

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 10934 | 41302 | A | 10996 | 219 | 688 | RRMHAYVSLDPLERPPFFFFFLF FFFFFFFLRRSFALVAQAGVHW RDLGSPQPPPPRFK*FSCLSLPSS WNYRHAPPRPANFVFLVETGL QLPTSGDLPASASQSVGITGVS HCAWPGNWLLKETRCGSSVGR QITGPITPDWVDPGIPDRYLQ |
| 10935 | 41303 | A | 10997 | 3 | 298 | FFFFFLRQSFALVAQAGVQWRD LCSPQPPPPRFK*FSCLSLPSSW NYRHGPPHPANF*FLVEMEFH HVGQACLKLLPSGDPPALASQS AGITGVSHRA |
| 10936 | 41304 | A | 10998 | 2 | 438 | APSVRSGNERDLARDEEAQETQ VRGCHASGGICTPAATAGASPP AWAGRRGTGQRLRSQPRQTGR QPPRVQPLAPPPGAPAPLPNPQ NCRKTRSHPRFWAGTLAPGPC PGLWCLPGLVQVDVLAAGRCD HLSCLPPLCPQAFLL |
| 10937 | 41305 | A | 10999 | 2856 | 3044 | GAATGEGGCCRLPGHPALAST A*AIPCRGPRVQETSPPPVLGW DPGSRAMSRALVFAWVGAG |
| 10938 | 41306 | A | 11000 | 1 | 908 | GLGDPGVVPLRSGGLGPPADLK GDQAVAE*LHEASGVTEHHPS AQPGPGGEAAEPAHLIV*EPEG GSPGHPGGGPGHPG*SEGPAGG KPGPAGGSAQGCRRSSEPSGT *SGRSPR*GPHGHPDCRTHPAR EGAQVHSRSLPGGAPVRRGCS QGPEQRLQQEDFLRVQQLSAA GPLRPQLYPQVWLCPEHQLE QYPRSYFSEIDVFKPCGVQQG CPVLDRASSKISPEDAAGSVVR LRSLWAASGLQQGASGLATFL QLLTCGVLWPDEELVHLLLDE VVASAALRCDPVPMEPTCG |

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| 10939 | 41307 | A | 11001 | 218 | 990 | VLQLLKAMRLELFLPPGGFMV LLASGVKLQTFATQVPSWLHP VDPSPGLEVELPASPVQCAHTP QPLGGRWDWVPWSRGQRSSG RLGPHGSPWRRWEAQAWQPA GPKPCPVGS*GPVRNRGQRRW AGTAGDPVHPPQPLAQVLSPSL PGADRAGQLLRVQGPPSPCPPG TPAGPQGRCAAPVPTGVSPSTP PCKLREQAPALASPERGSHSAA VG*RAPQVLPKW*PELMFRWV RSFFLLVGSWLTSGVKLHPFVV SVTALKGDASGVIPSSRWVHGL AGLRCEAADLRDSGAQLASPS GSLTRTGGAACQSRAVCPHSS AFGWSMGLGAMEQGAALIGEA RASREPMEEVGGSGMAACRSQ ALPRGQLRPSEKSRAAPVGVH CWGPSTPSAATGPGAKPLIARG RQGRPAAQSAGPAKPMPTRNSS WPARAVRSPGSHWRLSLHTSL QAERAGSGLGQPRKGLPQCSSG LKGSSSAKVVAQAEAAQRAS EGCEDYLARCHLSIRKMRRRN |
| 10940 | 41308 | A | 11002 | 3 | 644 | EPPGPTGPPSPQSPWHPGLPGR WSSTHVVFTHLHLAGPGWSCD HRWMGKQLPVSLASGVQGV RFRSQDMYQSSRNKFPSCAAH VPQEWAVPWKNQGNTHQSSRP SESGCCAQAEASNQCHQRQEA AGPSRLSLPDGRRLETPRHPN GPWYWNNSPQRLN*WRRGDPS WPEPQKPHGTGGARVPACQRR EICLSPFRGPRRRQKENIYEYL |
| 10941 | 41309 | A | 11003 | 202 | 438 | FHGHAPAGEMRGWPRVTKRSP AQSGKT\HFPPGSPGPPDTSTESI FRAWKAPGFPGRGRTADPET ARCGAWDEIVEPV |
| 10942 | 41310 | A | 11004 | 520 | 1094 | GPLSQCPPLPRLPPLGVYSKGR APHADTHSPGHRRTAHAHAQPA AAAATATR*QRRRRLPPRTPF RRPAARPDRRVP AHSSAVLPRP GKPGAFQALRKMDSDVDSGGP GEPGGKLG FARLRRAPPDRLPG CPSSHSFQTQSLSFMAHNVDEP LESATSLLGLLRRSWFCFTWQK QTVYWSTGRIRHSGEK |
| 10943 | 41311 | A | 11005 | 1 | 138 | SISLMNIDVKILNKILANQIQQH RKLIHHD*VGFIPCLRILVIYI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 10944 | 41312 | A | 11006 | 65 | 297 | NQRLPQPFLPTTPPPATRAT*D EEKSPYPGPGSDKKCPTLQLPSP PTPSAGGFPLGESGSPGGLVK AQIMEGISM |
| 10945 | 41313 | B | 11007 | 322 | 6900 | |
| 10946 | 41314 | A | 11008 | 3 | 215 | |
| 10947 | 41315 | A | 11009 | 1 | 234 | |
| 10948 | 41316 | A | 11010 | 149 | 300 | |
| 10949 | 41317 | B | 11011 | 28 | 162 | |
| 10950 | 41318 | A | 11012 | 700 | 861 | RRKCIPGRRNSKHKGPDGAGRP *VCREQQEQCAWTGYPGAQG PDPYCGKGPPYS |
| 10951 | 41319 | A | 11013 | 291 | 744 | LKRTKCDQLLKTSLDLGRGPI LKWLCTSKWGHQQIIIRA*GTE YKTTSFFFFFETASRLCHPGWE CSGAISAHS*FLLPGSCHSPASA S*VAVTTDTREHAQLIFF*HFSR DGFHVVARWLDLLTCDLPLSL QVLGYRNYIIIVRQLPSR |
| 10952 | 41320 | A | 11014 | 139 | 414 | SFKTAPPGFFFSF*LHLILMLKFT PGAIKLVFL/QFLLGISFFFLGKP PSSWFRNESCSVFRKESSQSWQ GRAHVWG*SDPWSSGRSRAH L |
| 10953 | 41321 | A | 11015 | 5 | 565 | VHTTEATCTTTGAKPCPWPSKL ATRQDHSVLSNSTNPRGPTPHKS GSPETAGALSSGDAGSRGEGPR TVSSERSSPGKGGSTLLGTTA*G PGPAHFASAVLGPSSKSLQAAS *EVDSFPSSLLKTAVSVLASTVR LSVSFMPPFITVSVTSSVISASSS PSELASMATLPGASG*AARAVN FELDEE |
| 10954 | 41322 | A | 11016 | 188 | 515 | SQTVSIVGELPIPRKRCEIGIWD AQKR/CPRLTGPWATISVPTISK KATGN/PQHNPNNPRARYQINAE *WKVHF*TNDRPSHECPCTLV VHRTLQDLRHKSSTSGGKTHG |
| 10955 | 41323 | A | 11017 | 80 | 397 | SVQRSVDHL*DHP*TSVDWELY LDGSSFANPCKVTLKTTTSPAS VTPEADWSMHSQSMRNSLRDS FSLKFGLIIHDFLTPTFNPLENP CGFLTRFCCVPNQISS |
| 10956 | 41324 | A | 11018 | 104 | 392 | PSQFHLKLLHMLLALLYPVGTC QVKDSSLLQKSTSVPPDSPQTG H\$KLGPFNPGRFR*RPQCQPGV LPPDVELSCHSWSNVLWTTAA KTPIFCSY |

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| 10957 | 41325 | A | 11019 | 125 | 1404 | NLALGMAMWNRPCQRLPQQP LVAEPTAEGEPHLPTGRELTEA NRFAYAALCGISLSQLFPEPEHS SFCTEFMAGLVKWLELSEA VLP TMTAFASGLGGEGTDVSVQTL LKDPILKDDPTVITQDLLSFSLK DGHYDARARVLVCHMTSLLQV PLEELDVL EEMFLES LKEIKEEE SEMAEASRKKKENRRKWKRYL LIGLATVGGGT VIGVTGGLAAP LVAAGAATIIGSAGAAALGSAA GIAIMTSLFGAAGAGLTGYKM KKRVGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYRTFSAPWA ALAH SREQYCLAW EAKYLMEL GNALETILSGLANMVAQEALK YTVLSGIVAALTWPASLLSVAN VIDNPWGVCLHRSAEVGKHLA HILLSRQQGRRPVTLIGFSLGAR VIYFCLQEMAQEK |
| 10958 | 41326 | A | 11020 | 3 | 1693 | CQRLPQQPLVAEPTAEGEPHLPT GRELTEANRFAYAALCGISLS QLFPEPEHR*VLLSCPLGTPVGL HSDAHYGQRLAVAVHVEGTLP FTSSTFAAASVFQKARPWQHPG EQMAFSGKPFLVAAVTSAGGS GAPSVGCTELISTSVLGYHTAL EMAGLVQWLELSEA VLPTMTA FASGLGGEGADV FVQILLKDPI LKDDPTVITQVHPTPGVKDGKL IF*ARVLVCHMTSLLQVPLEEL DVLEEMFLES LKEIKEEESE*ES PATKTEGGGEDKDRKHPLMGD KMTESKTDLWIYEMGNAGVLL FRRYLWLQPKKKENRRKWKR YLLIGLATVGGGT VIGESS*RCA PLVAAGAATIIGSAGAAALGSA AGIAIMTSLFGAAGAGLTGKVQ KE*VGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYREDQEDQA ALAH SREQYCLAW EAKYLMEL GNALETILSGLANMVAQEALK YTVLSGKCPHLPWPASLLSVAN VIDNPWGVCLHRSAEVGKHLA HILLSRQQVPGNGCVIGFSLGA RVIYFCLQEMAQEKGEHGLL |
| 10959 | 41327 | A | 11021 | 208 | 324 | VSLKAADNWL VNSYPFCNSV SSEFFFR*IRDFFLFWIH |
| 10960 | 41328 | A | 11022 | 1265 | 1459 | |
| 10961 | 41329 | C | 11023 | 188 | 730 | |

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| 10962 | 41330 | A | 11024 | 64 | 228 | QHLLRRWGRSGLLLNDR*VSN EIKMEINKFIELNNSDTIYQTL WDTANTVLKFM |
| 10963 | 41331 | A | 11025 | 1 | 648 | |
| 10964 | 41332 | A | 11026 | 26 | 613 | VGAGGRGWRFAAAVRRRAAGG GLRPGPAPGPRAGGGGPRGAH LALLRRAGALRAGKEYGKADA RWVYFDPTIVSVEILAVLDVS LALFLIYAIVKEKYRHFQITL CVCELYGCWMTFLPEWAHPEA PNLQQPATGWLYWLGFTLFFF* RCVGFILIPRNWLLWAVHGPRTS RKWHQKGNQFQWKEVFSGTF |
| 10965 | 41333 | A | 11027 | 2 | 252 | ARGRAGVAGGPR*AAELPGLP RDPFPASRPLRRSDCLGGLIRHK PPDPGAGARVEGEALPSWSPGG ALEEGVT*PGTRGPPWE |
| 10966 | 41334 | A | 11028 | 3 | 637 | RDQVRRGQGGEPRARIQCPRRRL GEGPGAPNRLGPPARDPRCSPW PRADSPRDPNRLSSPQLPRPAYL GPACFP*PSWGVSRSLPSLAPW RPHRLPDSQRFPNGGSRSRATS GSWTWKSKECREWRPSGSRGT RGSSSGSAGSSGSSAGVGRRAG HGRWHLR*GPLFPAAPASATCP LWHGWKGASLDLGLQPWATF YPRVTGARGGRTLGP |
| 10967 | 41335 | A | 11029 | 158 | 462 | |
| 10968 | 41336 | A | 11030 | 339 | 866 | QICHSPPGNKAHSHLLPYQTPV PSSQYPPSPSRTLQLPFPTWNP CQWPSRGSCGPSAVGTGPPFPT GIPSP*APSARG*HHSSACGCH PGCAGPQPARSHPGAPASGCH TVSGCCHALLQSCLAPGRPSPA GTWPHPPPGLPSAPGTEPCTA FEGFQPPCWLSQHPLSPCL |
| 10969 | 41337 | A | 11031 | 621 | 944 | TPQGGTAPSGGRHPWASASPHR LPPL*CSARPGCH/SSRMRSPGT RPSGPLAQDCHPPRPQTPHAGS HHTSAPQAPAGTF**RQRVAPG SSCWHLPSQSWSCSAWLGGC |
| 10970 | 41338 | A | 11032 | 3 | 257 | AGRASKGG*NPSKAVQGSVPG AEGSPPEGCGQGAGLGLPGA RQDCSRA*QHPPGPGGGQEVY LDISLAPGSTGIQGLEAKHL |
| 10971 | 41339 | A | 11033 | 94 | 227 | SSYVFKSILTAFGMTWMRLETII LSEVTQG*KTKHQMFSLICGS |

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| 10972 | 41340 | A | 11034 | 404 | 894 | FVYFFRGELCKISSTLGFKGTGQ GLQPSKVS**VPSRPAGNGRPA YPETSQPPPGPSGG*HWWLAGW Q*GGPEPGWTCIWP*GS*GTEIG SPSQPGPEPAGVPSPRDAGSAA TGCHTGLAGVWPPRLCHRRV TDGRKSMKRCLSRSYCTSSVRA SGGGAGRIT |
| 10973 | 41341 | A | 11035 | 1 | 408 | |
| 10974 | 41342 | A | 11036 | 68 | 204 | SFLWHPLGLHFHHTHH***NYKS SSK*MVRIRVTFSKFIVRNNYC |
| 10975 | 41343 | A | 11037 | 5 | 188 | PQCRLLHLRQGLALSPKLECSSAI TAHCSLELPGSSNPPSASRF*GS RSVAQAGVQQCYHSSLQPRTP GVKQSSLSFPFLRLQPKVSSATL PVRLQE |
| 10976 | 41344 | A | 11038 | 1 | 263 | |
| 10977 | 41345 | A | 11039 | 2 | 283 | |
| 10978 | 41346 | A | 11040 | 1 | 1965 | MAAENEASQESALGAYSPVDY MSITSFPRLPEDEPAPAAPLRGR KDEDAFLGDPDTGEAR*PRPCP ALGSPRSSFFCVKHPGSPLRETR KDPFSAAAAECSCRQDGLTVIV TACLTATGVTVALVMQIYFG DPQVRGTNGEGEETGEWVG* CLRNCGKGSSVDAAVAAALCL GIVAPHSSGLGG*GAVEVGVQP AYFLPPGL*ASCAARALREETL QRSWETKVGTLVRRESSGESLF IALLLTQALIC*VLAQDGFNVT HDLGQWGLGIWERHEVDGEG* NL*DLEPPPLPGSLLHRPDLAEV LDVLGTSGPAAFYAGGNLTLE MVAEVSARVVRVGACPKVPIA GHPRPHFFGVYRGDLSPGSQGP PSGEASQSMATSFWPFNLTSLV SREQALHWVAEVRLTRLPFPGF KDIRSGEIGYCHRADDMLRWV LGRTWGLQRQRWVWGKGQEK SSYELDGAPTAQVLIMGPDDF IVAMVRYASSDSEPGTRDPLNQ EGVGAG*RFSPWNRTANHSAPS LVGFASLLSWGP*GL*VGGAM AWLPLCGTYLALGANGAARGL SGLTQVRFTPWLAFSREPSCG LDCRCLS*QSNLLQVDSECRAE TSWGGHRDR*RKDSSQGCPWV HGSRRTNFNIIAVKDPRSPDAA |

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| 10979 | 41347 | A | 11041 | 1 | 363 | SSMTTVHATTATQKTVGETLA* LLQNIIPVSTSVAEAMGKVIPEP DKRLTGMAFCVPPTHNMLVVAL ICHLQKAAKYDGMRRRCFNATT GITFNGHFVRLLSWDEFGSSNR VVDLMVHTASKE |
| 10980 | 41348 | A | 11042 | 162 | 303 | CLLLKSCSQEAAAALALPALGL VFDVFL*1YFVRTKYLRVGFRN FF |
| 10981 | 41349 | C | 11043 | 56 | 118 | |
| 10982 | 41350 | C | 11044 | 345 | 410 | |
| 10983 | 41351 | C | 11045 | 7 | 439 | |
| 10984 | 41352 | A | 11046 | 2 | 80 | |
| 10985 | 41353 | B | 11047 | 205 | 5326 | |
| 10986 | 41354 | A | 11048 | 1 | 813 | |
| 10987 | 41355 | A | 11049 | 1 | 1454 | |
| 10988 | 41356 | A | 11050 | 2 | 1624 | |
| 10989 | 41357 | A | 11051 | 1 | 1185 | |
| 10990 | 41358 | A | 11052 | 1 | 2149 | MKEKMLRAAREKGRVTHK GK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTTRPVLK ELLKEALNMERNNWWYQPLQKH AKNMPNSIILIPKPGRDTTKKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIQMGQGW NIHKSINVIQHINRTIDKNHMIIS IDAEKAFDKIQQLFMLKTLNKL GIDGTYLKIRIKYLGILQLTREV DLFKENYKPLLNEIKEDTNKW KNIPCSWVGRINIMKMAILPKVI YRFNAISNKLPMFTFFTELEKTT NFIWNQKRARIAKSILSQKNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWGKDSL NKWCWENWLAVCRKLKLDPF LTPYTKJNSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPLAIREMQIKT TMRYHLTPVRMAIHKSGNNR QTESQIMSELPITIAASKRIKYL GLQTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWGRINIVKMI AILPKPTNVHVTNLAAQDTTAL EAAQISLEGHPQEKEISVTAMPL |
| 10991 | 41359 | A | 11053 | 1 | 2031 | |

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| 10992 | 41360 | A | 11054 | 1 | 1188 | |
| 10993 | 41361 | C | 11055 | 1 | 353 | |
| 10994 | 41362 | B | 11056 | 151 | 1608 | |
| 10995 | 41363 | A | 11057 | 1 | 373 | |
| 10996 | 41364 | B | 11058 | 1 | 488 | |
| 10997 | 41365 | A | 11059 | 1 | 1257 | |
| 10998 | 41366 | A | 11060 | 2 | 3527 | |
| 10999 | 41367 | A | 11061 | 1 | 2373 | |
| 11000 | 41368 | A | 11062 | 1 | 1755 | |
| 11001 | 41369 | A | 11063 | 1 | 1599 | |
| 11002 | 41370 | B | 11064 | 220 | 1286 | |
| 11003 | 41371 | A | 11065 | 1 | 1826 | |
| 11004 | 41372 | A | 11066 | 1 | 1645 | MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSQYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINILKMAILPKNW KKTTLKFIWNHHRACIAKSILS QRNKAGGITLPDFELYKATVT KTAWYWYQNRDIDQWNRTEP SEITPHIYNHMIFDKPDKNKKW GNDSLFDKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEESLGNTIQDIGIGK DFMSKTSKAMTTKAKIDKWDL IKLKSFCTAKETTIRVNRQPT WENIFAIYSSDKGLISRIYKELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKHKMKCSSLAI REMQIKTTMRYHLTPVRMAIK KSGNNRTRENYFKIHMESKKSQ NSQGNRKEKEQSWRHATRLQ TIVQGYTVAKTACYWYKNRPT DQSNRTENQEIRLHTYNHLIFD KPKDSNGETTPYSINGARJTG |
| 11005 | 41373 | A | 11067 | 1961 | 2588 | KLAQDRDALSPPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPIVSAQNLLK LISNFSKVSQYKINVQKSQAFL YTNNRQTESQTMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIK\EDTNKWKWNIPCSWV GRINIVKMAILPKVMYRFNAIP IKLPMTVFTELEKNYFKVHMGT KKEPASPSQS |
| 11006 | 41374 | A | 11068 | 2 | 278 | |
| 11007 | 41375 | A | 11069 | 3 | 274 | |

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| 11008 | 41376 | A | 11070 | 261 | 1382 | LELSFPPAGQRGVLSGDPQNLC TCPSGSWHVPRCWAVERQRPN LPRTVTQLVAEDGSRVYVVG AHFSDDSKRDVVKVSAATHIP DTGWCKLLPGSRDGLVRFTY RVSMMLKMDSTLLREAQELSLE KLQQA VRQVRSGQGSGSGSG SKPPHITEQLGMAPGGEFREA KEVGTG*GRGWPQCGSQAVT FKRAIAALSFQKVR LAWGLC FLSDPIR*GCPRPGRPAGWSV GMAEMIGEPDLHRTIVSERDV YLT YMLRQAARRLELPRASDG DGRPQAWDPL*G*GPRGHVPGI EKNWSTD LNIQEIMT*VPAPPC KPHPTSPQVAFFGLLGYSLYW MGRRTASLVLSLPAAQYCLQR |
| 11009 | 41377 | A | 11071 | 3 | 506 | KDCQF*VGPEQKALYKVHAPI QAALQLGPYE*ADQKRTCVR GRHTCETAFTFWKSLGLDKV TKPRSSSSQLLALAIRSSPGSTT DACLLDSFSGKSRISSWFGS |
| 11010 | 41378 | A | 11072 | 2 | 374 | IRRESTHLQQALGTTTPQDRLTC TGHS AQPPACASPLPPGPP*SS AWPLPPSTRLARQKQAAATAQ P*PLTTQTLGPWSSASTWTS AHKQPGAAAEWTSTAGSRQLLA GASGSSPSSCSVWTN |
| 11011 | 41379 | A | 11073 | 3 | 553 | |
| 11012 | 41380 | A | 11074 | 239 | 547 | GHHFQMNVCRCVWMLSLEP HPVGQIHSC**ERAKLCGKEFN RMHNL MGHMHLHSDSKPFKCL YCPSKFTLKGNLTRHMKVKHG VMERGLHSQVSRPSLEA |
| 11013 | 41381 | A | 11075 | 1 | 267 | MAISMVTTTRSTTIRTTAAGCHY ENDMAHNHSDRGGLPLKVVL TTPFLTTPPGKGGGAAGALERRTE EGDRDAGGAAQEGGLTPTSVP PSS*HTLWLRTVDPEASTSPSTP RHPYPNRGGGGRALEPHPRR*V *AGCHYENDMAHNHSDRGGLP LKVVLTTPFLTTPPGKGGGAAGA LERRTEEGDRDAGGAAQEGGL TPTSVPSS |
| 11014 | 41382 | A | 11076 | 1 | 1707 | |
| 11015 | 41383 | A | 11077 | 1 | 1407 | |

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| 11016 | 41384 | A | 11078 | 1 | 1275 | MVKGSIQQEELTILKIYAPNTG APRFIKQVLSDLQRDLDSHTIM TGFNTPLSTSDRSTRQKVND IQELNSALHQADLIDIYRTLHPK STEYTFFSAPHRTYSIIDLIGGSK ALLSKCKRIEITTNCLSDHSAIK LELRIKKLTQNRSTTWQLNNLL LNDYWVHNEMKAEIKMFFETN ENKDTTYQNLWDTFKA VCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTHSKASRRQEITKIR AELKEIETQKTIKISESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDQGDITTLERVVLEEPD TLHLLNYTPRKVL YRWNQSS TSVIETNKTSVELSLPFD EDYIIE IKPFSDGGDGSSEQIRIPKIS/NK KTK*PNPWRQK*G**LAVADA YARGSGASTSNACTLSAISTI |
| 11017 | 41385 | A | 11079 | 1 | 426 | MLHTKQHLMSGTEDMDDKLH FSDCSAASLVSLSTTTGGHVL NMSADIARYLPVLYRWNQSS TSVIETNKTSVELSLPFD EDYIIE IKPFSDGGDGSSEQIRIPKISNA *ARGSGASTPNACALSAISRIMI SLTARSSL |
| 11018 | 41386 | A | 11080 | 3 | 620 | DRTLAEAPHTAPARSGHRGWC PRPHRRRRNRGRQLLAPGRGA DPGAGEAATVQWRLLRGQPAA ALHVQQGAGDAANAGLQRGA HADSHDRAVPAGHAPGPVAAA GRGHDGQVPAALG*AGGPVGL RRPEPPLQTRGKRLAPATQQV GQARRLPTGRGQLLLRRPQPAA HHGPRPRLGGRGRGGSHKSPPH GIWPRLAGWRATLE |
| 11019 | 41387 | A | 11081 | 335 | 640 | PLGVLWSLWKSLVHSDAGAGE L*EVITGSTWPNP*QCCLVPNV DDEEEGEEQDDDDDEEEGL*D IDEEGDEDEGEEEEDDDDVEEG EEDEGEDDWKFAKE |
| 11020 | 41388 | A | 11082 | 2 | 204 | |

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| 11021 | 41389 | A | 11083 | 3 | 1471 | SKDTRKRDVDSKSPGMPLFEAE GVLSRTQIFPTTIKVIDPEFLEEP PALAFLYKDLYEAVGEKKKE EETASEGDSVNSEASFPSRNSDT DDGTGIYFEKYILKDDILHDTSL TQKDQGGGLEEKRVGKDDSYQ PIAAEGEIWKGFGTICREKSLEE PKGVIYGEGRISRPCGDRW*RS AESSHHRGRQSGYPENKLCGF LLKTPHHVLERADEAGSHGNE VGNASPEVNLNVPVQVSFPEEE FASGATHVQETSLEPKILVPPE PSEERLRNSPVQDEYEFTESLH NEVVPQDILSEELSSESTPEDVL SQKESFEHISENEFAAEQST PAEQKELGSEKKEEDQLSSEVV TEKAQKELKKSQIDTYCYTCKC PISATDKVFGTHKDHEVSTLDT AISAVKTVIRSDSKTKSGEGAY GREMKSPHKFPEGKIHNDKEH DRIVQEFLAETGPKVTRFNEQC RFRPRIYVYENNQTQIMVEEPQ |
| 11022 | 41390 | B | 11084 | 148 | 235 | |
| 11023 | 41391 | A | 11085 | 30 | 420 | VSGTRGPSPCLGTSWASGAWR PPLGGLPPSAGANGPGRVRSAA GCSLVAGCKVLGSWVSGFAGR SHVACAGSSGESVRARCPGTA* AAGGPGPQAFQAAY*QGSRMH RAPPRPNRQVQTWEEGAGTG |
| 11024 | 41392 | A | 11086 | 2 | 73 | ERLRMPGVAKGRPR*GNPRRG RG |
| 11025 | 41393 | B | 11087 | 1 | 1412 | |
| 11026 | 41394 | A | 11088 | 39 | 427 | PPYWGHFHSSAAASAALKGKD GGSSRSLVPPAQ*HSHSPSKTHC VHTPSRSCAQGLTHTLTQSPPSL KIAQSPSFDARAHARLRIWQIPS APRVPLSASLSPTRTAGSVRFE SQSTKTSRSHRFLPRT |
| 11027 | 41395 | B | 11089 | 1 | 813 | |
| 11028 | 41396 | A | 11090 | 3 | 365 | RTPSSKGCGRPPRGMGAQGSA GCGRRRSRRSRQARRWSHPC* PPSSPPWPRPARSPPGCSHRAAL SSPSPSSFLARHSARPLALAL GPPPWCSSGCASSAPFDLQHPE QSQNQDARG |
| 11029 | 41397 | C | 11091 | 295 | 412 | |
| 11030 | 41398 | A | 11092 | 21 | 164 | GAVTENDFYDLVRTIGGDLVE KVDLIDKFVHPK*VKSFLILPLTI SV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11031 | 41399 | A | 11093 | 1 | 1373 | GISTMVGSALRRGAHAYVYLV SKASHISRGHQHQA WGS RPPAA ECATQRAPGSVVELLGKSY PQD DHSNLTRKVLTRVGRNLHNQQ HHPLWLIKERVKEHFYKQYVG RFGTPLFSVYDNLSPVTTWQN FDSLLIPADHPSRKKGDNY YLN RTHMLRAHTSAHQWDL LHAG LDAFLVVG DVYRRDQIDSQHY PIFHQLEAVRLF SKHELFAGIKD GESLQLFEQSSRSAHKQETH TM EAVKLVEFDL KQTLTRLMAHL FGDELEIRWVDCYFPFTHPSFE MEINFHGE\WLEVLGCGVMEQ QLVNSAGA QDRIGWAFGLGLE RLAMILYDIPDIRLFWCED\ERF LKQFCVSNINQKV KFP LSKYP AVINDISFWLPSENYAE\NDF*Y LVRTIGSDLVERVDLIDKFVLPK THKTSHSYRIMYR\HMEPTLSQ\ REVRHI/HIQALQEAAVQL LGV |
| 11032 | 41400 | A | 11094 | 8 | 119 | |
| 11033 | 41401 | A | 11095 | 2 | 475 | QAGPSGGIPEGIAITGDDSSMHA IAPEDLPVGQDVEAEDSDTGDL DPVLT VFRRGVEREFFSNWYKT AWSFSKLAQKGLLSS*PSSLSSS SSSSDKAVTAGTELFASSLSSSS DPRRSISSSSLLFVAPLPVVSSTL AGPYLPTAFFTPGR LAFSFS |
| 11034 | 41402 | B | 11096 | 677 | 696 | |
| 11035 | 41403 | A | 11097 | 1 | 357 | STMIEAHVDVRTTDGYFLLFC VGFTKKHNNLIPKTSYA*HQQY ICLPHQDDRVTHQNPSLPDGSIA RVLSIYYLYISRREMNSIISQGL QKVHIHIVIPGSLMNQELDDL I TVFFKA |
| 11036 | 41404 | B | 11098 | 1 | 541 | |
| 11037 | 41405 | A | 11099 | 14 | 671 | PAPWRLGKNKRLTKGGKKG A\ KKKGVNPF SKKEWY\DV KAPA MFNIRNIGKTLVTRTQGT KIAS DGLK/GVRVFEVSLADLQ NDEV AFRK\FKLITEDVQGKNCLTN\F HGMDLY/TRDKMCSMVKK\WQ TMIEAHVDVKTTDGYLLRLFC VGFTKKRNQIRKTSYA\QHQQ \VRQIREGRWMEIMDPRRWQD QMDLEE VGHELIAGSIWKRHR KGLPIYLSSP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11038 | 41406 | A | 11100 | 1 | 217 | RQGLTLSFRLECPGVISAHC SLN LPGSSKPPASAPQVAGTTGVYH HAS*FFIFFVEMGFHHVAQPGL CNFVF |
| 11039 | 41407 | A | 11101 | 2 | 442 | LDVQIQEAQRTPGKFIKRYSP RHFVIRLSKLKTKERILRAVRQ KHQVITYKGKPIRLAADFSTETL QARRDRGPISLLKQNNYQPRI LYPEKLSIIYEGKIQSFSQKQML REFAIRKPPLQELLKGS LNLETN PGNT*KQNFFKA |
| 11040 | 41408 | A | 11102 | 2 | 545 | EPRPGEKTAHVYGPDC LCGSCV QLSFSGAFFSTRWVS YE QANCK GEQVFVEKGEYAHWDWWTSS QRT/DLSSLRPIKVDSQE HKIILY ENPNFTGKKMEIIDD D \VPSFHA \HGYQEKVSSVWLRSGTWVGY *YPGYRGLQYLLEKGDYKDSS DFGARHPQVQSVRCIHD MQGH QCGAFHPSK |
| 11041 | 41409 | A | 11103 | 2 | 389 | EIIDD DVPSFHAHGYQEKVSSV WVRSGM*VHCQPWLTLPQELR LWGPRSGETLALTSAPVSKTCD FGARHPQVQSVRCIHD MQGHQ CGAFHPLGTQEEEEAGQKEQM EQVPFWLARGDICELSGK KSV |
| 11042 | 41410 | A | 11104 | 1 | 446 | MEEEELEFVEELEAVLQLTPEV QLAIEQVFPSQDPLDRADFN AV EYINTLFPTEQLPMPSAHGGVSS CGNAGGPVSFATRENARCGIW GSGGVCDGVFGA/GAAGWGGV *GGGALGWMLSGRRIVLRS AIF TSPVSRAGSPERGWS CDC |
| 11043 | 41411 | A | 11105 | 1 | 210 | SSDGRHLAFDQGS PG*VLGHVG KQRAVDVQPSVAVRVRQPLLL LSTIMGSGLLGWEQGIDILNSIEI CSI |
| 11044 | 41412 | A | 11106 | 2 | 287 | AAESPGRSTRTDGAGLTRSLPR GSR CAGAWVAAGGLSWARGG GRQEAGWRNDG*GGTGARGG AGSRAAAHARGAAGHRASVSK PGPSRSSRFQCC |
| 11045 | 41413 | A | 11107 | 150 | 389 | GEEIAWLGAARPGKPTPSRIPL* PSLFPWRPHKFPERSVFAGSQP ASQSPPLRPPPPSHPEGSC LGS R LPPPGYLLPLR |
| 11046 | 41414 | C | 11108 | 43 | 213 | |
| 11047 | 41415 | A | 11109 | 3 | 246 | SSFPAPAREGALAPCRCLAGISV TLQGNP*GRCHHHHHHHHHHHH HRCYDSQESGKLPRPGPKAELE GPPAWLLVGPGAHP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11048 | 41416 | A | 11113 | 1 | 726 | |
| 11049 | 41417 | A | 11114 | 2 | 251 | LSCGRSLHQGSVTSCKTINALT LTVDTWRGCAW*GCACTFHCR SATNMIRAYVVFSTISVLSLQEI RLSLRAILADLRLSICF |
| 11050 | 41418 | A | 11115 | 1 | 1041 | |
| 11051 | 41419 | A | 11116 | 1 | 398 | MGPNSTLENLLKGATSVFYNR DQEEAQKKERKLRGRTKALAA ALQ/SWQSPGAPRCIH*LLSVW QARVF*RGMPRQQDEATSTLSI QWQKPVETELSPDMEVTGFRA SLTDERVHLPEVLPQEYTEQRR QGHL |
| 11052 | 41420 | A | 11117 | 5 | 137 | |
| 11053 | 41421 | A | 11118 | 5 | 272 | |
| 11054 | 41422 | A | 11119 | 2 | 211 | WNQPRCPSTVNWIMKIWYIYT MEHYAAIKRNMIMSFAATWME LEAIFLSKMPQ*QKNKYCVFLH ACLES |
| 11055 | 41423 | B | 11120 | 1 | 1560 | |
| 11056 | 41424 | A | 11121 | 1 | 588 | |
| 11057 | 41425 | A | 11122 | 80 | 574 | EPAAQGNVLVDLLC*MKNRNR WLPNELSQVLHVTSQSFSKTG MSAKHTAFAMRMSPAQMTDIV VGLSTGQSPFMVLMQGGGHS AQETRIASLPVTAIPAGMKIPCV TAGSACMVGPSVRVNEWFSAY GMAGMAYSRVSTFVRGLSPRY LTTREAPGCGSSAGH |
| 11058 | 41426 | A | 11123 | 48 | 131 | |
| 11059 | 41427 | A | 11124 | 1 | 1195 | |
| 11060 | 41428 | A | 11125 | 2 | 1028 | |
| 11061 | 41429 | A | 11126 | 1 | 1008 | NMMEQVLDIPSL*VISKDNANV TIDAVCFIQVIDAPRAAYEVSNL ELAIINLTMTNIRTVLGSMELE MLSQRDSINSRLLRIVDEATNPL ALKIAARMIEDGELDKRIAQRY SGWNSQLGQILKGQMSLADL AKYAQEHHLSPVHHQVAEWM RARNGQLFRLRSNHLTLLVEQN NFYARGAKIYPDIHIDRSLKKCP SDLFAANARCGICQSDERCLR YQPRRERGLYRIDITYPGKSYTT TALPSRFVWFVTGKAQSTQAS ALSYIDSLLYHHLDLYGQRLGH LDDGTDSDWNHVPTLNGQCTLV LIHEYVDTRGPEIKTILVISWWN ILVFH |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11062 | 41430 | A | 11127 | 3 | 333 | DIGIGEENRKRWLRTGKCSFLP KEREWMDRLMSWGLVDTRH ANPQTADRFSWFDYRSKGFDD NRGLRIDLLLASQPLAECCV*T GIDYEIRSMEKPSDHAPVWATF RR |
| 11063 | 41431 | A | 11128 | 2 | 136 | YCKLACLQVDSRGSQVFALDV AARHR*QFAMPESDAVAMLKH LS |
| 11064 | 41432 | A | 11129 | 3 | 431 | GVFGRVSEKQRPAAPAAGERPL PRPRPLPCGAAARTGPFAAQAA *RAAAAPRSERRRHGAEEGH QRCIYRHAADRALGEAARTG YALRPAGEPELAAAARRR*RAP DPGPRVPRHLGLLATRACPPGG AHCSPERGAISW |
| 11065 | 41433 | A | 11130 | 64 | 2436 | RRQGLEGWWAIGLEGLTGKAL AWLFTVPGVRGLQWSPRFFLTR LRTLCKVLGVLFVSVAGGKKG PTCILQILKGQRRQEA*CISGWA ERVWASGQA*WEVWLHWAKS RNWFLFWKQHVHALRVRLDTT LFSLEEGSSFWNQGLTWKVVR RTFSESINHTPRITLGVPSVHSF QLPGLLNFGFKVCFVLSPRIFN LTHENFLSSEGPEIGLLGATFN CLNKRLAKYMRNVHPKPKLV RYLHSRLPPEPAAAP*AWCGPR HLSCRQMSSSSQIGNDSFQLQV TPVHLLPLSHTTRKNPEMYDLP LLFFNPQESAILQLFHQDGECLH CSPIVGDWCHLGHSQACPSFSV PSGLFVPSLLCGAAFGRLVANV LKRYSVCVRVCAHVHVCARVR VYACVWVRMTISLTVILIESTN EITYGLPIMVTLMVSTLPPGPCQ AQGHVRPTGPIFRSLEWETEV EMDK*GHDFAHVLVSECISSEA *GMLLFCCGPDRSLFSTFRAVW SLSRLDVSIAAGKQ*A*RT*SV GYSLLCPDLKGDPSAVSILRTT VHHAFFVVTENRGNEKEFMKG NQLISNNIKFKVKKTA*EERQV RDKRSRLTRLSALELRNMCDE HIASEEPAEKEDLLQQMLERR* EPGGAPTARRATQRWGEPLAQ MFPLTFHGLILRSQVLTLVRG VCYSESQSVSLSEAEISQARPDE |
| 11066 | 41434 | A | 11133 | 3 | 80 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11067 | 41435 | A | 11134 | 2 | 958 | LKCELS\DQGLAPAIQTVRLTHE SLTALEIPNALLQTIQDLILDLR VRCVMATLQHTAEEIKRLAEK EDWIVDNEGLTSLPCQFEQCIV CSLQSLKGVLECKPGEASVFQQ PKTQEEVCQLSINITQVFIYCLE QLSTKPDADIDTTHLSGDVSSP DLFGSIHEDFSLTSEQRLIVLS NCCYLERHTFLNIAEHFEKHNF QGIE*ITQVSMASLKELDQRLFE NYIELKADPIVGSLEP*YIAGYF DCKDCLPPTGVRNYLKEALVNI IAVHAEVFTISKELVPRVLSKGI EAVSERAQSTDAVCFILQQKWS |
| 11068 | 41436 | A | 11135 | 52 | 1053 | MDEEERVYRACYILCISLLSSPG NPGLHSPMLDLNDTRPSVLG HLSLFLIQKYNHSILFFSPLAWR YKTPHRVAFVEKLTCLVLSQLP YF*IISNMFYFVFLIFKTAEKSNP INHI*TRLCLFLVF*KMIQEVMS SLVKLTRGALLPLSIRDGEAKQ YGGWEVALRSHSAHFCLDVFFV RRLTHESLTALEIPNDLLQTIQD LIFRPGSQL*PVSRIFFSAGTFRF KNHLHDFTGFHTCLTGAPRGPV GGCASDDGQAAADTSQWLS*I* VLYL*LFLASMFSLSDVFSL AP*R*FSKHLFCF*EQRLIVLSN CCYLERHTFLNISHGSP |
| 11069 | 41437 | A | 11136 | 50 | 426 | |
| 11070 | 41438 | A | 11137 | 2 | 949 | QQVWKQNCFKHYSNETDNSTT QLVGVQTLQVVVPSLILCEHCM NFSSPHVWCCMVQAVPGGQGO TIMQVPVSGTQGLQQVSNI*KY *AVYQRRGFKE*IITGQTQQIII QQPQTAVTAGQTQVIPLALSHR SKTDLEESDN*VRYQPVNADGT ILQQGKCTHKLP*DFLGQLFCPL DN*HTTSSGQGTVTVTLPVAGN VVNSGGMVMVRKCIFQLCL*N FLEHAT*CLLKEEPLYVNAKQY HRILKRRQARAKLEAEGKIPKE RRVCITLGRI*ERRIAGFYF*NY LFSPKEKDSPHMQVGRHIHFILL FITLY |
| 11071 | 41439 | B | 11138 | 26 | 80 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11072 | 41440 | A | 11139 | 203 | 797 | HRHIARHLFPRTTPTP*LSWQGS *TPRWKGVRAVVTQPRKERRA ESEQFQATKPRSRL*LOPPTPSL VSSCQLKTTAASRPLT*PSKSVY PSAPFHPWLPC/SKPERSVSPES NDSISEELNHFKPIVCSPCTPPK RLPDGRVLSPLIKSTP/PQPKQK PAEADFL*GQSTDPQKVGTDLS GAADQKDPFKSHSYLSGS |
| 11073 | 41441 | A | 11140 | 33 | 379 | EATSNFKQPPSLPFWCLKSRTSL KPRQSKVCSSSFVI*GKTGNEL ALQIP*FKSSCGPRFPD***PAGR /SAPSLGPPPSQSCAHQ*EHWVQ VCIKHGITNAEPPAEHLKVLVR E |
| 11074 | 41442 | A | 11141 | 248 | 622 | SESSGRFWLCGLGPGTSPLLSL KFPHLLPASRGRSPSPRPRVPR GKATQVVWAWGYRCVDEDPA RCLGTPGRTD/PHCGQGLLCPL GKSCSTSQPLSQGDGRGTSWDR SHACSPGGHPHRCIGCM |
| 11075 | 41443 | C | 11142 | 1 | 1311 | |
| 11076 | 41444 | A | 11143 | 452 | 1286 | |
| 11077 | 41445 | A | 11144 | 2 | 299 | GLPLAHGLLGRFGMDRIYEGQ VEMTGD*CDVESIDGQPGAFTC YLDVGLARTITGNKVFGALKG AVDKGCSVPHSTR*FPACDSAE FALGIPYFVQPN1 |
| 11078 | 41446 | B | 11145 | 49 | 832 | |
| 11079 | 41447 | A | 11146 | 1 | 1074 | |
| 11080 | 41448 | A | 11147 | 1 | 360 | |
| 11081 | 41449 | A | 11148 | 1 | 1155 | |
| 11082 | 41450 | A | 11149 | 75 | 266 | |
| 11083 | 41451 | A | 11150 | 2 | 222 | |
| 11084 | 41452 | A | 11151 | 1 | 549 | |
| 11085 | 41453 | C | 11152 | 453 | 665 | |
| 11086 | 41454 | A | 11153 | 1 | 1962 | |
| 11087 | 41455 | A | 11154 | 1 | 295 | ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN |
| 11088 | 41456 | A | 11155 | 1 | 363 | |
| 11089 | 41457 | B | 11156 | 1 | 375 | |
| 11090 | 41458 | A | 11157 | 1 | 197 | |
| 11091 | 41459 | C | 11158 | 1 | 270 | |
| 11092 | 41460 | C | 11159 | 1 | 146 | |
| 11093 | 41461 | C | 11160 | 1 | 268 | |
| 11094 | 41462 | C | 11161 | 1 | 301 | |
| 11095 | 41463 | A | 11162 | 1 | 289 | |
| 11096 | 41464 | B | 11163 | 19 | 240 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11097 | 41465 | A | 11164 | 2 | 253 | |
| 11098 | 41466 | B | 11165 | 1 | 978 | |
| 11099 | 41467 | B | 11166 | 1 | 316 | |
| 11100 | 41468 | A | 11167 | 191 | 319 | |
| 11101 | 41469 | A | 11168 | 608 | 763 | |
| 11102 | 41470 | A | 11169 | 274 | 437 | |
| 11103 | 41471 | A | 11170 | 1 | 417 | |
| 11104 | 41472 | C | 11171 | 1 | 792 | |
| 11105 | 41473 | A | 11172 | 3 | 449 | IYLTKEKLDLYKECKTLLKEIT DDTNKWKHIPSSWMGRINIVK MTTLPKAIYKFNAIPFRIPPSFFT ALEDTILKFIWNQKR/CPHSQCK IKQKEQIWRHHTT*FQAIL*GHS HQNS/IGTWMKLENIILSKLLQG QKTKHCMFSLIGGN |
| 11106 | 41474 | A | 11173 | 1 | 441 | |
| 11107 | 41475 | B | 11174 | 1 | 597 | |
| 11108 | 41476 | A | 11175 | 5 | 265 | |
| 11109 | 41477 | A | 11176 | 3 | 280 | SIYPNTCTRMFIVALLTIAKTWN QAICPTMIDWIKMWHIYSME YYAAIKNDEFMSFVGTWMKLE TIIFSKLSQGQK\TKHRMFSLIGG ELEQ |
| 11110 | 41478 | A | 11177 | 590 | 747 | KAYQPEKAQDQVDSQPNSTRG TWMKLETIILSKLTQEQQ\TKHC IFSLISGS |
| 11111 | 41479 | A | 11178 | 3 | 274 | FYYKDTCTHMFIVALFTIAKTW NQPKCPSVIDW/IMKNMWHIYT MEYYAAIKNDEFMSFSGTWMK LETIILSKLTQE\QKTKHCMFSLI SGS |
| 11112 | 41480 | A | 11179 | 1940 | 2061 | |
| 11113 | 41481 | A | 11180 | 493 | 743 | KATRSVNC/WWDHL*RPFWGS PH |
| 11114 | 41482 | B | 11181 | 1 | 1248 | |
| 11115 | 41483 | B | 11182 | 50 | 8445 | |
| 11116 | 41484 | A | 11183 | 40 | 125 | |
| 11117 | 41485 | B | 11184 | 1 | 1896 | |
| 11118 | 41486 | A | 11185 | 1 | 624 | |
| 11119 | 41487 | A | 11186 | 1 | 357 | |
| 11120 | 41488 | A | 11187 | 1 | 304 | |
| 11121 | 41489 | A | 11188 | 681 | 834 | |
| 11122 | 41490 | A | 11189 | 3 | 2128 | |
| 11123 | 41491 | A | 11190 | 175 | 402 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11124 | 41492 | A | 11191 | 46 | 790 | NPGAVKMPAYHSSIMDPDTKLI GNM/AHLLPIRSQFKGPAPRET KDT\DIVDEAIFLPSGPNVFFKN YEIKNE\ADRTLIIYITLYISECLK KLQK\CQFPKAQGGGKEMFYA GESTNFSHFLGEPGFPTLTAILC PNPANK\QEDEVMRALFTNQF KGKRLGLRLCEKSFSDP\QNG*T PAKWVDLAFVKRQFMNKSLS GPWTVEGSPGQPTVSRGPAAAF FQQDVTQSFCLYLVKFYRDERR ACLYLKNS |
| 11125 | 41493 | A | 11192 | 1 | 828 | |
| 11126 | 41494 | A | 11193 | 1 | 525 | |
| 11127 | 41495 | A | 11194 | 43 | 1826 | THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLPLPAAGRNVVRRRL AVVRSGSRSLSTADMTKGLVL GIYSKEKEDDV\QFTSAGENFD KSLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDPCG DAQAAAEGAVLGLYEYDDLK QKKKMAVS AKLYGSGDQEA QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIKLNLSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFVGKGITFDGGISIKASA NMDLMRADMGGAATICSIVS AAKLNLPINIIGLAPLCENMPSG KANKPGDVVRAKNGKTIQVDN TDA\EGRLILADALCYAHTFNP KVILNAATLTGAMDVALGSGA TGVFTNSSWLWNKLFESIETG DRVWRMPLFEHYTRQVVDCQL AD\VNNIGKYRSAGACTAAAF KEFVTHPKWAHLDIAGVMTNK DEV PQSTGKA*LGRPTRTLNEF L\LRFSQDNCLVQILKNVFHSL NWTVELKKVFE |
| 11128 | 41496 | A | 11195 | 1 | 273 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11129 | 41497 | A | 11196 | 2996 | 8256 | LPTRRSWAVFFKGGESGAHTLR RKARKKRKKQVKGGSPKKGEE AKKVEAPRLPKLAAPGGGAGA KGGAGGTSDMRLWSWVLHLG LLSAALGCGLAERPRRARRDPR AGRPPRPAAGPATCATRGPRPP RLAAAAAAGRAWEAVRVPR RRQQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAF TLQVWLRAEGGQRSPA VITGL YDKCSYISRDRGWVVGHIHTISD QDNKDPRYFFSLKTDRARQV |
| 11130 | 41498 | A | 11197 | 75 | 266 | |
| 11131 | 41499 | B | 11198 | 1 | 363 | |
| 11132 | 41500 | A | 11199 | 1 | 649 | PRIRHEVIEEVIRMMLEINSCLT NSLHHNPNLVYALLYKRDLE Q\FRTHPSFQDIMQNIDLVISFFS SRLAQAGAELSERVLEIISQV ALRCPKDRLEISQKLKFKYVE EEQPRGVF*SPYVWSLVQLQ SALYWEFHRTFQLFHPWDSRLR GRDASSPPGTPSSQGRPFQSSFIS GVTEVGQTGYLVYLLKEDCT SVFSSHTLIWRIGC |
| 11133 | 41501 | A | 11200 | 108 | 210 | |
| 11134 | 41502 | A | 11201 | 53 | 259 | |
| 11135 | 41503 | A | 11202 | 1 | 2679 | |
| 11136 | 41504 | A | 11203 | 1 | 675 | |
| 11137 | 41505 | A | 11204 | 834 | 1077 | KGLWTVPPSFGDTVSGPPVPTG GSAGHTVPPPPR*CRRQPPSP WRRLFLPQLRSRSSQPPAGPAR HLPPPAARPECFCA |
| 11138 | 41506 | A | 11205 | 1 | 681 | |
| 11139 | 41507 | A | 11206 | 1777 | 1940 | VPILPQPLLLHPIILLS*VPILPQP/ PAPPPYNPFITSPHTWSGLQFH SVTSPPPPAQFTLKRVAEAKGI VK |
| 11140 | 41508 | A | 11207 | 3 | 547 | |
| 11141 | 41509 | A | 11208 | 1 | 578 | |
| 11142 | 41510 | A | 11209 | 194 | 379 | |
| 11143 | 41511 | A | 11210 | 1 | 927 | |
| 11144 | 41512 | B | 11211 | 1 | 916 | |
| 11145 | 41513 | A | 11212 | 1 | 441 | RRKLQKQALGPEQNLETLLNL ATSVFYNRDQEEQVQKEKRDQ RKAAALVMALRQTNLGGSERT EHEAGQSPGKACYQCGLLGHF KKDCPMRNKLPPR/RVSTMLRQ SLEGALPQRMKVPWVRSPQPD DPTTGLRVP GASASSCHHPH |
| 11146 | 41514 | A | 11213 | 164 | 359 | |
| 11147 | 41515 | C | 11214 | 157 | 189 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 11148 | 41516 | A | 11215 | 13 | 399 | VEAFPTGSEKATAVISSLLSDIIP QSRLPTSIPSDNRRAFISQISQAV FQALSIP*NLYIPYGPSSSRKH/T LTKLSHQLKKDWTILLPLSLLRI QACPRNATGYSPFKVLYRHSFL LRPSLIPDTRPT |
| 11149 | 41517 | A | 11216 | 2 | 152 | WYGEIMGDVVSQGCER*WAMF LRAASSGIRGGVGT*SGRH*AE GRFYGDFRGNRAASVFSR |
| 11150 | 41518 | A | 11217 | 1 | 1143 | |
| 11151 | 41519 | A | 11218 | 28 | 453 | |
| 11152 | 41520 | A | 11219 | 275 | 1128 | DISTPSLATDHMPITIPNLIT/TY PTQRQYPIPPHALKGLKPVITDL LQHRLKPINSPYNPILPVQKP DKSYRLVQDLRLTNQIVLPIHP VVPNLYTLLSSIPSSSTTHYSVLH LKDAFFTIPLHPSSQPLFAVTWT DPDTQQSQQLTWAVLPQGFRD SPHYFSQALSHDLLSFHPSASHL IQYIDDLLCSPSFESSQQDTLL LLQHLFSGYQSDDRPAFTSQI TQAVSQALGIQWNLHIPYHPQS SGKVEWTNGLLKLKLLLLLTANI DDTSYLQIPHKGLQ |
| 11153 | 41521 | A | 11220 | 1 | 606 | |
| 11154 | 41522 | A | 11221 | 713 | 835 | LSQWRSDNGPAFISQITQAVSQ APGIQ*NLYIPYHPQSSGK |
| 11155 | 41523 | A | 11222 | 1 | 1133 | AEALPVQFYFHLSDIRGMLLHE PDLQKGIAVSQEDPQWSYQA DSPGIARRDYMVSRLVEGLKK AAYKAVNYDKLKKTTQVTIVP GPDFNLASHIIPDTTPDPHDCYL SDTPGIHSISHISFFAIPHPDHTW FIDGSSTTPNRHTPAKAGYAIVP STSIIEAALPPSATSRQAKLIAL TRTLTLAKELCVNIYTDKYAF HILHHHAVIWAERGFLTQGW SNINASLIKTLKATLLPKEAGV IHCKGHQKASDPQAQGNQYAD KIAKEAASGPTSVPHGQFFSFL VTPTYSPKTSTYPSLLTQGW FLDQGGKYLPAKASHILPSFH NLFHVGYPKLAHLLEYLISFLS WKSILKEITSQ*SICYSTTPQG |
| 11156 | 41524 | B | 11223 | 1 | 1156 | |
| 11157 | 41525 | A | 11224 | 1 | 4991 | |
| 11158 | 41526 | A | 11225 | 3 | 590 | |
| 11159 | 41527 | A | 11226 | 203 | 1772 | |
| 11160 | 41528 | A | 11227 | 1 | 1669 | |
| 11161 | 41529 | A | 11228 | 1473 | 1604 | |
| 11162 | 41530 | A | 11229 | 82 | 159 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11163 | 41531 | A | 11230 | 1 | 1323 | |
| 11164 | 41532 | A | 11231 | 377 | 631 | LLKGKLTNRKDIHTKTPSVRHH HRRPKPGRDTTKKIILNQYPW* TSMQKSSIKYWQTESSSTSKSL TMIKLASSLGCKNWKKL |
| 11165 | 41533 | C | 11232 | 1 | 1677 | |
| 11166 | 41534 | A | 11233 | 753 | 966 | FVFLWSLMMV TYRWGFGVDV LSVC*FSFQQS\EPQLQVCWSLL EVHS*PCLPGYQQRN SCWPRG SCDVVIT |
| 11167 | 41535 | A | 11234 | 1253 | 1459 | LSDSPKLK*RKKC*GQPERKVG LPTKGSPSD*QQISWQKLCKPE ESGGQYSTFLKKRIFNPEFHIQQ |
| 11168 | 41536 | B | 11235 | 1 | 924 | |
| 11169 | 41537 | A | 11236 | 299 | 436 | |
| 11170 | 41538 | A | 11237 | 259 | 536 | FQKEWYQLLLVPLV/EIWL*IHL VLDF*LVNY*LLPQFQSMLLV SSEIQLLPGLVLGECMCQGIYPF LLDFLWSLMMV TYRWGFGVD VLCVC |
| 11171 | 41539 | B | 11238 | 79 | 1587 | |
| 11172 | 41540 | A | 11239 | 1608 | 1763 | |
| 11173 | 41541 | A | 11240 | 1 | 2001 | |
| 11174 | 41542 | B | 11241 | 1 | 741 | |
| 11175 | 41543 | B | 11242 | 1 | 1368 | |
| 11176 | 41544 | C | 11243 | 1 | 3924 | |
| 11177 | 41545 | A | 11244 | 470 | 619 | KVTRGWGSPHQDAG*SPCQSH QDQTP*GILKEHQEKARRK*RQ LCVLQL |
| 11178 | 41546 | B | 11245 | 1 | 3546 | |
| 11179 | 41547 | A | 11246 | 363 | 476 | |
| 11180 | 41548 | A | 11247 | 1 | 759 | |
| 11181 | 41549 | C | 11248 | 376 | 986 | |
| 11182 | 41550 | A | 11249 | 556 | 821 | MSIRSTWRRAEFNSWVSFLTFR LVDLSLVFDDGDVQVGFWC GC PSCLLVFL/ISQDPQLQVCWSL QEVHSRPCSPGYQQQLQYSEY |
| 11183 | 41551 | A | 11250 | 119 | 340 | |
| 11184 | 41552 | B | 11251 | 1 | 942 | |
| 11185 | 41553 | A | 11252 | 436 | 732 | LHIWPFLLPCKAQNQVHCSKFC PLGRFPFMAVLQGCPRKGL*CC SCPLLGGIWISCRICAFRTYLRP IMYIPLPFADGMLLCTAHSMAR CFGYCSLVV |
| 11186 | 41554 | C | 11253 | 1 | 1878 | |
| 11187 | 41555 | A | 11254 | 720 | 1535 | ILPEVQGGAGTI*LSLFLIE*PLF LSPA*LPWPELPTLC*IGVVRDG TPVLCQFSKGMLPVFAHSV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11188 | 41556 | A | 11255 | 2 | 1059 | WLLAASPLWLCRIRP/LILAAF MGWQSR SALGTQ SQESGK GSPD QVLVPQ DCGPW LGSVEL VSV GSQAGE EPI LSENK GRVTQ MKI PEERSG SNICCS AIFAV LQPPL LI PRQTR SGVDL QQNPT DLQLR VL TVRRK TNKEK GHPHQ NPTCT SP ASKTK GALRF IKQVLR DLERAL DSHTIM GDFNT PLSTLD RSTRQ KVNKDI QELNS ALHQVD LIDIY RTLHPK STEYTV FSAPH HTYSKI DHTVGS KALLSK CKRIE ILTNC LSDHSA IKLEL RIKKLT QNHST TL KLNNLL LNDYW VHKET KAEIK MVFEID ENKDT IYQNL WDTFK AVCRGK FIALKA HKKRQ QERVT |
| 11189 | 41557 | A | 11256 | 82 | 159 | |
| 11190 | 41558 | A | 11257 | 820 | 1358 | HTDGF LVWMP FLFVS FSPNS QD RQLQVC WRLL EVHSR PCFPGY QQRWL QNNRY /SVNR KCCCL IV PLEVLS QRSTH QHVG EWLCL LGRKFP AGME ACTAM LCSSSV L EAATLS FSVQ HRACT GGS*K PQ QGRVYP SEG REHNG AAAF GPE CSSECP ASCPD PGTQPC APGT YIPFF SCQT |
| 11191 | 41559 | A | 11258 | 2435 | 3261 | QVRGY RCRFV TWVNC MSLR FG VQRIP SPSLT GTQPP VGAD* HLT RPGT PLR* NFQR NDQAV TFAVH VHIH FVQPL LLIPM QTGSG VDLR QTPT DLQL RVLT VRRK TNKQK GHPHR NPICM SPSSK TKAR QAN IQIQEI QRT PQRY SSRR ATPR HII VRFTK VEMKE KKLRA AREK GR VTHKG KPIRL TVDLL AETL QAR REWGP IFNIL KEKNF QPRIS YPA KLNFI SEEEI KSFTD KQML RDFV TTRPAL QELLK EALNM ERNNQ YQPLQ NHAKL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11192 | 41560 | A | 11260 | 1439 | 2544 | VSSTTKEKALSVPWRWCILQKK NPPNHQPVSLPEVFLPQILKFSG PPHWRRIEYKVMRLNIGDM KTKKKMLEKYEQLERHQQS RT*KAVCCIT*LSRHII LLGQAPL VQQSM*QPESHHQVNPPESTSYG IHQTPKLS*IGIK*RPWIM/MSEV KGYKVGNNFFAKAPNRPPL KPRQTGSGVDLQQT PADLQLR VLTVRNTNKQKGHPHQNPICT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPMVE DQMNMKQEEKFREKRMKRN EQSLQEIRDYVKRPNRLRIGVPE SDGNGTKLENTLQDIIQENFPS LARQANIQIEIQRMPPQR |
| 11193 | 41561 | A | 11261 | 2772 | 3111 | QSGPSAAGLLEFAGGPLQTLFA WVSAAEVGKCKGSGSSLS*PK KGVMMDGTWKIGSLPPEYCAFP G*KNGAP/LRLYPTPGSEGPTPT ESP*/FASTAVGDQATARQQRGW GRGARH |
| 11194 | 41562 | A | 11262 | 248 | 597 | DRCPAAWDRHPAGIQSSRREPS KATWTLRSKLSVQDGRDSSL RLNCKVAARLGAGHPMLRLG LRC*YPGKQGLEWTSSKLQQTC H*GS*LLKGKLTNRKDIHSKTPS VRHYHQR |
| 11195 | 41563 | B | 11263 | 1 | 2250 | |
| 11196 | 41564 | A | 11264 | 1298 | 1681 | GVSVPLLWGASQLGYLGVMDB LAEAVCPFSDLQLHSGRTSTVF KAALGQSGAHCPCVSAQS* AD*RALREHKQ*FGSTLCGPVM VVAMELGSSTMVELVSSPANS VKVFLFLHIFSSTCCFLTFS |
| 11197 | 41565 | A | 11265 | 1272 | 1497 | SGLLPIKVAFTKPQFLFILLRIWL *RGYVFCSWKVTTPREQPQCIT DGYQIFIFMQKTLSCLSILGKRT MSLMQ |
| 11198 | 41566 | A | 11266 | 1 | 1071 | |
| 11199 | 41567 | A | 11267 | 788 | 1286 | |
| 11200 | 41568 | A | 11268 | 3 | 455 | |
| 11201 | 41569 | A | 11269 | 1 | 711 | |
| 11202 | 41570 | A | 11270 | 225 | 525 | GGGENFSYPWYLLVGCGWFSS SPIVPDVPPFSLLLPAQKKKPAP PK\PEPKPKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11203 | 41571 | A | 11271 | 914 | 1261 | TAKPKTNWCCRAPTSRLASTFA TMPFKKAECVGDAHPATVKDE PQRISARLS\AKPAPPKPEPKPK KAPAKKGKGVKPKGKKGKAD\A GKEG\NNPAEN\GDAKTDQAQK A\EGA\GDAK |
| 11204 | 41572 | A | 11272 | 3 | 359 | |
| 11205 | 41573 | A | 11273 | 440 | 642 | WKAEREEIEPR/PKKAPAKKGE KVPKGKKKGKAEAGQDGDNPTE NGDAKTDQGQKAEGAGDAKR TVSHQN |
| 11206 | 41574 | A | 11274 | 499 | 723 | |
| 11207 | 41575 | A | 11275 | 147 | 459 | STYVPLPSPSSMPKRKAEGHA MGDKAKVKDEPQRRFARLS\A KPAPPKPEPKPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK |
| 11208 | 41576 | B | 11276 | 179 | 400 | |
| 11209 | 41577 | A | 11277 | 24 | 601 | |
| 11210 | 41578 | A | 11278 | 266 | 441 | |
| 11211 | 41579 | A | 11279 | 17 | 570 | HQPKKDLTGFKWPRYIRLQR QRAILYKRLKVHLAINQFTQAL ARQTATQLLKLAKHYRPETKQ EKKQRLARAEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIAHDVGPIELVVFLPA LCRKMGPVYCQ\IKGKARLG\R LVHRK\TCTTCRFTQ\VNS\EDK GALAK\VEAIRTNYNDRYDEI R\RHWGGNVLGPKSVARIAKL EKAKAKELAH*TGGSYQDQLQ |
| 11212 | 41580 | A | 11280 | 175 | 289 | RPCVKESGKPHLKSSTMWTTL KLLRI*PRRTTCSPLRS |
| 11213 | 41581 | A | 11281 | 205 | 361 | |
| 11214 | 41582 | A | 11282 | 144 | 396 | CLEVLHKILFFEMESHSVTQAG VQWRDLGSLQPLPPG\SSNSPTS ASQVAGIRSMRQKGRANFFVFL VEMGFHHVGQADLELLTL |
| 11215 | 41583 | A | 11283 | 241 | 550 | |
| 11216 | 41584 | A | 11284 | 2 | 106 | |
| 11217 | 41585 | A | 11285 | 2 | 447 | PPLSRLLCPRPHSGWPEGYSPE HLRCGLRSGTLRSRQALHCQVS SNP*PPSLWF*GCGNVL*ELCLF VLPVSVNLYQVLLSEIWEFHRT |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11218 | 41586 | A | 11286 | 1 | 2172 | PAGRCRTAWAVAAQQLMLSA ALRTLKHVLYYSRQCLMVSRN LGSVGYDPNEKTFDKILVANRG EIACRVIRTCKKMGIKTVAIHSD VDASSVHVKMADEAVCVGPAP TSKSYLNMDAIMEAIKKTRAQ AVHPGYGFLSENKEFARCLAAE DVVFIGPDTHAIQAMGDKIESK LLAKKAEVNTIPGFDGVVKDA EEAVRIAREIGYPVMIKASAGG GGKGMRIAWDDEETRDGFRLS SQEAASSFGDDRLLIEKFIDNPR HIEIQVLGDKHGNALWLNREC SIQRRNQKVVEEAPSIFLDAETR RAMGEQAVALARAVKYSSAGT VEFLVDSKKNFYFLEMNTRLQ VEHPVTECITGLDLVQEMIRVA KGYPLRHKQADIRINGWAVEC RVYAEDPYKSFGLPSIGRLSQY QEPLHLPGVRVDSGIQPGSDISI YYDPMISKLITYGSDRTEALKR MADALDNYVIRGVTHNIALLR EVIINSRFGKRNLNT*FLASKGF PEAFKGHLLTKSEKTQFLAIASV SLFVAFQLRAQHFQENSRRMPVI KPDIANWELSVKLHDKVHTVV ASNNGSVFSVEVDGSKLNVST WNLIASPLLSVSVDEHSEGLFQ CLSREAGGNMSIQFLGTVYKV NILTRLAAELNKFMLEKVTEDT SSVLRSPMPGVVAVSVKPGD AVAEGQEICVIEAMKMQNSMT |
| 11219 | 41587 | A | 11287 | 62 | 2600 | |
| 11220 | 41588 | C | 11288 | 277 | 508 | |
| 11221 | 41589 | B | 11289 | 94 | 1440 | |
| 11222 | 41590 | A | 11290 | 57 | 237 | FLHAENKAHRPGISLCGLRAQP RQPASRHAW*SMRSEQRPWLT ASGRSSGQTRSSRSLG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11223 | 41591 | A | 11291 | 3 | 1968 | EFDYSEDKSSWDNQQENPPPTK KIGKKPVAKMPLRRPKMKKTP EKLDNTPASPPRSPAEPNDIPIA KGTYTFDIDKWDDPNFNPFSST SKMQESP KLPQQSYNFDPDTC ESVDPFKTSSKTPSSPSKSPASFE IPASAMEANGVDGDGLNKP KKKTPLKTDTRVKKSPKRSPL SDPPSQDPTPAATPETPPVISAV VHATDEEKLAVTNQKWTCMT VDLEADKQDYPQPSDLSTFVNE TKFSSPTEELDYRNSYEIEYME KIGSSLPQDDAPKKQALYLMF DTSQESPVKSSPVRMSESPTPCS GS/SFEETEALVNTAAKNQHPV PRGLAPNQESHQVPEKSSQKE LEAMGLGTPSEAIEITAPEGSA SADALLSRLAHPVSLCG\ALDY LEPDLAEKNPPLFAQKLQREA\ VHPTDVSISKTALYSRIRTEVE KPAGLLFQQPDLDSALQIARAE I\TKEREVSEWKDKYEESR\RE VMEMRKIVAEYEKTIAQMIEDE QREKSVSHQTVQQLVLEKEQA LADLNSVEKSLADLFRRYEKM KEVLEGFRKNEEVLKRCQAEY LSRVKKEEQRYQALKVHAEEK LDRANAEIAQVRGKAQQEQAA HQASLRKEQLRVDALERTLEQ KNKEIEELTKICDELIAMGKS |
| 11224 | 41592 | A | 11292 | 63 | 2203 | |
| 11225 | 41593 | A | 11293 | 27 | 586 | |
| 11226 | 41594 | A | 11294 | 89 | 288 | |
| 11227 | 41595 | A | 11295 | 1 | 522 | HERFETTYFKKFP\GYVVTGDG CQRDQDGYWITGRIDDMLNV SGHLLSTA EVESALVEH*RLLQ EAAVVGHPHPCEGVNASYCFV TLCDGHTFSPKLTEELKKA\VM RKRLAPFATPDYIQNAPGLPKT\ RSGKIMRRVLRKIAQNDHDLG DMSTVADPSVISHLFSHRCLTI |
| 11228 | 41596 | A | 11296 | 2 | 569 | |
| 11229 | 41597 | B | 11297 | 1 | 990 | |
| 11230 | 41598 | A | 11298 | 1 | 252 | |
| 11231 | 41599 | A | 11299 | 39 | 174 | RHIYSSNEVH*KEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEIPLSSL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11232 | 41600 | A | 11300 | 16 | 379 | ILDTSMPMRWTQKNFSMILAQPE QQCKTLSQNKNKDRRIKKKEE KKKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKEKKKEKE EKKKK/QEEEEEEEEEEEEEEEE EEEEEEEEEEEEERRRR |
| 11233 | 41601 | A | 11301 | 1 | 249 | |
| 11234 | 41602 | A | 11302 | 1 | 353 | |
| 11235 | 41603 | A | 11303 | 1 | 847 | |
| 11236 | 41604 | A | 11304 | 3 | 224 | QEKRRRKEKKK\KEEEEEEEEE EEEEEEEEEEEEKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKGRKTDLAVDPV |
| 11237 | 41605 | A | 11305 | 1 | 417 | |
| 11238 | 41606 | A | 11306 | 1 | 1314 | |
| 11239 | 41607 | B | 11307 | 1 | 133 | |
| 11240 | 41608 | A | 11308 | 45 | 266 | |
| 11241 | 41609 | A | 11309 | 35 | 313 | FLQMEDTYIVTKLLLLLRFAWL YLDLVFVLI*YRKKRRKKRKK KEKEKEKEKKKKKKKKKKKKK KKKKKKKKKKKKRKKEMALQS CSLWYLYA |
| 11242 | 41610 | C | 11310 | 240 | 391 | |
| 11243 | 41611 | A | 11311 | 1 | 579 | |
| 11244 | 41612 | A | 11312 | 141 | 410 | PEPILTMESKGMWQLFELTL/H NSKVNTLSKELHSEFSEVMNEI WASDQIRSAVLISSKPGCFIAGA DINMLAACKDPSRSNTAIRKH RE |
| 11245 | 41613 | A | 11313 | 1 | 358 | KWFTPMFEIKGGYA*SKNWR LSVRCGGWPLRRLMEEGSLPNP SRIYYRNKLRLKSQNNSSVDPC MRNLDECEVCRDGWELFCCDT CSRVFHDDCHIPPESEKMKES AGSQCCQES |
| 11246 | 41614 | A | 11314 | 1 | 921 | |
| 11247 | 41615 | A | 11315 | 108 | 2765 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11248 | 41616 | A | 11316 | 98 | 2418 | AKLMAQQGQQGQMASGDSNL NFRMVAEIQNVEGQNLQEQVC PEPIFRFFRENKVEIASAITRPPF FLMGLRDRSFISEQMYEHFQEA FRNLVPVTRVMYCVLSELEKTF GWSHLEALFSRINLMAYPDLNE IYRSFQNVCEHSPLQMNNVN DLEDPRLLPYGKQENSNACHE MDDIAPQEQALSSSARCEPGFS SESCEQLALPKAGGGDAEDAPS LLPVSKLAIQIDEGESEEMPKL LPYDTEETFDLKTPTVTNEGEP EKGLCLLPGEGEESDDCSEMC DGEERQEASSSLARRGSVSSEL ENHPMNEEGESEELASSLLYDN VPGAEQSAYENEKCSVMCFS EEVPGSPEARTESDQACGTMDT VDIANNSTLGKPKRKRKRKRGR HGWSRMRMRQKNSQQNDNS KADGQVVSSEKKANVNLKDL KIRGRKRKGKPGTRFTQSDRAAQ KRVRSRASRKHKDETVDFAKAP LLPVTCCGGVKGILHKKKLQQGI LVKCIQTEDGKWFTPTFEFIKG GHARSKNWRLSVRCGGWPLR WLMENGFLPDPPRJRYRKKKRI LKSQNNSSVDPCMRNLDECEV CRDGGELFCCDTCRVFHEDCH IPPVEAERTPWNCIFCRMKESPG SQCCQSEVLERQMCPEEQLK CEFLLLKVYCCSESSFFAKIPYY YYIREACQGLKEPMWLDKIKK |
| 11249 | 41617 | A | 11317 | 1 | 1210 | |
| 11250 | 41618 | A | 11318 | 1 | 743 | MRYKKEQPLFLPKYDLGADAA ILQPQEEDCGSTQVRGGHHRK TEETGLLVTSLNQGIKPHDSVT KLLSPQRSSVLFLLLITSGVHTD SSKAVLESRRSLGYEASFLEYF QSFYKLPVDRLYAWHCSDHR NTTVTAINTDRPGLLTSLTVTI GQGSKKAPSGFSHISPAPTVKQ QPILCDDRDFSPSSFPSTNTPSQF ATNEVLTTGPPPGAG/CCQYSTI TRKTGPNCQAGGCPGGARPAK |
| 11251 | 41619 | A | 11319 | 314 | 486 | |
| 11252 | 41620 | A | 11320 | 3 | 122 | |
| 11253 | 41621 | A | 11321 | 1 | 289 | |
| 11254 | 41622 | A | 11322 | 1 | 399 | |
| 11255 | 41623 | A | 11323 | 3 | 259 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11256 | 41624 | A | 11324 | 1 | 369 | MPATWEAEARESHKREFETHL/ VQHSETPSEKEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEGEEEEEEEEEEEEEEEEEEEE GEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEGEEEEEEEEEEEEEEEEEEEE EEGEEEEEEEEEEEEEEEEEEEEEEEE |
| 11257 | 41625 | B | 11325 | 1 | 441 | |
| 11258 | 41626 | A | 11326 | 1 | 267 | |
| 11259 | 41627 | B | 11327 | 1 | 234 | |
| 11260 | 41628 | A | 11328 | 1 | 383 | MVRPFLYKKIKEEEEEEEEEEEE EEEEGEEEEEEEEEEEEEEEEEEEE EGEEEEEEEEEEEEEEEEEEEEEDKD DEEER/EKKEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEKKHSL*DPD LGEKENKGQRKRKLARGTSQP SLSPGGSDPLGA |
| 11261 | 41629 | A | 11329 | 305 | 625 | VAPGDRHAFPLAPSGLSPELTLP QTQCCAQATVQGLEGTRSWSQ SGTSSLSPWSHTSLRRRRKEEG EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEE/IEEGEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEAAKTQ |
| 11262 | 41630 | A | 11330 | 294 | 501 | AFDKQPRGRGRVVKEEVLKKK KKEEEEKEEGEEEEEEEEEEEEEE E/EEDEEEEEEEEEEEEEEEEEEEEE EEEEEEEE |
| 11263 | 41631 | C | 11331 | 618 | 966 | |
| 11264 | 41632 | B | 11332 | 1 | 332 | |
| 11265 | 41633 | A | 11333 | 1 | 705 | |
| 11266 | 41634 | A | 11334 | 1 | 417 | |
| 11267 | 41635 | A | 11335 | 1 | 639 | |
| 11268 | 41636 | A | 11336 | 2 | 2347 | LMLVVIFNGTERIEDLRKPPSFD AILGGGLRVLFFQNEAHPPFAS WRNNEEARTDRPSQQLRSLNG KWRLMRYFLLTHLCETLVKVK DAEDQLGARVGYIELDLNSGKI LESFRPEERFPMMSTFKGLLCG AVLSRIDAGQEQLGRRIHYSQN DLGEYSPVTEKHLTDGMTVRE LCSAAITMSDNTAANLLTTIG GPNELTAF LHNMGDHSVTRLDR SEPENEAIPNDERDTRCLGQW QQRSQTINWPTTTTLP |
| 11269 | 41637 | A | 11337 | 56 | 243 | YSCLMFPQDGE*LEKEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11270 | 41638 | A | 11338 | 1 | 503 | MKHQHFALLVPEKFLIAQSTAS RVDRRQIWRDVSSERGEISQCL KVGTSLSNSTDVSAVEAVRATV LGSGTLTPTVLRSNAGPYTRIST VPACLLGQEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEK/EEEE/EEE EEEEEEEEEEEEEEEEEEEEEEEE EEGEEEEERRKS |
| 11271 | 41639 | A | 11339 | 1 | 651 | |
| 11272 | 41640 | A | 11340 | 1 | 2184 | MNIDANIPNKILENRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTKDKNCMIISIDAEK AFDKIQQCFMLETNLKLGIGGT YLKIIIRAIYDKPTANIILNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGVQLGKE EVKLSLFADDMIVYLENPIVSA QHLLKLISNFSKVSGYKINVQK SQAFLYTNNRQTENQIMSELPF TIASKRIKYRGIQLTRDLKDLFK ENDKPLLKEIKED/DKEMEEHS MLMGRKNQYRENSHAAQELE KNYFKVHMEPKKSPHYQVNP PKEQSGRHHVT*LQTLQGYSN QNSMVLVPKQTYRSMEQNRSL RNNATYLLQSDL*QTQEKQAM GKGFP**MVLGKLASHM*KPE TGSLPYTLYKNQFKVD*RLKR* T*NHKNQRRKPRHYHSGHRHG QGLHV*NTKINGNKNQN*QMG SN*TKELLHSKRNYRQSDQATY KMGENFHNLLIRQRANIQNVQ* TQTNLQEKKNQPHQKVGEHGE QTLKRRHLCSQKTHEK\NSPSL AIREMQIKTTMRYHLTPVRMAI IKKSGNSRKHIQKKEEEEEEEEA EEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEE EEKCSLKHTEAPCVKGIETIFW NKFSLCDITKSYLSGVQKLEER AHKVKLALKFKKEIKMALHGG |
| 11273 | 41641 | A | 11341 | 1 | 870 | |
| 11274 | 41642 | A | 11342 | 2 | 259 | GSTISCARCAELRGSASRFRPLP AAAMKWMFKEDHSLEHRCVE SAKIRAKYPDRVPALTMGQLYE KEKDEDGFLCVAYSAGENTFGF |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11275 | 41643 | A | 11343 | 1 | 461 | GCRRCRRRCCCARCAELRGS ASRFRPLPAAAMKWMFKEDR WLEHRCVESAK\IRAKYPDRVP VIVEK/VSQGSQIVDIDKRKYL VPSDITVAAQFMWIIRKRIQLPSE KA\IFLFVDKTVPQSSLTMGQLY EKEK\DEDGFLYVA\YSGRGTLF |
| 11276 | 41644 | A | 11344 | 1 | 966 | |
| 11277 | 41645 | A | 11345 | 1 | 1037 | RPPFPVPGVQKCPLPTRGGLHIG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSPVASGREM VVLSVPAEVTVILLDIEGTTTP IAFVKG/DILFPYIERKMLK\EYL QTHWEEEEFQ\QDVSLEFEGNK A\EEDAHLDGAVPIPGKHLGIG VDD\LQQM\QAVVDNVCWQM SLDRKTTALK\QLQGH\MWRAA FTAGRMK\AEFFADVPA\VR\K WREAG\MKVYIYSSGSVEAQKL LFGHSTEGDILEL\VDGH\ADTKI GHKRRRVKVTRKIADSI\GCST\N KHVFVWTDVTSRRASAGLRE AGCCTLAV\VRPG\NAGINR*L RKTTYSLITSFQWNYLPSST |
| 11278 | 41646 | A | 11346 | 346 | 858 | |
| 11279 | 41647 | A | 11347 | 1 | 234 | |
| 11280 | 41648 | A | 11348 | 1 | 1696 | |
| 11281 | 41649 | A | 11349 | 1 | 234 | |
| 11282 | 41650 | A | 11350 | 1 | 1696 | |
| 11283 | 41651 | A | 11351 | 1 | 211 | |
| 11284 | 41652 | A | 11352 | 1 | 417 | |
| 11285 | 41653 | A | 11353 | 1 | 1458 | |
| 11286 | 41654 | A | 11354 | 219 | 329 | |
| 11287 | 41655 | A | 11355 | 132 | 451 | |
| 11288 | 41656 | A | 11356 | 1 | 996 | |
| 11289 | 41657 | A | 11357 | 1 | 867 | MARLWGALSLWPLWAAVPWG GAAAVGVRACSSTAAPDGVEG PALRRSYWRHLRRLVLGPPEPP FSHVCQVGDPVLRGVAAPVER AQLGGPELQRLTQRLVQVMRR RRCVGLSAPQLGVPRQVLAL PEALCRECPPRQALRQMEPP LRVFNPSLRVLDLRLVTFPEG CESVAGFLACVPRFQAVQISGL DPNGEQVVWQASGWAARIQH EMDHLQGCLFIDKMSRTFTN VYWMKVND*SFATGAEDSGY QDANTFTLSWANLTWHQLGW LAYDRKLDLCQGMAD |
| 11290 | 41658 | A | 11358 | 3 | 226 | |
| 11291 | 41659 | A | 11359 | 1 | 756 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11292 | 41660 | A | 11360 | 35 | 142 | |
| 11293 | 41661 | C | 11361 | 151 | 484 | |
| 11294 | 41662 | A | 11362 | 1 | 1245 | |
| 11295 | 41663 | A | 11363 | 2 | 1464 | CQAKFIMNRLKK/NERQKVQDI KEVKQNIHLIRASFAGKGKQLE EKMQPLEPEAIMLSELMQEQT KCRMFSLSISGKHGVHMSKTG ATDSGAYLRVEEIQTIREYYK HLYANKLENLEEMDKFLDKYT LPRLNQEEVESLNRPITGAEILAI ISSLPTKKSPGPDGFTAIFYLRY KEELVPFLLKLSQSIEREGILPNS FYEASIIIPKPGRDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNL RKSINVIQHINRAKDKNHMISI HEEKAFDKIQPFMLKTLNKL IDGTYLKIIRAIYDKPTANIILNG QKLEAFPLKTGTRQGCPSPLL FNIVLEVLAIRQEKEIKGIHL GKEEVTLSLFADDMIVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASRRIKYLGIQLTRDMKD LFKENYKPLLSEIVTVF |
| 11296 | 41664 | A | 11364 | 41 | 559 | |
| 11297 | 41665 | C | 11365 | 63 | 370 | |
| 11298 | 41666 | A | 11366 | 3 | 211 | |
| 11299 | 41667 | A | 11367 | 47 | 358 | PDMGLEDEQKMLTESGDPEEE EEEEELVIGLRLSVHTGNLGRP GM*NFPLLSIQN*MGDPHSAIS GGQCGSASWPSARIPLQQVREQ CRASWKKCVK\ARERLE\ CDE R*SSRSHTEDCT\EELFD\H A\RDHC\VAHKLL*QLAFCTDPP TTSERAMPSQLEEMCKRPGSG |
| 11300 | 41668 | A | 11368 | 1 | 2082 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11301 | 41669 | A | 11369 | 1 | 2013 | MKHLKRWWWSAGGGLLHLTLL LSLAGLRVDLDLYLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRALGVFPVPRTSV DAWLVSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGGCASEE NGVLREKHEAVDHSSQHEENE ERVSAQKENSLLQNDDEENKI AEKPDWEAEKTTESRNEGISLG DIPLPGSISDGMNSSAHYHVNF QAIQDVNLHEAILLCPNNTFR RDPTARTSQSQEPFLQLNSHTT NPEQTLPGTNLTGFLSPVDNHM RNLTQDLDLYDLINIFDEINLM SLATEDNFD\PIDVSHLFDEPDS DSGLTLDSSHNNTSDIKSNSSHS VCDEGAIGYCTDHE\SSSHDL EGAVGGYYPEPSKLCHLDQSDS DFHGDLTQHVFNHTYHLQP TAP\ESTS\EPFPWPGGRSQEG RE*DTLKD\TDRNLSRDEQRAK ALHIPF\SVDEIVGMPVDSFNSM LSRYLTDLQVSLIRDIRRGK NKVAAQNCRRKLDIILNLEDD VCNLQAKKETLKREQAQCENKA INIMKQKLHDLYHDIFSRLRDD QGRPVNPNHYALQCTHDGSILI VPKELVASGHKKETQKGKRRK |
| 11302 | 41670 | A | 11370 | 3 | 255 | |
| 11303 | 41671 | A | 11371 | 1 | 1611 | |
| 11304 | 41672 | A | 11372 | 109 | 207 | MLCLQRFYMIFVDFQSRPQF*L KSCQHIISCHQ |
| 11305 | 41673 | A | 11373 | 1 | 666 | |
| 11306 | 41674 | A | 11374 | 1 | 1254 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11307 | 41675 | A | 11375 | 33 | 1458 | KLPLKAKMGKEKTHINIVVIGH VDSGKSTTTGHLIYKCGGIDKR TIEKFEKEAAEMGKGSFKYAW VLDKLKAERERGITIDISLWKFE TSKYYVTIIDAPGHRDFIKNMIT GTSQADCAVLIVAAGVGEFEA GISKNGQTREHALLAYTLGVK QLIVGVNKMDSPEPPYSQKRYE EIVKEVSTYIKKIGYNPDTVAFV PISGWNGDNMLEPSANMPWFK GWKVTRKDGNASGTTLLLEALD CILPPTRPTDKPLRLPLQDVYKI GGIGTVPVGRVETGVLPKPMV VTFAPDNVTTEV*SVEMHHEA LSEALPGDN/VGAFNVKNVSVK DVRRGNVAGDSKNDPPMEAA GFTAQVILNHPGQISAGYAPV LDCHTVAHIACKFAELKKK\DR RF\GKKLED\GPK\FWKSGDAAI VDMVP\GKPMCVESFSDYPPL GPFAVHDMRQT\VAGGAHQKQ VDKK\AAGA\GKVTK\SAQKAQ |
| 11308 | 41676 | A | 11376 | 1 | 880 | |
| 11309 | 41677 | A | 11377 | 1304 | 2340 | KETEAQRKRLRRNEPEEQEIRT RKTRSPQTPDQQTYYKGRNER LCGISQPTKEPTRGGFCRFRNPP SNRIFACWGKPAWTACCNSLR ARRMLMERNARAAGSRKRMG RMDCWARVLD\NLAAEAKSEP EKKAGVKRICKRRCTGSSFDL\ DY*LFNGDYDDRMYSYPARVP PPPPIARA VVP\SKRQRVSGNTS RRGKSGFNSKSGQRGSSKSGKL KGDD\LQAIKE\ELTQIKRKSGF LFLGKTWEKIEKEQSKQAVEM KK**SQKEEQSSQLR*KKDET*C *RLEV LKGG\EDSA\EEGDLLD DDDNEDRGDDQLELIKDDKE\A EEEEEDDRD\SANGRIDDSLST |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11310 | 41678 | A | 11378 | 80 | 1141 | ETQNRISPPSPSCEIFLIFSIFRL CEKPYHQTRSASNVTNKTDPRS MNSRVFIGNLNTLVVKKSDVE AIFSKYGKI\VGCSVHKGFALSE SMLMKRNARA AVAG\EDGRMI AGQVLD\NLAAEPKVN RGKAG VKRSAAEMYG/SQ*QNTLLRPL YFSSSFDLDYDFQRDY YDRMY SYPARVPPPPPIARA VVPSKRQR VSGNTSRRGK\SGFNSKEWNSG VSSKFWKR*KGDDLQ\AIKEEL TQIKQKVDSL\LENLEKIEKEQS KQAVEMKNDKSEEE\QSSSS\LK KDET\NLKMESEGGCRLTLPEE GDP\LD**YDE**RSGGNDPAGS *SKDDEK\EAEE\GEDDRD\ISAN G\EDDS |
| 11311 | 41679 | A | 11379 | 1 | 1134 | |
| 11312 | 41680 | A | 11380 | 1 | 642 | |
| 11313 | 41681 | A | 11381 | 397 | 898 | |
| 11314 | 41682 | A | 11382 | 1 | 663 | |
| 11315 | 41683 | A | 11383 | 44 | 398 | ATMLGLNIISRK WFYKSSEKSL GLRGGLGRPLAFTLYSLLQAAL LCVNAIAVLHE/ERRISSKNICA GGTRTIGIGWIWEKEPGIKSQL MNLIRSVRTEM RVPLIIVNSIAI VLLLLFG |
| 11316 | 41684 | A | 11384 | 3 | 754 | GLYYRK CQLISKEDVTHDTRLF CLMLPPSTHLQVPI/GEHVYLKL PITGTEIVKPYTPVSGSLLSEFKE PVL PNNKYIYFLIKIYPTGLFTPE LDRLQIGDFVS VSSPEGNFKISK FQELEDLFLLAAGTGFTPMVKI LNYALTDIPSLRKVKLMFFNKT EDDIIWRSQLEKLAFKDKRLDV EFVLSAPISEWNGKQGHISBALL SEFWKRNL DKS KVLVCICGPVP FTEQGVRL LHDLNFSKNEIHSFT |
| 11317 | 41685 | A | 11385 | 1 | 1785 | |
| 11318 | 41686 | A | 11386 | 95 | 369 | |
| 11319 | 41687 | A | 11387 | 511 | 728 | |
| 11320 | 41688 | A | 11388 | 1 | 100 | |
| 11321 | 41689 | A | 11389 | 1 | 777 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11322 | 41690 | A | 11390 | 2 | 707 | PNPKCR*VFPVFLFYRPI*PFPSS PA/SLIARPS*VPILPQPPLL/TPY NPPTTSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVNAHVP FSLSDLSQISQHLGSFSSDPTKYI QEFRYLTLSYNLTWSDLNVILT STLSPDERERVFPVSQSH/V**P/ SGFMSQTSRKALEQFPERIPQW NYQANSPGKNFKN*NLALKPH NRN*STLPSTCTIHERKQPDGNA FLSYNYLPP |
| 11323 | 41691 | A | 11391 | 2 | 339 | LLFRSLPAKLNQAPILPWPL/PP PPYNPSITSPVHTWFSLQFHSET SPPPPAQQFPLRAVAGTEGIVR MNGKEFFLQPNLTLITAGFKSQ TSRKALEQFPERIPNGTIRQIPQ |
| 11324 | 41692 | A | 11392 | 1 | 993 | |
| 11325 | 41693 | A | 11393 | 3 | 1127 | TKETRFIHGPKTPAPVTDWEGS LPLVFNHCRDASLIHSRFGVR PHRDTCLGPSPLAASPFLGKG QAAHCQAELSPNSSASTPPPY NPSITSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVRVHVP FSLSDLSQISQCLGSFSSDPTKY TQEFQCLTSLYNLTWSDLNVIL TSTLSPDEWERVSSLAQSHADN VPGFTSQTSRKALEQFPE/TDPQ WNHQANSPGIARRDYMVSCLV EGLKKAAYKAVNYDKLKETTQ GEDENPAQVVARLAATLRRFT ALDPEGPEGRILNMHFITQSAP DITKKLQKLESGPQTPOQELINL TFKVHNNGEETDAARSPWKPP GPSRTPSFRACFPCPHNFCGY |
| 11326 | 41694 | A | 11394 | 1 | 312 | |
| 11327 | 41695 | A | 11395 | 1 | 244 | MFADR*LFSTTHQSIVPLYLALF GA*AGVLATAISLLIRAELGQP GNLLGNDHIYNVIVTAHAFVHIF FIVIPHIIGGFGN*LVPLIIGAPDM AFPRINNISF*LLPPSLLLLASA IVEAGAGTRLNKSYPPLAGNY SHPWKPPVDLTIFSLHLAGVSSI LGAINFITTIINIKPPAITQYQTPL FV*STTHQSHRTTIPIYSAHELA SSPQPLSLLIRAELGQPGNLLGN DHIYNVIVTAHAFVHIFVIVPIIIG GFGN |
| 11328 | 41696 | A | 11396 | 1 | 1287 | |
| 11329 | 41697 | A | 11397 | 3 | 583 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 11330 | 41698 | A | 11398 | 3 | 419 | ILSISKLR TSLAGEGSVDTPKAS GVTRHIKGP GVAAEMSAFILPL PG*VSPGWEWAASAVLNLRT TLALRRGVCLIRSRPGLGLED GASPRTESLHTGTACKGAVDGS SEVDEKLKRIALDFLGLHGGDD PRSSWH |
| 11331 | 41699 | B | 11399 | 1 | 1242 | |
| 11332 | 41700 | C | 11400 | 504 | 755 | |
| 11333 | 41701 | A | 11401 | 155 | 710 | ETETTGEREGSLSNHPSNPTAA GLSLDTMKSHCPNHSSLLSTAA SPPKLWRCFKEEH\ELAVLGAP PKLLPPTSHRDPTSASVYLRA P THVVWSL FKHPLS*TPCCMGFI AFA\YSVKSRDRKIGCERDPGPI AYASTAK\CLNIWALILGLLHD HSGSSSPVLIVPGLWDRSGGIT GGQELCP |
| 11334 | 41702 | A | 11402 | 1 | 1158 | |
| 11335 | 41703 | A | 11403 | 80 | 996 | LKGKFLMSG\ALDVLQMKEE DVLKFLAA\GTHLGGTNLD\FH MEQYIYKRKSDGIYIYLMRTW EKLL\LAARAIVAIENPADVSAI SSRNTGQRAVLKFAAATGATPI AGRFTPGTFTNHIQAARE\PRIL LVVTDPRADHQPLTEASYVNL P TIALCNTDSPLRYVDIAIPCNNK GAHSVGLMWWMLAREVLRM RGTISREHPWEVMPDLYFYRDP EEIEKEEQAAAEKAVTKEEFQ G EWTAPAPEFTATQPEVADWSE GVQVPSVPIQQFPTEDWSAQPA TEDWSAAPTATQATEWVGATTD WS |
| 11336 | 41704 | A | 11404 | 1 | 819 | |
| 11337 | 41705 | A | 11405 | 1 | 1032 | |
| 11338 | 41706 | B | 11406 | 63 | 344 | |
| 11339 | 41707 | A | 11407 | 49 | 281 | FFKSTVCSFQKQFQTLVPPIGGS IMY*DISDHRGQR**NVGPCGH |
| 11340 | 41708 | A | 11408 | 985 | 1213 | TQCVTINY*GMKWGSFGYIVFH KDGCALIDKRFTFCVSFKGSQ IQSSAAFLIPDVQVHQRLQKDF QGLMPVIVGS |
| 11341 | 41709 | A | 11409 | 1 | 774 | |
| 11342 | 41710 | A | 11410 | 3 | 249 | |
| 11343 | 41711 | A | 11411 | 3 | 619 | |
| 11344 | 41712 | A | 11412 | 3 | 493 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11345 | 41713 | A | 11413 | 3 | 292 | DALPRWPSGSGDGGAVREAGQ QGTRLERPAAVLIRAADPGRRT QALA/GLPRG*PHPRMDPPESFQ ATGGTQQMTSTAPSWLTM*LR SVSGW*ELKD |
| 11346 | 41714 | B | 11414 | 190 | 315 | |
| 11347 | 41715 | A | 11415 | 227 | 545 | |
| 11348 | 41716 | A | 11416 | 1 | 1896 | |
| 11349 | 41717 | B | 11417 | 52 | 1822 | |
| 11350 | 41718 | A | 11418 | 1 | 458 | |
| 11351 | 41719 | C | 11419 | 196 | 327 | |
| 11352 | 41720 | A | 11420 | 258 | 375 | TRALSKFGSSRVEQS*AGYSGP GTP*EGGSGILGETVC |
| 11353 | 41721 | A | 11421 | 3 | 854 | |
| 11354 | 41722 | A | 11422 | 1 | 434 | MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDKEKACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF |
| 11355 | 41723 | A | 11423 | 1 | 642 | |
| 11356 | 41724 | A | 11424 | 260 | 534 | |
| 11357 | 41725 | A | 11425 | 1 | 438 | |
| 11358 | 41726 | C | 11426 | 391 | 750 | |
| 11359 | 41727 | A | 11427 | 786 | 926 | AQQQRQETIQGGRSLSRTL* GRSGTSLSQKLAQLSSLTGDST |
| 11360 | 41728 | A | 11428 | 488 | 649 | VLQLLKVAHPELFIPPGGFVFSL TSGVKLHT*ALQLLKVAHPELL IPPGSWSH |
| 11361 | 41729 | A | 11429 | 1 | 2028 | |
| 11362 | 41730 | A | 11430 | 1022 | 1417 | SLMGTSTSSALGMHVPRITRD VLSAPVIVSGNTAKFCTMLGHF LKKTRTERRDIQAP*SFISLPPKS TWEKLSSAAMVSTLR*GASDQ K/C*LLGGNDRVSLIVIQVEGAPL QDPGTLGRLLQSLTVKRISV |
| 11363 | 41731 | A | 11431 | 1 | 535 | |
| 11364 | 41732 | A | 11432 | 3 | 1186 | |
| 11365 | 41733 | A | 11433 | 201 | 458 | QVDGCIPELV*F*KKRGRRRGR RGRRRRRRRGRREEGGGGGGG SFWRTHHTKPKDQHKKDTMG HFRSCAFQEGFVVHVPLLSSEK |
| 11366 | 41734 | A | 11434 | 1392 | 1532 | AQQQRQETIQGGRSLSRTL* GRSGTSLSQKLAQLSSLTGDST |
| 11367 | 41735 | A | 11435 | 1253 | 2820 | |
| 11368 | 41736 | A | 11436 | 1504 | 1718 | VIGIWALALGILARPQRGFHV HLQDVGGAAA*AAKGLLRNVV R**VDQVQVSGAQGIAGVVVT VGGEEDF |
| 11369 | 41737 | B | 11437 | 1 | 1383 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11370 | 41738 | A | 11438 | 3 | 310 | VHGRASSLGVG/TPIPKGHGQIK P/DRLKPPVYGACKLLDMELEM AFFVGPGNRLGEP/IPISKAHEPI FGMVLNNAWSARHIQKWEYV PLGPFLGKSFGTPVKSS |
| 11371 | 41739 | A | 11439 | 1 | 1337 | MSFIPVAEDSDFPIHNLPGVFS TRGDPRPRIGVAIGDQILDLSIK HLFTGPVLSKHQDVFNQPTLNS FMGLGQAAWKEARVFLQNLLS VSQARLRDDTELKCAFISQAS ATMHLPATIGDYTDFYSSRQHA TNVGIMFRDKENALMPNWLHL PVGYHGRASSVVSGTPIRRPM GQMKPDDSKPPVYGACKLLDM ELEMAFFVGPGNRLGEPISKA HEHIFGMVLMNDWSARDIQKW EYVPLGPFLGEEFWGHCLLPW VVPMDALMPFAVNPQKQPRG PCRYLCHDEPYTFDINLSVNLK G\EGMSQAATICKVQILKMYMY WT\MLQQAHSPTLSNGC\NL\RP GDLLGFLGP\NSGPGAQKNFGS\ MLELSWKGTKPID\LGNGQTR KFLLD\GDEVIIITAMATRDFKW YS\QGDGY\RIGFGQ\CAGKVLP ALLPIMRFFLLF |
| 11372 | 41740 | B | 11440 | 100 | 383 | |
| 11373 | 41741 | A | 11441 | 1 | 263 | MEYYAAIKKDEFMSFVRIWMK LETIILSKLSQGQKTKHRRFSLI DG/IHRSFTRTENSQRTGRKC WN**PTCGLARSWFGKTWSGN |
| 11374 | 41742 | A | 11442 | 2 | 160 | |
| 11375 | 41743 | A | 11443 | 150 | 308 | CLHR*GRGSPRPGGGSTGGA GPGAGPSLAPPLPAQNAEGLGG RRRGNKYL |
| 11376 | 41744 | A | 11444 | 1 | 372 | |
| 11377 | 41745 | A | 11445 | 49 | 177 | SQQGLYAKPTSSQAL*GDGQAS AEMGRILSYE*EHAVFGFSSL |
| 11378 | 41746 | B | 11446 | 1 | 420 | |
| 11379 | 41747 | C | 11447 | 1 | 334 | |
| 11380 | 41748 | C | 11448 | 1 | 268 | |
| 11381 | 41749 | C | 11449 | 1 | 564 | |
| 11382 | 41750 | A | 11450 | 1 | 264 | |
| 11383 | 41751 | A | 11451 | 33 | 194 | |
| 11384 | 41752 | C | 11452 | 1 | 309 | |
| 11385 | 41753 | A | 11453 | 1 | 738 | |
| 11386 | 41754 | A | 11454 | 1 | 2028 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11387 | 41755 | A | 11455 | 3 | 1008 | LKDAVFSIRISPESQKLFAFQWE DPESGVTTQYTWTLTQGFENS PTIFGEALARDLQKFPKDLGCI LLLYMDDLGLGHSTAVRCAKG MDALLQHLEDGKGVSKKKA QICRQQVTKWGDWERFEWEPL QQQAFCKLKEKFMSAPALGLP DLTKPFTLYVSEKTAAGVLI QTVGPWPTPVAYLSKQLDGVS KGWPPCLRALAATALLAQEAD KLTLVQNLNIKAPHAVGTSAG KPELIALTRALESEGTMKLE THLSKLSQGGK/DQTLHVLGTIS RST*ACSCLASLQVGLETGSQL SLENPLRVGIQRRRCFTCAVDG EGFLLGVPMA |
| 11388 | 41756 | A | 11456 | 677 | 879 | KRRNHQILEIRSHLQSVEDNLK SGLGSTASL*MSWTQPRNGAE VGFLILGYIKETPRNAETPSMV |
| 11389 | 41757 | A | 11457 | 1 | 624 | |
| 11390 | 41758 | A | 11458 | 3 | 130 | VEEEQGHSEFRNAR*IISW*RNEN GLDRMDCSCRNGERDKGHG |
| 11391 | 41759 | A | 11459 | 1 | 1477 | MADPPWSSVQVKNKYDSGLLSS VSAEPLASSASSHPGMSDNAPA SLESGSSSTPTNCSTSSAIPQPGA ATKPWRSKLSVKHSATVSML SVKPPGPEAPRPTPEAMKPAPN NQKSMLEKLLFNSKGGSKAG EGPGSRDTSCERLETLPSEFESE ELEAASRMLTTVGPASSSPKIAL KGIAQRTFSRALTNNKSSLKGN EKEKEKQQREKDKESKDLAK RASVTERLDLKEEPKEDPSGAA VPEMPKKSSKIASFIPKGGKLNS AKKEPMAPSHSGIPKPGMKSM GKSPSAPAPSKEGERSRSGKLSS GLPQQKPQLDGRHSSSSSLASS EGKGPGGTTLNHSSSQTVSGS VGTTQTGNTSVSVQLPQPQQQ YNHPNTATVAPF*EGFHLP*HA *VITF*TANYASSDNDLVGYT H*LTASEFFQSRSSSLGEVAGLH AHTC*A*LGSNIPFSVRLRPVA ASAEDLRGHQGLIKDRAQVS |
| 11392 | 41760 | A | 11460 | 1 | 327 | LLLMGLKHNVLKLPKPMVTL RESVWETLNFLK*SFV*LNMLIF KKSS*RLQ*VRFHFLCPRVLIVQ LPFMSENMRCLVFCSCVSLLRM MVSSFIHVPPFKVLSFFALG |
| 11393 | 41761 | B | 11461 | 119 | 203 | |
| 11394 | 41762 | B | 11462 | 1 | 677 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11395 | 41763 | A | 11463 | 2 | 74 | |
| 11396 | 41764 | A | 11464 | 1 | 1256 | MSASQDSRSRDNGPDGMEPEC VIESNWNEIVDSFDDMNLSESL LRDIAYGFEEKPSAIQQQAILPC IRGYNVIAQARSGTGKMATFAI SILQQIELDLKATQALVLAPTRE LAQQIQKVVMALVDYMGASC HACVRGTNMRAEVQKLQMEA PHIIVGTPSRVFDMLYR\RYLAP\ KSIRMLVLNEADEMLSRGFKG QIY\DISKRNLNSTTK\VVLLSAT MPFD\LEVTKKFMGRPH\IRIL VKKEELPLEGIRHFYINVEPEE\F NLDTLCDWYEP*PIT\QAVIFHQ PPGGKVDW/LSPEKMHARDST VPPMHGDMTKKE\RD\VIMREF RSGS*PEF*ITPLTLPQRPLMC QPGFL*SFKLMTLPPPTRGKLLI HRNRSRVDRFGRKGVA\INMVT EED\KRTL\RDIEIFYNTSIEEMP |
| 11397 | 41765 | A | 11465 | 1 | 402 | KSRGRGLPYTMDAFMLGMGM LKYPNFVAT*ARGYPGFAPSYG YQFPGFPAAAYGPVAAAAVAA ARGSGSNPARPGGFGANSPGP VADLYGPASQDSGVGNYSAA PQPGSGFR/HTGIAGPLIATAFT NGYH |
| 11398 | 41766 | A | 11466 | 226 | 486 | |
| 11399 | 41767 | A | 11467 | 2 | 432 | |
| 11400 | 41768 | A | 11468 | 1 | 834 | |
| 11401 | 41769 | A | 11469 | 205 | 570 | |
| 11402 | 41770 | B | 11470 | 61 | 939 | |
| 11403 | 41771 | A | 11471 | 96 | 269 | |
| 11404 | 41772 | A | 11472 | 123 | 593 | VAVLEARLLSPVRASKMTKKR RNNGRAKKGRGHVQPIRCTNC ARCVPKDKA\IKKFVIRNIVEAA A\VRDISEASVFDAAYVLPKL\YV KLHYCVSCAIHSNVVMESISVK ARKD\RTPPPRFRPGGCWPHVP PPKPNVRELEFFKDLKDRLISS WEEK |
| 11405 | 41773 | A | 11473 | 1 | 228 | |
| 11406 | 41774 | C | 11474 | 187 | 423 | |
| 11407 | 41775 | A | 11475 | 1 | 546 | |
| 11408 | 41776 | A | 11476 | 1 | 1254 | |
| 11409 | 41777 | A | 11477 | 1 | 1386 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11410 | 41778 | A | 11478 | 1 | 1445 | HLKAKMGKEKTHINIVVIGHVD SGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVL DKLKAERERGITIDISLWKFETS KYYVTIIDAPGHRDFIKNMITGT SQADCAVLIVAAGVGEFEAGIS KNGQTREHALLAYTLGVKQLI VGVNKM DST EPPYSQKRYEEIV KEVSTYIKKIGYNPDTVAFVPIS GWNGDNMLEPSANMPWFKGW KVTRKDGNASGTTLLEALDCIL PPTRPTDKPLALPLQGVH\KLG GIGTVSSAPMET\GFSNPGMVV TFAPSPR*QRKVKSVE\MH\HEA L\NEALSGEQCGLSMSKKVSVK ECFVRGN\VAG*PAKNDPTQWE ASWLSLLQVIILEPSQAQISAGL CPLYWDC\HTGSHLHAKFAELK EKIDRR\SGKKV\EDGPKIL/RS LDAAIVDMV\PG\RPMCVESFS DYPPLGRFAVRDMRQTVAVGV IKAVDKKAAGAGKV\TKSAQK |
| 11411 | 41779 | A | 11479 | 1 | 996 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11412 | 41780 | A | 11480 | 1 | 1875 | MPSDLAKKKAACKKEAAKAR QRPRKGHEENGDVVTEPQVAE KNEANGRETTEVDLLTKELEDF EMKKAARAVTGV LASHPNST DVHIINLSLTFHGQELLSDTKLE LNSGRRYGLIGLNGIGKSMLLS AIGKREVPPIEHIDIYHLTREM PSDKTPLHCVMEVDTERAMLE KEAERLAHEDAECLELMELYE RLEELDADKAEMRASRILHGLG FTPAMQRKKLKDFSGGWRMR VALARALFIRPFMLLLDEPTNH LDLDACVWLEELKTFKRILVL VSHSQDFLNGVCTNIIHMHNKK LKYYTGNYDQYVKTRLELEEN QMKRFHWEQDQIAHMKNYIAR FGHGSAKLARQAQSKEKTLQK MMASGLTERVVS DKTLSFYFPP CGKIPPPVIMVQNV SFKYTKDG PCIYNNLEFGIDL DTRVALVGP NGAGKSTLLKLLTGELLPTDG MIRKHSVVKIGRYHQHLQEQ LDLSPLEYMMKCYPEIKEKEE MRKIIIGRYGLTGKQQVSPIRNL SDGQKCRVCLAWLAWQNPHM LFLDEPTNHLDIETIDALADAIN EFEGGMMMLVSHDFRLIQQVAQ EIWVCEKQTITKWPGLDILAYK EHLKSKLVD EEPQLTKELPTTC |
| 11413 | 41781 | A | 11481 | 194 | 418 | YGLASVSPTQISSSSCNPWMFE GGTLVGGDWIGSHDSEGLTR SGCLISVWHFSCAVSPATL*RR LLLLRLPP |
| 11414 | 41782 | A | 11482 | 1 | 675 | |
| 11415 | 41783 | A | 11483 | 1 | 1125 | |
| 11416 | 41784 | A | 11484 | 1 | 711 | |
| 11417 | 41785 | A | 11485 | 673 | 796 | |
| 11418 | 41786 | A | 11486 | 3 | 570 | RLQEFGTRNRHLPVNSPKLTNT KGKRRGTRVYMF SRPFRKHGV VPLATYMRIYKKGDIVDIKGM GTVQKGMPHKCYHGKTGRVY NVTQHA/VMGIVVYKQA*GQR FLPKRI*CCVIEH\KHSKSRDSF \LK\RVKENDQKKKEAKE\KGT W\VQL\NRQLAPPREAHFVRTN G\KEPGACWNPIPYEFHGHNR |
| 11419 | 41787 | A | 11487 | 1 | 2091 | |
| 11420 | 41788 | A | 11488 | 1 | 2208 | |
| 11421 | 41789 | A | 11489 | 430 | 1032 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11422 | 41790 | A | 11490 | 3 | 1158 | EDQIDRLDFIRNQMNLLTLDVK KKIKEVTEEVANKVSCAMTDEI CRLSVLVDFCSEFHPNPDVLKI YKSELNKHIEDGMGRNLADRC TDEVNALVLQTQQEIIENLKPLL PAGIQDKLHTLIPCKKFDLSYNL NYHKLCSDFQEDIVFRFSLGWS SLVHRFLGPRNAQRVLLGLSEPI FQLPRSLASTPTAPTTATPDNA SQEELMITLVTGLASVTSRTSM GIIIVGGVIWKTIGWKLLSVSLT MYGALYLYERLSWTTHAKERA FKQQFVNYATEKLRMIVSSTSA NCSHQVKQQIATTFARLCQQV DITQKQLEEEIARLPKEIDQLEKI QNNSKLLRNKAVQLENELENF TKQFLPSSNEGSVTIEIALVTLIG GNNRL |
| 11423 | 41791 | A | 11491 | 132 | 381 | SKAESVFPPTLPRQRPAAAAGP HWGAG*GQDEAGLHPGPEDRG FLRETPADPGLQAGLGQVHPPR SRADPPAPYQVPPRMGT |
| 11424 | 41792 | B | 11492 | 129 | 470 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11425 | 41793 | A | 11493 | 1 | 1955 | FVSCQAPWSHPPAQLSPVGADA MTLTLSVLICLGLSVGPRTC VQAGTLPKPTLWAEPASVIARG KPVTLWCQGPLETEEYRLDKEGL PWARKRQNPLEPGAKAKFHIPST VYDSAGRYRCYYETPAGWSEP SDPLELVATGFYAEPTLLALPSP VVASGGNVTLQCDTLDGLLTF VLVEEEQKLPRTLYSQKLPKGP SQALFPVGPVTPSCRWRFR CYYYYRKNPQVWSNPSDLLEIL VPGVSRKPSLLIPQGSVVAR GGSLTLQCRSDVG YDIFVLYKEGEHDLVQGS GQQPQAGLSQANFTLGPV SRSHGGQYRCYGAHNLS PRWSAPSDPLDILIAGLIP DIPALSVQPGPKVASGEN VTLLCQSWHQIDTFFLT KEGAHPPLCLKSKYQSY RHHQAEFMSMPVTS AQGGTYRCYSAIRSY PYLLSSPSYPQELVV SGPSGDPSLSPTG STPTPGPEDQPLTPT GLDPQSGLGRHLG VVTVSVAFVLLLFL LLFLLLRHRHQS KHRTSAHFYRPAGA AGPEPKDQGLQKR ASPVADIQEEILNAA VKDTQPKDGVEMD ARAAASEAPVQDV TYAQLHSLTLRREA TEPPPSQEREPPA EPSIYAPLAIHLA HG GPRSHTQQKET QRLQKARELPP VDTNEPQPAWDP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11426 | 41794 | A | 11494 | 22 | 1991 | GLIPLQSAGSPEGDAMTPALTA LLCLGLSLGPRTRVQAGPFPKP TLWAEPGSVISWGSPVTIWCCG SLEAQEYQLDKEGSPEPLDRNN PLEPKNKARFSIPSMTQHHAGR YRCHYYSSAGWSEPSDPLELV MTGAYSKPTLSALPSPVVASGG NMTLRCSQKRYHHFVLMKEG EHQLPRTLDSQQLHSGGFQALF PVGPVNPSHRWRFTCYYYMN TPRVWSHPSDPLEILPSGVSRKP SLLTLQGPVLAPGQSLTLQCGS DVGYDRFVLYKEGERDFLQRP GQQPQAGLSQANFTLGPVSPSN GGQYRCYGAHNLSSEWSAPSD PLNILMAGQIYDTVLSAQPGP TVASGENVTLLCQSWWQFDTF LLTKEGAHPPLRLRSMYGAH KYQAEFPMSPVTSAHAGTYRC YGSRSSNPYLLSHPSEPLELVVS GHSGGSSLPTGPPSTPGLGRYL EVLIGVSAFVLLLFLLLFLLLR RQRHSHKRTSGLRLCPSSPRPE K\ADFQRPAGAAETEPKDRGLL RRSSPAADVQEENLYAAVKDT QSEDGVEIYTRQSPHDEDPQAV TYAEVKHSRPRREMASPPSPLS GEFLDTKDRQAEEDRQMDTEA AASEAPQDVTYAQLHSLTLRRE ATEPPPSQEGPSPAVPSIYATLAI |
| 11427 | 41795 | A | 11495 | 1 | 1818 | |
| 11428 | 41796 | A | 11496 | 3 | 574 | IRCSSVDPRVRPRVRGASGAAA YCCRHVSIPRDHTTHNQSRKW HRNGIKKPRSQRYESLKGVDPK FLRNMRFAKKHNTKGLKKMQ ANN\AKAMSARAEAIKALVKP KEVKPKIPKGGQPINLIRLAYIA HP\KLGKRARARI\AKGLKLCRP K\AKAKAKAKAKDQTKAQAA APASVPAQAPKRTQAPT KASE |
| 11429 | 41797 | B | 11497 | 45 | 331 | |
| 11430 | 41798 | A | 11498 | 1 | 1779 | |
| 11431 | 41799 | A | 11499 | 1 | 837 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11432 | 41800 | A | 11500 | 3 | 557 | ERGYSFTTTAERDIVRDIKEKLC YVA\LDFEQEMATAASSSSLEES YE\LPDGGVITIGNE\RFRCPEAL FQPSFLGMESCGIHETTF\NSIM K\CDVDIRKDLYANTVLSGGTT MYPGFADRMQKEITALAPSTM KIKIIAPPERKYSVWIGGSILAS LSTFQQMWISKQEYD\ESGPS\I VHRKCF |
| 11433 | 41801 | A | 11501 | 1 | 1188 | |
| 11434 | 41802 | A | 11502 | 1 | 684 | |
| 11435 | 41803 | A | 11503 | 1 | 1398 | |
| 11436 | 41804 | A | 11504 | 22 | 1239 | |
| 11437 | 41805 | A | 11505 | 837 | 971 | |
| 11438 | 41806 | C | 11506 | 1 | 3018 | |
| 11439 | 41807 | A | 11507 | 23 | 368 | |
| 11440 | 41808 | A | 11508 | 1 | 816 | |
| 11441 | 41809 | A | 11509 | 1 | 441 | |
| 11442 | 41810 | A | 11510 | 195 | 293 | IKVSPSGRDPVRDN*ITW*FLPY CSSTTGSLH |
| 11443 | 41811 | A | 11511 | 56 | 372 | MELPASPALFARTPQPLGGRW DWAPWSRGWRSSRRLGPHRSP RRGSEAQA WRAAGPEPCPAGR QLRPVNIEWLFALILTHTFGTQ VLA*TSQALI*NPRVLYPD |
| 11444 | 41812 | B | 11512 | 108 | 326 | |
| 11445 | 41813 | A | 11513 | 3 | 326 | GSKKKFH*HSRILERSRSWRTS YQGRPQEPSWLHPVDPHRGCR WSCLPVPCRAPSTPQPLGGRWD WAPWSRGRRLSGRLGPHRSPR NRGRLRHGGLQVPSRASQEGS |
| 11446 | 41814 | A | 11514 | 3 | 619 | VRDIHGSPTTHRPGLRGKNGF VGEARDPRYRSGHCFRECRTO ALVAFT*C*SCGFTEVK*GLSC LPAGQGS GPAARHV*ASHPLHG LPCGPSLP/NRAPPTPRRPVPST TQGLRNASARRGTGRQLHLQP WCGIH*VKPAGLLSLLHGQAC GDPATPSRERLSQPAVPTALGS RRRLLLGPA GSPGSSLPPSRQPP GGRRRPP |
| 11447 | 41815 | B | 11515 | 1 | 1524 | |
| 11448 | 41816 | A | 11516 | 1 | 1365 | |
| 11449 | 41817 | B | 11517 | 1 | 654 | |
| 11450 | 41818 | B | 11518 | 1 | 795 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11451 | 41819 | A | 11519 | 486 | 929 | QKQEESWPEDTYPRALAAFP GRARDLQAMPEPPTLSMGSC APEPPRGAPPPAPRRRIPSTTQG LRSSGAGRRTCRQLHLQPRCRI HWVKPAGLLSLWLFQMHSASC WWNYHSGAWRMVALFSWLH* ECPSGESGAPILHFPFALP |
| 11452 | 41820 | A | 11520 | 35 | 473 | VLQLLRHVWSCSFPPGVVVS ALAVKLQTFVTQEPSWLHPVD PAPGLQVELPASPLQCTRSTSQPL GGRWDWAPWSRGRSSGRLGP HRSPWRG*EAQAWRAAGPEP/ WPRGKA/C*GPARNRAKRRFPH CTF*EEVTVCSPPQKRGGD |
| 11453 | 41821 | A | 11521 | 23 | 229 | RSWNPQTLFVGMYNATAAWK PI*QFLKKNMKLP*DPGREPLN QTG*KGKRGGQEAFLKGISSR MSQ |
| 11454 | 41822 | B | 11522 | 152 | 901 | |
| 11455 | 41823 | A | 11523 | 1 | 3063 | |
| 11456 | 41824 | A | 11524 | 242 | 263 | VLQLIKAVWTQRTQEPSWLHP VDPALGLQVELPASAPCACTP QPLG\PLLPGLPLWRHLRSPSVH HCTVGAPFWAGQGRSPLPQRR CALFLAGP |
| 11457 | 41825 | A | 11525 | 1584 | 2082 | QRAGSPHSPRSLVPPPLPGLPLW RHLRSPSAHRCMTMGAPFWAGQ GHSRLPQLAGRRGGRGASGNR CCVQRLQASWSSRWAWRA PHSEQPAGPAGPGQ*GTWHPG QRLQRMVWVLQQCRLTGAVL DFSPGLSCLPAGQGS GPAARHA *AFHPLHGLLCGRSLPD |
| 11458 | 41826 | A | 11526 | 1293 | 1558 | CIQHCHHCCCRCRASAAGAA SLQGSTHVRIQH\CTP\CPVLLTP SVRLRDVCTRSIWPLVVTGLPS AMNVSSWCSTSSPAFGVLVLWI |
| 11459 | 41827 | B | 11527 | 179 | 1031 | |
| 11460 | 41828 | A | 11529 | 1 | 342 | |
| 11461 | 41829 | A | 11530 | 1 | 3081 | |
| 11462 | 41830 | A | 11531 | 1 | 371 | |
| 11463 | 41831 | A | 11532 | 1 | 501 | |
| 11464 | 41832 | A | 11533 | 1 | 836 | |
| 11465 | 41833 | A | 11534 | 88 | 573 | |
| 11466 | 41834 | A | 11535 | 1 | 675 | |
| 11467 | 41835 | A | 11536 | 1239 | 1556 | FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFFLRFWSFAVVAQAV\ VQWHNLSSLPGFKQFSCLSLP SSWDYRCPPPRPANFCIFTRDG VSPCCPGWSRTSDLR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11468 | 41836 | A | 11537 | 2 | 375 | ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTLDPEKALRDA KLDKSQIHDIIVGGSTRIPKIQ KLLQDFYEAVAYGA AVQAAIL SGDKSENVQDLLSLDVTPFP LGIETAGGVMTVPH |
| 11469 | 41837 | A | 11538 | 2 | 295 | NRMGNHFIAEFKRKHKKDISEN KRAVRLRTACERAKRTL/SSST QASIEIDSLYEGIDFYTSITRAPF EELNAWGISWWWLPPPVGAS SGPTIEEVD |
| 11470 | 41838 | A | 11539 | 1 | 1659 | |
| 11471 | 41839 | A | 11540 | 1 | 810 | AGKPHCGGEFCTPNVHHFFR*F *ANPKRTII/ENKEALTPPTV/C* RAKPTLSSAPRAVI/EIDSS*E/GI GLYTSITPPRFEELNADLFLAPL TPVEKALRNA\KLDKSQIHDIIVL \GGSTRIPKIQSFLQDFNGKE LNKSINPDEAVAYGA AVQAAIL SGDKSENVQDLLLDVTPLSLG IETAGGVMTVLIKRNTTIPTKQT QTFTTYSN\NQPGVLIQVYEGER AMTKDNNLLGKFELTGMPGG MPGGFPGGGAPPSGGASSGPTI EEVD |
| 11472 | 41840 | B | 11541 | 848 | 2399 | |
| 11473 | 41841 | A | 11542 | 1 | 876 | |
| 11474 | 41842 | A | 11543 | 16 | 1203 | SIPHEPWPVSLLLFQEQVPGKK ELRKGLALLEAIISICGSLDKVL KEKRKLFHSMGEGTINGLLDE LLQTRVLNQEEMEKVKRENAT VMDKTRALIDSVIPKGAQACQI CITYICEEDSYLAETLGLSADQT SGNYLNMQDSQGVLSFPAPQ AVQDNPAMPTSSGSEGNVKLC SLEEAQRIW\EQKSAEIYPIMDK SSRT\RVALLICNEEFDSIPRRTG AEVDITGMTMLLQNLGYSVDV KKNLASDMTTELEAFARPE HKTSDSTFLVFMHSHGIREGICG KKHSEQVPDILQLNAIFNMLNT KNCPSLKDKPKVIIIQACRGDSP GVVWFKDSVGVSGNLSLPTTE EFEDDAIKKAHIEKDFIAFCST PDNVSWRHPTMGVSFIGRLIEH |
| 11475 | 41843 | A | 11544 | 2 | 654 | |
| 11476 | 41844 | A | 11545 | 3 | 291 | LIPLLRPLVQSGGIPMGKFMK PGKVVLVLAGRYSGRAVIVR YSVDIPLDKTVVNKDVFDPAL KRKARREAKVKFEERYKTGKN KWWFQKLR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11477 | 41845 | A | 11546 | 157 | 386 | |
| 11478 | 41846 | A | 11547 | 2 | 531 | FWQESASGHLWLSGFLSGPFSL LSAEMGKFMKPGKVVLVLAGR YSGRKAIVVKNIDGTSRDPYS HALVAGIDRYPRKVTAAMGKK KIAKRSKIKSFVKVYNYNHLM TRYSDIPLADKTVVNKDGFTD PALKRNARMEA\KVKFEERYK TGKNKWFF\QKLRVLD AFVLI KNYKE |
| 11479 | 41847 | A | 11548 | 1 | 414 | LGGLKGTWGETKPAMAAAE DGGPEGPNRERGGAGATKLL YTG NHLFSPQWLETRPERQ VCKAGISREKVVGESLLTF HFLRLKTPQICRLPV*LFLPP* GFQPF GDTGGFHF SFGVGA FPFGF FNPSY |
| 11480 | 41848 | A | 11549 | 1 | 654 | |
| 11481 | 41849 | A | 11550 | 3 | 663 | RGQEVVSGLLGRVYVYLGG LKG TWGETKPAMASAE E\SGAPN VPNRERGGAG RPKTPFECNICL ETARE AVVSVC GHL YCW PCLH QWLETRIPERQECPVCKAG ISREKVVP L YGRGS/Q RSPQDPRIK NSPRPPGGR GPAE\SRGGSQPF GDT GGFHF SFGVGA FPFGF FTT VFNAHEPFRRGTG VDLG\QGH PSLQLGKE FPLPGFSAIFFLFWL |
| 11482 | 41850 | A | 11551 | 3 | 369 | |
| 11483 | 41851 | A | 11552 | 375 | 851 | |
| 11484 | 41852 | A | 11553 | 1 | 927 | |
| 11485 | 41853 | A | 11554 | 104 | 845 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11486 | 41854 | A | 11555 | 200 | 1496 | ETIQAVVFMSLHFLYYCSEPTL DVKIAFCQGFQDKQVDVSYIAKH YNMSKSKVDNQFY SVEVG DST FTVLKRYQNLKPIGSGAQGIVC AAYDAVLDRNVAIKKLSRPFQ NQTHAKRAYRELVL MKCVNH KNIISLLNVFTPQKTLEEFQDVY LVMELMDANLCQVIQME LDHE RMSYLLYQMLCGIKHLHSAGII HRDLKPSNIVVKS DCTLKILDF GLARTAGTSFM MTPYVVTRY Y RAPEVILGMGYKENVDIWSVG CIMGEMVRHKILFPGRDYIDQW NKVIEQLGTPCPEFMKKLQPTV RNYVENRPKYAGLTFPKLFPDS LFPADSEHNKLKASQARDLLSK MLVIDPAKRISVDDALQHPYIN VWYDPAEVEAPPPQIYDKQLD EREHTIEEWKELIYKEVMD SVEE KT*KWC*LKGQPS\SAQVQQ |
| 11487 | 41855 | B | 11556 | 56 | 1564 | |
| 11488 | 41856 | A | 11557 | 1 | 970 | |
| 11489 | 41857 | A | 11558 | 1 | 903 | |
| 11490 | 41858 | A | 11559 | 237 | 479 | PVGTNTECEIPFQPMETGHSSR VDASGYK*PCLLC SVYSRGKTA GECTLF*VHHFLSSLCPVNLGA NNQLHYIPWFSTDG |
| 11491 | 41859 | A | 11560 | 1 | 477 | |
| 11492 | 41860 | A | 11561 | 125 | 1133 | |
| 11493 | 41861 | A | 11562 | 1 | 837 | |
| 11494 | 41862 | A | 11563 | 2 | 708 | CQHYKFRYHQQGEQEPP LN PHGAARAEVYL RKCTFDMFNF LASQHRVLPEGATCDEEDEVQ LRSTRATSLELPMAMRFRHLK KTSKEAVGVYRSAIHGRGLFCK RNIDAGEMVIEYSGVIRSVLTD MRKKFYDGKGIG\CYMF SMDD FDVV DATMHGNAARFINHSCE PNCFSGVIPGGGPENKIVIFGLR RILGGEEVNLRTKKFPIE\DAK\N KLPC\NCGAKRCRRFLN |
| 11495 | 41863 | A | 11564 | 2 | 136 | |
| 11496 | 41864 | A | 11565 | 1 | 551 | AILYAKRASVFVKLQKPNAAIR DCDRAIEINPDSAQPYKWRGKA H/RAQKIAEHRRKYERKREEREI KERIERVKKAREEHERA QREEE ARRQSGAQYGSFPGGFPGGMP GNFPGGIPGMGGGMPGMAGM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQN PANMSKYQSNPK VMNLISKLSAKK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11497 | 41865 | A | 11566 | 1 | 804 | |
| 11498 | 41866 | A | 11567 | 64 | 1215 | PPSFAHHLPTMDPRKVNELRAF VKMCKQDPSVLYTEEMRFLRE WVESIGGKVPPATQKAISEENT KEEKPDSSKVEEDLKADEPSSE ESDLEIDKEGVIEPDTDAPQEM GDENAEITEEMMDQANDKKVA AIEALNDGELQKAIDLFTDAIKL NPRLAILYAKRASVFKLQKPN AAIRDCDRAIEINPDSAQPYKW RGKAHRL\LGHWEEAAHDLAL ACKLDYDEDASAMLKEVQPR QKIAEHRRKYERKREEREIKERI ERVKKAREEHERAQR\EEARR QSG\AQYGSFPGGFLGG\MPGN FP\GG\MPGMGGG\MPGMG\GM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPA\NMSKYQSNP K\VMNLISKLSAKFGGQA |
| 11499 | 41867 | A | 11568 | 1 | 265 | VKAKIQDKEGIPPDQQLIFAG KQLEDGRTLSDYNIQKESTLHL VLRLRGGIIEPSLRQLAQKYNC DKMICR/KKCGHTNNLRPKKK |
| 11500 | 41868 | A | 11569 | 3 | 318 | |
| 11501 | 41869 | A | 11570 | 7 | 57 | RFFNFLGGIP/P*SGPKGMTL/DQ TQGSKSKQIQWPALTFKPLVER NIPSSVTAVEFLVDKQLDFLTE DSAFQPYQVRNFRLLFKIKG*L NFIDIQTFFKQYSLNISSNF*LC EKPNECSQLILLIG*TVY*FFNFL GGIPLNLGQKE |
| 11502 | 41870 | A | 11571 | 1 | 2109 | |
| 11503 | 41871 | A | 11572 | 50 | 251 | |
| 11504 | 41872 | A | 11573 | 1 | 1922 | |
| 11505 | 41873 | A | 11574 | 2 | 479 | |
| 11506 | 41874 | A | 11575 | 1 | 909 | LILTSVLLFQRHGYCTLGEAFN RLDFSSAIQDIRTFNYVVKLLQL IAKSQLTSLSGVAQKNYFNILD KIVQKVLDDHHNPRLIKDLLQD LSSTLCILIRGVGKSVLVGNINI WICRLETILAWQQQLQDLQMT KQVNNGLTLSDLPLHMLTNILY RFS DGWDIITLGQVTP\TLYML SEDRQLWKKLCQYHFAEKQFC RHLILSEKGHIEWEVCNFAF RKHYPAKEQYGRQHCIFCRHCS ILFWKDSGHPCTAADPDSCFTP \VSSQQFIALFQVLRAPCHPY WRFVNPAVCAGLIVSVL |
| 11507 | 41875 | A | 11576 | 1 | 1035 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11508 | 41876 | A | 11577 | 63 | 606 | FAKNERTQRGKRRG\TRYMFSR PFARKIHGVVPLGPHICRIYRK DIVDTQGNQVLFKKGMPHKCY PWPKLEGVLQLLPQHA\VAIVV NQPVLGQSFFPRE*IVRIEHI\KH SKSPR*ASLK/RVLKENDSEKER SPNEKGTWGSNLKRHLAPPQK KHTL*RTNGKEPEL\LEPIPYEFH GHNRC |
| 11509 | 41877 | A | 11578 | 1 | 490 | |
| 11510 | 41878 | A | 11579 | 150 | 536 | NCKISFLHFCYIFVKALKKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLRAL *G*DLTHHIIILFPFFFL**PAPP REAHFVRTNGKEPELL |
| 11511 | 41879 | A | 11580 | 336 | 476 | GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV LCG |
| 11512 | 41880 | A | 11581 | 1 | 626 | WAFRPEPPSSSKFAQNDGPQRG KRRGTTRYMFSRPF*ENHGVVP LAHIFMR\IYKKGDIVRHPRGM GYCSKKGMPPTSCYPWQKLGR VYNVTPAMLFIVCKQTKLKG NDSLPRG/ILMWRI*AHLRHF*G ARD/RASLKTCGRENGSRKKER KPKGGKVTWGFQLKRRHLGFP PQEEATFLLKEPIGGREP*ACLE PYFPYWISWGINRC |
| 11513 | 41881 | A | 11582 | 499 | 723 | |
| 11514 | 41882 | A | 11583 | 96 | 411 | PAPTSRCRRRRAPLPKKAEGD AKGNKAKVKDEPQRRSARLSA KPAPPKPEPKPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKAIEGAIGDAK |
| 11515 | 41883 | A | 11584 | 3 | 493 | |
| 11516 | 41884 | A | 11585 | 588 | 759 | GEGCGWAEVGRCRPGPPDPAG PAGAAGP\GAARGGLFRGVLS SSRCGGGSSSSRSRGR |
| 11517 | 41885 | A | 11586 | 213 | 626 | |
| 11518 | 41886 | A | 11587 | 1 | 645 | |
| 11519 | 41887 | A | 11588 | 1 | 739 | |
| 11520 | 41888 | A | 11589 | 327 | 676 | NPNPSWNLAHVWDMDRK*EQ RGIQ/V**SNINKS*KEKMSMQC LEMPRNPDH*GRIDVSFQNLMLR LTR*SQMGYLPWDLKQELETFS KLS*KQVMLSVVVTFVRNMLQ LRFLTSTFSG |
| 11521 | 41889 | A | 11590 | 11 | 328 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11522 | 41890 | A | 11591 | 1 | 378 | LFIVTVCPAFLRFSSAICDSFLIC PQVGGCVRRVLLVTGVLLSIS LDMAATGVSLGSSWSLFLGIW LMIRFQVS*WYPNWLLILSWRN ISITSTPSYYFTYFPTFCYQISPPN QLFCFCLCSWFL |
| 11523 | 41891 | A | 11592 | 1 | 780 | |
| 11524 | 41892 | A | 11593 | 1 | 1461 | MVTLMGHAALCLHYVMQLGT TGGAWYFPRASSQAREMPQCP TLESQEGENSEEKGDSSKEDPK ETVALAFVRENPGAQNGLQNA QQQGKKKRKKKRIIIISGKVLED FLALAMHFADEETGQKRCSLN QTIQLLITPDTGSIWHQAFLSSIV RRAAQYGFREGGEDDDWTL YWTDYSVSLERVMEMKSYQKI NHFGPMSEICRKDLLARNMSR MLKMFPKDFRFFPRTWCLPADP AQLDLWSQTFWPRPRTAPDGT GADGLGLRLGSLGK/VSFWFPA CHGLG*PEASYTAS/MACGSLP/ WKLSTFSAYLEDHSYNVEQIW RDIEDVIAKTLISAHPIRHNYHT CFPNHTLNSACFEILGFDILLDH KLKPWLLETEKMQTAGALFISP ALPSYSNFPLQVARREFQTSVV SRDIDTAAKFIGAGAATVGVAG SRAGIGTVFGSLIIGYARNPSLK QQLFSYAILGFALSEAMGLFCL MVAFLILFAM |
| 11525 | 41893 | A | 11594 | 1 | 2301 | |
| 11526 | 41894 | A | 11595 | 3 | 381 | |
| 11527 | 41895 | A | 11596 | 1 | 729 | |
| 11528 | 41896 | A | 11597 | 1 | 1006 | MVKVKARVNEFGYTGCLVTRA AFNSGKVDIVAINDPFIDLNYLA YMLQYDSTHGKFHGTIKAENG KLIVINGNPITIFQE*DPTKIKWG DAGTEYVVESTSIFTAMEKVGA HLQRGAKRVMIFAPSTEAIMFM MKVNYEKYDNSLKIISNASCTT NCLAPLAKVIHDNSGIVERLMI TVHVITTTQKTVDGPCRKLRPD GHRALQNIIPASTSTAKAMVKV IPELNKKLTGMASHVPTAKVLV VDPTCHL/EKPAKYDIKKMM KQASEDPIKGILGYTEHQIVSSD FNSDTQSSTFDAGAGITLNDHF VKLISWYDNEFGYSNRVVDLM AHMASKE |
| 11529 | 41897 | A | 11598 | 3 | 508 | |
| 11530 | 41898 | B | 11599 | 1 | 5068 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11531 | 41899 | A | 11600 | 58 | 659 | PVATTCECIFIHLGEADVWIGN AA/WELYYLEQSIQHDSMPMPD KTTG*GDN*FYASS\GAGKFVS RAVFINLEPIVTDEVCTGTYHQ LFHPEQLITDKEDAAHNYAWG HHDIGKIIGCYSTNKTCTIQFV DWCFTSLKVGINCQLPTVVPAG NLANIKRAACMLSNTIAIAEAW VCLGHKSDLSYANCSFVHQFFN KSIH |
| 11532 | 41900 | A | 11601 | 511 | 1173 | |
| 11533 | 41901 | A | 11602 | 3 | 497 | WCDGPQNRALICQQC/YSHNG MALKEEFYIAFRCA YCFFLNP ARKTRPQAPRLPEFSFEKRQVV EGSSSVGPLPSGVLSSDNQFNE ESLEHDVLDNTEQTDDKIPAT EQTNQVIEKASDSEEPEEKQET ENEEASVIETNSTVPGADSIPDP ELSGESLTAE |
| 11534 | 41902 | A | 11603 | 2 | 764 | |
| 11535 | 41903 | A | 11604 | 1 | 444 | |
| 11536 | 41904 | B | 11605 | 44 | 1748 | |
| 11537 | 41905 | B | 11606 | 1 | 1134 | |
| 11538 | 41906 | A | 11607 | 1 | 549 | |
| 11539 | 41907 | A | 11608 | 212 | 548 | |
| 11540 | 41908 | A | 11609 | 1 | 905 | ESVAAAARAFPTAPKELERQQ RRRFRFHHLFLPSLRTPCRVS SLQPWLWKATEVMAMFEQMR ANVGKLLKGIDRYNPENLATLE R\YVETQ\AKENAYDLEPNLA V LKLYQFNPAFFQTTVTAQILLK ALTNLPHDTFTLCKCMIDQATI QERNGPDPQIFVPSGTLLEDPA HFPGPFWQTPGNGRACQKAWD ENHWTLFGKVL\TGF*RLLVRK FIC\HVVGYYHLPSHIDR\WLLAE MLGDLASDKPAKRCWMSKIRLR EDDRRGQIFICS\QE*EHLNPRN\ IVEKIDFDSVSSIMASSQ |
| 11541 | 41909 | A | 11610 | 186 | 209 | QLWPN*LLSRNKEATLRYSQLP TCHSICY*MPAF*HTISDLSFNK NINCKSYHLRVFYKYV*IVCHF *VPKVYWTKYYQTSCT*WR* SGVE*PPISSSSSACCLLRRLPT EGTCPEIFWNPRLGISAECRDSC GPTSF |
| 11542 | 41910 | A | 11611 | 2 | 2948 | |
| 11543 | 41911 | B | 11612 | 1 | 999 | |
| 11544 | 41912 | A | 11613 | 1 | 657 | |
| 11545 | 41913 | A | 11614 | 1 | 707 | |
| 11546 | 41914 | A | 11615 | 1 | 297 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11547 | 41915 | A | 11616 | 1 | 1287 | |
| 11548 | 41916 | A | 11617 | 242 | 540 | LTNEKKVQDQMDSQPNSTRGT RRSLYPFLLKLFQLEKEGILPNS FYEASIIIPKPGRDTTTTKKEF* TNIPDEHRCKNPQ*NTSKPNPA AHPKAYPP |
| 11549 | 41917 | A | 11618 | 193 | 916 | |
| 11550 | 41918 | A | 11619 | 1 | 2169 | |
| 11551 | 41919 | A | 11620 | 1 | 615 | |
| 11552 | 41920 | A | 11621 | 39 | 568 | NSAWARRPLVLPLMSLVSPWK SSQHIFRVLNPPNLDGRRKNSP LPITCHLRVWARRYAHV\LRK AD\DLTK\RAGEL\TEDEVERVI TILQ\NPRQYKIPD\WFLNRQKD VKDGKYSQVLANGLDNKLRED L\ERLKEDSAPIEGLRHFWGLR\ VRGQHTQDQLGRRGRHRGASA GARR |
| 11553 | 41921 | A | 11622 | 1 | 378 | |
| 11554 | 41922 | A | 11623 | 1 | 222 | |
| 11555 | 41923 | A | 11624 | 2 | 367 | |
| 11556 | 41924 | A | 11625 | 2 | 376 | QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW |
| 11557 | 41925 | A | 11626 | 1 | 633 | |
| 11558 | 41926 | A | 11627 | 164 | 714 | IGVNRHLIQESPSWNLGAPLE QIFQRKEQAAIFAILQPLLVISRQ TGSGVDPQQTPADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSELKEHVVTQCKEAKNLE KMLQELLTRITSLEKNINDLME LKNTAQELREAYTIINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE |
| 11559 | 41927 | A | 11628 | 504 | 936 | TESSSININKKDDHAKTPPKDH NSSPAREQNKTENEFDELTEIGC RRWVITNSSELKEHVVTQCKEA KNLEKMLQELLTRITSLEKNIN DLMELKNTAQELREAYTIINSQ TDQAEERISEIEDQLNEIKGEDN IREKTVKRIE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11560 | 41928 | A | 11629 | 1949 | 3232 | PGKQDLEWTSSKLQQTCTRRGT LLVEGKLTNRKE*HQHQQKLR PHGNLIQRDHNCSPARE\QNW ENEFDKLTEVGFRRTITNSSK LKERVLTQCKEATNLAKRLEK LLTRITSLEKNKNDLMELKNTA QELREAYTSISGRINQAEQRTSE IEDQLNEIKRRGVSVCQPSED PRSTARVPKGMVPRPRVPLVT PPREKKEAPWLACLRTRALRILI DPPSQVWDIVSCDAENETKLEN TLQDIQENFPNLARQAN\VQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEK\MLRAAREK\GQVT HKAKPIRLTADLSAENLQAR/R TEWGPINFILKEKNF\QPRISYPA K\LSFISEGEIKYFTDKQMLRDF VTTRPALK\ELLKEALNMERD N\RYQP\LQNHAKFVKTIAREE TCINLMCQITS |
| 11561 | 41929 | A | 11630 | 1 | 421 | |
| 11562 | 41930 | A | 11631 | 2 | 415 | |
| 11563 | 41931 | A | 11632 | 59 | 492 | GHIGVRPSLHPVTSTTSGNVSP LARAMASISELACVYLALILHD DEVIIMEVNINTLIKAASVNVE/ PFWPGLFGKALANVNIGSLICN VGAGGPALAAGAAPAGGPAPSI AAASAEKKMEAKKEESEESD DDMGFGLFTKPVL |
| 11564 | 41932 | A | 11633 | 100 | 527 | PPRTGQRQPLHSARRHGPSVSE LACIYSAISARTDEVTVT\EDK INALIKSSPL*MLSPFWPWLC RPLA\NVNIGSL\ICNVRG PVEPA ASQPGA\GPARKVLAPSTAAAP S*RRRKLEAKKRKNPKEVLNDE HGLLVFLN |
| 11565 | 41933 | A | 11634 | 1 | 675 | |
| 11566 | 41934 | A | 11635 | 1 | 1032 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11567 | 41935 | A | 11636 | 3 | 976 | HEAKHQMADDAGGS/AGGPEG PGGPWDGKTPLLSGEVFGIVIR GRGSRP/RGRGRGR\GRGARGG KGPRIK/WIGMPVHQVGAALVK DH*RSKFPWKEIYLFSLP\IKGIK DS*FSFLAGPLSKDEGFEGLCPV QKQTRAGQAQQVSRPFVAIGG LQMAHVGSGLSAPKE\ VATG HPVGAIILAKLSIRPRAQKGIWG TKYWQSPNTVP\CKV\TGRCGF VVVRLIP\APRGSIVSAPVA\K KLLMMAGIDDCYT\SAPGCTAT LG\NFAKGHPLIAIFK\TYKLP*P PDLWK\ETVFTKVPYQ\EF\TDH LVKDPHPRESSVQRDLRLQLVAT |
| 11568 | 41936 | C | 11637 | 279 | 322 | |
| 11569 | 41937 | A | 11638 | 1 | 107 | |
| 11570 | 41938 | C | 11639 | 69 | 134 | |
| 11571 | 41939 | B | 11640 | 223 | 950 | |
| 11572 | 41940 | B | 11641 | 1 | 684 | |
| 11573 | 41941 | A | 11642 | 1 | 564 | EFGTRDNRVLLPLVNPTVFFDI AVD/GVYPLGRVSFELFADKVP KTAENFRALSTGEKGF\YKGS\ CFHRLFP\GFMCCGW*L*SHHN GT\GGKSHLWGRNLKDENFIL KHTGPGILS\MANAG\PTNGSP VFLTSCTA\KTE\WLDGKH\AGL GKVKEGMNIVEAMER\FGSRN GKTSKKIISIA\DCGTTSN |
| 11574 | 41942 | A | 11643 | 1 | 877 | MSGALDVLQMKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLAAR AVVAIENPADVSVISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIQAAFREPRLLVVTDPRA DHQPLTESSYVNLPTIALCNTDS PLRYVD/ICNNKGAHSGVGLMW WMLAREVLRMRGTISRHPWE VMPDLYFYRDPEEIEKEEQAAA EKAVTKEEFQGEWTAPAPEFTA TQPEVADLSEGVQVPSVPIQQF PTDDWSTQPATENWSAAPTAAQ ATEWVGATTDWS |
| 11575 | 41943 | A | 11644 | 1 | 1674 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11576 | 41944 | A | 11645 | 1 | 1121 | MLEAVLEESPREEA AFSWVMK GNLAAGKTIQAQDRDAVGILSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQMKEEDVL KFLAA\GTHLGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWEKLL \\LAA\RAIVA IENPADVSVISSRN TGPEGLCLKFAA\ATGATPIAG\ RFTPG\TFTNQIQAAAFREATGF LVVTWTPGLD\HQLPTEASYV YLPTIA\LCNTDS\PLARYVDIAIP CNNKGAHSVGLMW\WMLARE VLRMRG\TISREHPWE\VM PDL YFYRDPEEIEKEEQAAA EKAVT KEEFQGEWTAPAPEFTATQPEV ADWSEGVQVPSVP IQQFPTED WSAQPATEDWSAAPT AQATE WVGATTDWS |
| 11577 | 41945 | A | 11648 | 1 | 396 | |
| 11578 | 41946 | A | 11649 | 1 | 567 | |
| 11579 | 41947 | A | 11650 | 1 | 226 | |
| 11580 | 41948 | A | 11651 | 3 | 377 | |
| 11581 | 41949 | A | 11652 | 19 | 450 | PDRRWSSLDTMNHTGQTFFSPV NSGQPPNYEMLKEEHEVAVLG APHPNPAPTSTVIHIRSETSVPD HVVWSL FNTLFMNPCCLGFI AF AYSVKSRDRKMVG DVTGAQA YASTAK\ALNIWALILGILMTIL LIVIPGLIFQAYG |
| 11582 | 41950 | A | 11653 | 210 | 2206 | |
| 11583 | 41951 | A | 11654 | 450 | 644 | SLRLWVTERTAVTNLPSSSRGV GDKPPVGSPHLFLSLVVA FNPL QSTRNPASASQPQ\PCSAEQPAR RG* AEPALRTVLPIHAEMWLPR LHEFEEHRLVHRCFTLTFVDET DHCAVLPRGAGSGQGGGFERIL SQSPGSLWESC*PGLWLNILSNP PPCPLPAPLGRTAQ |
| 11584 | 41952 | A | 11655 | 66 | 157 | RGTWSIIA*KSQGISWDRFEEVT LCREPFT |
| 11585 | 41953 | A | 11656 | 1 | 2538 | |
| 11586 | 41954 | B | 11657 | 68 | 1602 | |
| 11587 | 41955 | B | 11658 | 1 | 1464 | |
| 11588 | 41956 | A | 11659 | 587 | 1081 | ILSWLTLWSILRLYIVTLTGKIC SLTSEASEATSPPRGTNNSRVA LAVVTLVWRVCSFIFDSKAFIL AFAFFFSHWFSILPFPQHGATL WYFWGDFECSRGPRIHTDDR ARLVPMTERGGPPQGGEPART RSPRQGGRGGM EGGE*YPCPPH LGGQERKPG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11589 | 41957 | A | 11660 | 180 | 583 | YTEVLKGPDGAENHGTRTT** MHKPH*PIRSTGRKADKQLQQS LR\NKINVQKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQL TMDVKDLFKENYKPLLKEIRG YKQMGEHSMLMGRKNQYSEN GHTAQ |
| 11590 | 41958 | A | 11661 | 82 | 159 | |
| 11591 | 41959 | A | 11662 | 2 | 1008 | NAAPLQQRNKAGCR/YDLDEL REEGFRRSNFFKLKAEVRTQCK ETKNLEKTLDKWLTRKTSVEK SLNDLMELKTMVQGLRDKCTN FSNGFDQLEERVSVIEEQMNEM KQEKKYREKKDRSMTQKVNK DIQELDSALHQEELIDIYRTVHP KSTEYTFFSAPHRITYFKIDHIVG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNRSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDDTTYENLWDTFKAVCR GKFRALNVHKKRKQERSKIDTLI SQLKELERQELTHSKASRMQEI TKIRAEQKEKETEKNIQKNQRI QELFLLKDQQN |
| 11592 | 41960 | B | 11663 | 1 | 1529 | |
| 11593 | 41961 | B | 11664 | 111 | 1350 | |
| 11594 | 41962 | C | 11665 | 1 | 2127 | |
| 11595 | 41963 | B | 11666 | 1 | 1350 | |
| 11596 | 41964 | A | 11667 | 1 | 1506 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11597 | 41965 | A | 11668 | 1 | 1855 | MIIIVPLYSSLGDRVKSCCKRE RERERRKKERKKERKKERKKE RKKASSKERE EGRKKERRKKL RKKEEKERKKRKKRREGRKE RKKEKERKEGKKEERKNIPGKR RESTDPLKEMDHRCLLPEMLK GTWWTTPARASGPAVPLLCEF RQWTVDTTSVVPETHMPGQM TQIPAPDSHNMDEAGGHYPK QTNRPENQILHVFTDKWELNT EYKDPKKRTTDTRAYLRVEAT LAADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRGRMTPHM AGYSSETKLPEERSGSSICGSPIS AVLQPPLLIPRQTGSGVDLQQT PTDLQLRVLMERSSSPATEQSW MENDFDEMDEGFRRSNYSEL KEEVQTYCKEVCGRGKFKALNA HKRKQETSKIDTLTSQLEKEK QEETHSKASRRQEITKIRAELEK IETQKTLQKINESRSWFFKINK IHRPLARLIKKKTEKNQINAIKN DKWDITNNLTEIQATIREYYKH LYANKLENLEEMDKFLDTYTL PRL*N/CRQSLIAYQKIKVQDQ MDSQSNSTRGTRRSWYHSF |
| 11598 | 41966 | A | 11669 | 2678 | 2897 | PDGAKKHGKRTTRDERTSFSSEF NQLEERVSVIENQMNMKREE KFREKRVKRNEQSLQEIWDM* KDQMRSTS |
| 11599 | 41967 | A | 11670 | 843 | 2004 | NNQCREVLKGVDAESQGSRT REERRSLRSRCDQLEERVSVID QNMNMKREGKFREKRIKRNEQ SLQEIWVYVVRPNLRLIGVPES DGNGTKLENTLQDIIQENFPN LTRQANIQIEIQRTPQRYSSRR ATPRHIVVRFTKVEMKEKMLR AAREKGRVTHKGKPIRLTADLS AGTLQARREWGPIFNILKEKNF PPRISYPAKLSFISEGEIKYFTDK QMLTIVHLKTLDIIMYNIRRPK GGEKKADQEVNSEPRNNIVLET KGDRGPQAPASPGGPPRRVRR SASGSRAGITFHPVHYLTRRPA HRFHYQSHGYGVGSVQSAELR HKTNSAARAALRDGGVDCRGR ERGSACQKRSDDDEAGGLVLS LPRVMSGSWEVRR |
| 11600 | 41968 | B | 11671 | 1 | 3221 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11601 | 41969 | A | 11672 | 82 | 160 | |
| 11602 | 41970 | A | 11673 | 1 | 551 | AAAMADSGTAGGAALAAPAP GPGSGGPGPRVYFQSPPGAAGE GPGGADDEGPVRRQGVTVS YDRKELRKRL\NL\EDWIL*QLN GAFYDCQ\EEEEIPELEIDVDELL D\MESD\DARAA\RVKELLVDC YKPTEAFISGLLDKIRGMQKLS TPPEEVRVPDPGRTVAPTGQSL PPDLVATAITGGT |
| 11603 | 41971 | A | 11674 | 362 | 650 | |
| 11604 | 41972 | A | 11675 | 1 | 651 | |
| 11605 | 41973 | A | 11676 | 1 | 3101 | |
| 11606 | 41974 | B | 11677 | 1 | 2838 | |
| 11607 | 41975 | A | 11678 | 1326 | 1980 | TSEASRQSERVDSAALSALLS RSSKCRPWGTARVARAGGCLT PLLSRRFLETRPFTGPWDPGLG VTCWCCPPKRRLKSTPRPKFSV CVLGDQQHCDEAKAVDATFEV CLGDQVLSNANGFLSLSAKKY DAFLASESLIKQIPRILGPGLNK AGKFPSLLREEGQAICYSSSTNLT *SSLPSSQVLCLAVAVGHVKMT DDELVYNIHLAVNFLVSLLK |
| 11608 | 41976 | A | 11679 | 11 | 720 | EAMSSKVSRDTLYEAVREVLH GTQRKRRKFL\ETVELQISLKNY DPQ\KDKRFSGT\VRLKSHSPAL SFSVCVLGD\RQHCD\EAKA\V DIPPHGPSEAAEKTSTKNKKLV QKSWPKKV*MPFLA\SESSDQA RFPRIPRAPGLNKAGK\FP\SLLT HNGKHGGPKVDEVKVPQSRFQ MKKVLCLAVAVGHVKMTD\DE LVFNIHLA\VNFL\VSLLK\KNW QKCSGALYYQEAPMGQSPKRL |
| 11609 | 41977 | A | 11680 | 34 | 507 | |
| 11610 | 41978 | A | 11681 | 407 | 806 | LRVGMLQRSKANGPDDDHLLG ASCTCGPSTGSPSPRLPSLPQRP QKGLLHQ/RATRMKPGNIAKGL WKRLSKGTVMKLWLLTAVPRL SGLLVCPLVHQLLLAFKFLKRF PIFCLWFRAANRHARFSILFKLS RP |
| 11611 | 41979 | A | 11682 | 1 | 1551 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11612 | 41980 | A | 11683 | 1 | 751 | MAGYSSETKLPEERSDSSIRGSR KSTVLQTLILLIPRQTGIKKLTQN RSTTWKLNLLNDYWVHNE MKAIEKMFFETNENKDTTYQN LWD/YIQSSV*REIYSTKCPQEK AGKIQMDTLTSQLKELEKQEQ THSKASRRQEITKIRAEPKEIQT QKTLQKINESRSLFFKRINKIDR PLARLIKKREKNQIDAINEK GISPPIPQNYKLPSENTTNTSMQ IN*KI*KKWINSWTHTPSQE*TR KKLNL |
| 11613 | 41981 | A | 11684 | 49 | 551 | VRATYFHHAPANCTEFVPRQL VSRAENLPQATSLPTEKASRAF RVLLIPRQTRSGVDLQQTPTDL QLRVLIVRRKTNKQKGHPHQN PICTSPRRSNFFELKEEVRTHG KDAKNLEKRLDKWLTRISSVE KSLNDLMELRTMA*ELCDECTS FSS*FNQLEERSVSI |
| 11614 | 41982 | A | 11685 | 1 | 1566 | MNSLLTGQIPESQQIHRDSSAAT WWKKIYRQKMGNIEKSEVRG GLTPHTAGYSSETKLPEKRSGS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRRKS NKQKGHPHQKPICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTCSKIDHIVGSKALL/EQM*KN RNYQKLSLRPQCQNQ\LELRIKKL TQNHSTTWKLNLLNDYWM QKRPLKIQQC FMLKTLNKL GID GTYLKIIRAIYDKPTANIILNGQ KLEAFLKGTGRQGCPLSPLL NVVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLPKLISNFSKVSGYKIN VQKSQTFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFTELEKTTLK FIWNQKRACIAKSILSQKNKAG GITLPEFRLYTRLQ |
| 11615 | 41983 | A | 11686 | 1 | 4962 | |
| 11616 | 41984 | B | 11687 | 101 | 3772 | |
| 11617 | 41985 | B | 11688 | 1 | 1047 | |
| 11618 | 41986 | A | 11689 | 21 | 287 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11619 | 41987 | A | 11690 | 131 | 723 | LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSAEDEINEMKRE EKFREKRVKRNEQSLQEIWLYL KRPNLRLIGVPESDGENGTKE NTLQDIIQENFPNLRQANIQIQ EIQRMPQRYSLRRATPRHIIVR TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL |
| 11620 | 41988 | A | 11691 | 1 | 1257 | |
| 11621 | 41989 | A | 11692 | 1 | 759 | |
| 11622 | 41990 | B | 11693 | 107 | 511 | |
| 11623 | 41991 | A | 11694 | 170 | 726 | LLEGKLTNRKDIHTETPSVCHH HQRPKDIIQENFPNLRQANIQIQ QEIQRTTPQRYSSRRATPRHIIVR FTK/VEMKEKMLRAAREKGRV THKVKPIRLTADLLAETLQARR EWGLIFNILKEKNFQPRISYPAK LSFISEGEIKYFTDKQMLRDFVT TRPALKELLKETLNVERNRYQ PLQKHAKL |
| 11624 | 41992 | A | 11695 | 1 | 569 | MAGYSSETKLPEERSGSNICCSP ISAVLQPPLIPRQTGSGVDLW QTPTDLQLRVLTVRRKINKQKG HPHQNPICSTPSSKTKGQIRAE KEIETQKALQKINESRNWVFEK INKIDRPPARLIKKKREKNQIDA IKNDRGDITIDPTEIQTIREYYK HLYANKLENLEERDKFLNTYTL PRLNQEEVESLNRPIGTSEIEAI NSLPTKKSPGPDGFTDAFYQRY KEDLVPFLLKLFQSIEKDRILSN SFYEASIFLIPKLGRDTTKKEN* QTERTSTPKPHLYITIEDQRPD QSRTEGNRDTKSPSKNQ*IQEL/ WFLKRSTKLIATSKTNKEEKRE ESNRCNKK**RGYHHRSHRNT NYHQRIL*TPLCK*TRKSGRKG* IPQHIHSPKTKPGRS |
| 11625 | 41993 | A | 11696 | 3 | 1039 | |
| 11626 | 41994 | C | 11697 | 1 | 1251 | |
| 11627 | 41995 | A | 11698 | 1 | 807 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11628 | 41996 | A | 11699 | 1 | 713 | MNSLLTGQIPESQQIHRDSSAAT WWKKIYRQKMGNIDIEKSEVRG GLTPHTAGYSSETKLPEKRSGS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRRKS NKQKGHPHQKPICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFFSAPH HTCSKIDHIVGSKALL/KQM*K NRNYQKLSLRPQC�NQTRTQD*E THSKPLNYMETEQPAPE |
| 11629 | 41997 | A | 11700 | 1 | 1768 | MNLSRHLNEVKGELLWSLEWR DPDGGSIIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFGGLQKKMDLKG VFKSCFKI YCSSKHLLKTGFISEAVLCYGE GGEGDTVLTMKERWPHECIVLI QCNKGRLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQKPICMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQQEELTILNIYAPNTEAPR FIKQVLSDLQRDLDSHIIIMGDF NTPISTLDRSMRQKVNKDIQEL KSALQQADLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHIVGSKAL LSKCKRMEIITNCLSDHSAIKLE LRIKKLTQNRSTTWKLNNVLLN DYWVHNKMKAEIKMFFETNG NKDDTYQNLWD/YIQRSV*REI YSTKCPQEKAGRI*N*HPNIQL KELEKQEQTSHKVSRRQEITKIR AELKEIETQKTQKINESRSWFF EKFNKIDRRLARLIKKKREKNQ IDAIKNDK\GISPLIPQKYKLPSE NTINTSTQIN*KI*KKWINSSTHT |
| 11630 | 41998 | A | 11701 | 535 | 666 | KGRNIQLNGLVIGTSLN*LKCL KMFFTMPLGYINGGISSDFFLH |
| 11631 | 41999 | A | 11702 | 20 | 262 | |
| 11632 | 42000 | B | 11703 | 1 | 1254 | |
| 11633 | 42001 | A | 11704 | 1 | 1032 | |
| 11634 | 42002 | A | 11705 | 481 | 1491 | |
| 11635 | 42003 | A | 11706 | 2 | 717 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11636 | 42004 | A | 11707 | 348 | 1976 | SRVRPVVHLRRAPMVCQGHTT PPVCGSLAGPGDCVHYSVPAG YSSETKLPEERSGSNICCSPISAV LQPQLLIPRRTGSGVDLQQTPT DLQLRVLTVRRKTNKQKGHPH QKPICMSPSSKTKGSNSHITILT NVNGLNAPIKRHRLANWIKSQ DPSVCCIQETHLTCRDTHRIKIK GWREIYQANGKQKKAGVAILV SDKTDFKPTKIKRDKEGHYMM VKGSIQQEELTTLNIYAPNTGAP RFIKQVLRDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDIQ DLNSALHQVDLIDIYRTLHPKS TEYTFFSALHHIYSKIDHIVGSK ALLSKYKTTEIITNCLSDHSAIK LELRIKKLTQNRSTTWKLNLL LNDYWVHNKMKAEINTLFETN ENKDDTTYQNLWD/YIQSSV*REI HSTKCPQEKAGKI*N*HPNIQL KELEKQEQTSHKASRRQEITKIR AKLKEIETQKILQKINESRSWFF EKINKIDRPLARPIKKKREKNQI DAIKNÆKGISPLIPQYKLPSEN TINTSMQIN*KI*KKWINSSTHT PSQD*TRKKLNL*INTSMQIN |
| 11637 | 42005 | A | 11708 | 1124 | 1717 | LLEGKLTNRKDIHTKNPSVRHH HQRPKVDKTTKMGRKQSRKTG NSKNQSASPPPKERSSSPATEQN WTENDFDELREEGFRRSNYSEL KEEVRTNAKEVKNFEEKLDEW ITRITNAEKSLKDLMEKTTAR ELRDECTSPSSQCNQLEERISAM EDKMNEMKREEKFREKRIKRK EQSLQEIWVYVKRPNLCLIGVP |
| 11638 | 42006 | A | 11709 | 1 | 3549 | |
| 11639 | 42007 | B | 11710 | 209 | 403 | |
| 11640 | 42008 | A | 11711 | 3 | 248 | |
| 11641 | 42009 | A | 11712 | 61 | 594 | IQPLVSVLDEKPSNGVLVHMK LLIKTFLDGIFDDLMEENVLNT DEIHLIGKCLKFVVSNAENLVD DITETAQTAGKIFREHLWNSKK QLSSVHGSEHEDKALTCHWVG HPGFPEKLKERKKFCGIMVVGL FGFTTDSGKAGADIHGRFLQGN FCNDAVTKAHVEKDFIAFKSST |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11642 | 42010 | A | 11713 | 1 | 430 | FSAVREDGGCYLWQIYPIKERM DRJRLVLIICNKEFDHLPPRNGA DFAIMEMKKLLEDLGYSVDVE ENLTAR/HNVSQGETGTGKGLPIF ITQLIACFQRYSWRCHLAEVFW KVQQAFESPEATVQMPTIERVS MTRYFYLFPGN |
| 11643 | 42011 | A | 11714 | 3 | 1195 | |
| 11644 | 42012 | A | 11715 | 35 | 1288 | |
| 11645 | 42013 | A | 11716 | 1 | 1641 | |
| 11646 | 42014 | A | 11717 | 1 | 2933 | MVCSAAPLLLLATTPLLLGSPV AQASQPLWPMAGQTMWAQT STLTLTEELGQSQAGGESGSG QLLDQENGAGESALVSYYVHL DFPDKTWPPELSRTLTPAASA SSSPRPLLTLRLTTECNVNHK GNFYCACLSGYQWNTSICLHYP PCQSLHNHQPCGCLVFSHPEPG YCQLLPPVPGILNLNSQLQMPG DTLSLTLHLSQEATNLSWFLRH PGSPSPILLQPGTQVSVTSSHGQ AALSVSNSMSHHWAGE |
| 11647 | 42015 | A | 11718 | 1 | 357 | |
| 11648 | 42016 | A | 11719 | 73 | 1494 | KSSHCIKMGPQIFHKTSEFLPA TSCPSCPDQNEEDVSQTQYKEC CGGGWCSSHIFAVWHFI*RPDA T*FG*SSAYGFVASDQCP*GSS* LYHLWYSYSGSENKQCG*RAA LGAGFSDKTPAHTVTMACISAN QAMTTGVGLIASGQCDVIVAG GVELMSDVPIRHSRKMRLML DLNKAKSMGQRLSLISKFRFNF LAPELPAVSEFSTSETMGHSAD RLAAAFVSRLEQDEYALRSHS LAKKAQDEGLLSDVVPFKVPG KDTVTKDNGIRPSSLEQMAKLLK PAFIKPYGTVTAANSSFL/LTDG ASAMLIMAEKALAMGYKPKA YL/RRDFMYVSQDPKD\HLLLG PTYATPKVLEKAGL\TMNDIDA FEFHEAFSG\QILANFKAMDSD WFAE\NYMG*KKPRFGLPPLWR RFNNWVG\SLSLGHPFGATGCR LVMT\AANRLREEGRASMA*V AACAAGGQGH\MI\VEAYPK |
| 11649 | 42017 | A | 11720 | 1 | 642 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11650 | 42018 | A | 11721 | 17 | 960 | KSGARSLQPQFLRAPEDGGPLS LPNAAMARGPKKHL\RVAA\P KHWMLDKLTGGCA\PRHSPVP HKL\RECLPLIIFLRNRLKYALT GDEVKKICMQRFIK\NDGKV\RT *YNPTPAGFHGMSSAFDKTGEE NFPS*SIDTKGSAFA\VHPYLTTL EEGQSTSLVPKVKKRSFVGHKK GIPSSWVTS*WPATIR*PRSPSSK VN*YHFRLDLETWQRLD\FIKF \DTGN\LCMGDWGGA\NLGRN WVLITN\RERHPSGSDPW\HFVK DANG\SFATRLSNIFVIGKGNK PWISLPRGKGIRLTIAEERDKRL AAKQSSG |
| 11651 | 42019 | A | 11722 | 1 | 460 | |
| 11652 | 42020 | A | 11723 | 1 | 243 | |
| 11653 | 42021 | A | 11724 | 94 | 311 | |
| 11654 | 42022 | A | 11725 | 400 | 792 | |
| 11655 | 42023 | B | 11726 | 473 | 596 | |
| 11656 | 42024 | A | 11727 | 1 | 1707 | |
| 11657 | 42025 | A | 11728 | 3 | 484 | |
| 11658 | 42026 | A | 11729 | 122 | 253 | |
| 11659 | 42027 | A | 11730 | 1 | 803 | RGGRGGAGAAGAELAGPLPSP APFESPGFTPPGPWGSICPAFA HALHSGTVPARSGRTMARGAA LALLFGLLGVLVAAPDGGFDL SDALPDNENKKPTAIPKKPSAG DDFDLGDAVVDGENDDP\PPN PPKMPNPNPNHPSSSGSFS\DA DLADGVSGGEGKGGSDGGGSH RKEGEEVADAPGVIPGIVGAVV VAVAGAISSFIA\YQKK\KLCFK\ EN\AEQGEVDMES\HRNAQRQK PAVQRTLLEKIEDCPEKQPQAF GSRVRTAA |
| 11660 | 42028 | A | 11731 | 335 | 476 | |
| 11661 | 42029 | A | 11732 | 2 | 169 | |
| 11662 | 42030 | A | 11733 | 49 | 289 | VPVVQVPAAPGPLPGPATGSCS ASAAPRPDP\PPGHPEGHGHHS P/GVLGFVGVGIFS\YCQE\QPQKCV TIKIFESPP\IRRL |
| 11663 | 42031 | A | 11734 | 22 | 412 | ARVGFLLGQEGKAGARASGPA DDVC\GKGASAIRSHMRASRSP PSPRRCHHHHEATGTASGSAAG GPGAGCVWLCRLALTPSAQDG RNSTFQTYKKEVCLPRHSHPCW MHAAGTTAGGS\AVMSACCPSS SR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11664 | 42032 | A | 11735 | 250 | 571 | KGPRVTQGATVPKRQAPSAGL D/GSPISQFPWSY/DV*AIAILCG QGV*PLPVSPGGPAPPESVAL AEWVCSGSRRLSNSGIARRPIG VIQPLDFLQNWPKPVLRC |
| 11665 | 42033 | B | 11736 | 1 | 1593 | |
| 11666 | 42034 | A | 11737 | 2 | 1175 | |
| 11667 | 42035 | B | 11738 | 206 | 354 | |
| 11668 | 42036 | B | 11739 | 850 | 1461 | |
| 11669 | 42037 | A | 11740 | 2 | 663 | VLLDERSAALDGA KR DGT LAL AAGALCREARAAQVFLKGGY EAFSASCPELCSKQ/INVSANCP NHFEGHYQYKSILCGMTTHKA DISSWFNEAIDFIDSIKNAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFVPV SIPDHSTNSALS YLQSLITTSSHC |
| 11670 | 42038 | A | 11741 | 1 | 474 | |
| 11671 | 42039 | A | 11742 | 3 | 1354 | WAVCATRVGGAVGGTAKKPR SPEPRVTLLSQSKSGFWGAER PGGLAFPRKAPPCWPREQTKS TAGPITLGALRPAMVMEVGT DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIAGSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAALD GAKRDGT LALAAGALCREARA AQVFLKGGYEAFSASCPELCS KQSTPMGLSLPLSTSVPSAES GCSSCSTPLYDQGGPVEILPFLY LGSAYHASRKDMLDALGITALI NVSANCPNHFEGHYQYKSIPVE DNHKADISSWFNEAIDFIDSIKN AGGRVFVHCQAGISRSATICLA YLMRTNRVKLDEAFEFVKQRR SIISPNFSFMGQLLQF*VPQD/VL VPHCSAEGWEAPDMAVLDRG TSTTTVFNFVPVFI VPHSTNSAL SLPFRGPINGPFPAG |
| 11672 | 42040 | A | 11743 | 196 | 1260 | |
| 11673 | 42041 | A | 11744 | 5 | 447 | |
| 11674 | 42042 | A | 11745 | 1 | 328 | |
| 11675 | 42043 | A | 11746 | 3 | 364 | |
| 11676 | 42044 | A | 11747 | 1 | 816 | |
| 11677 | 42045 | A | 11748 | 1 | 1377 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11678 | 42046 | A | 11749 | 1 | 989 | EGRTVLGGGLGSAAAMASRLL LNNGAKMPILGLGTWKSPPGQ VTEAVKVAIDVGYRHIDCAHV YQNEVEVGVAIQEKLREQVVK REELFIVSKLWCTYHEKGLVKG ACQKTLSDLKLDYLDLYLIHWP TGFKPGKEFFPLDESGNVVPSD TNILDTWAAMEELVDEGLVKA IGISNFNHLQVEMILNKPGLKY KPAVNQIECHPYLTQEKLQYC QSKGIVVTAYSPLGSPDRPWAK PEDPSLLEDPRIKAIAAKHNKIT TAQVLIRFPMQRNLVVIPKSVT PERIAENFKVDFELSSQD\MTT LLSYNRRNWRVCALLSCTSHKD |
| 11679 | 42047 | A | 11750 | 1 | 855 | |
| 11680 | 42048 | A | 11751 | 2 | 367 | |
| 11681 | 42049 | A | 11752 | 2 | 376 | QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW |
| 11682 | 42050 | A | 11753 | 1 | 1536 | |
| 11683 | 42051 | A | 11754 | 1 | 2541 | |
| 11684 | 42052 | A | 11755 | 1 | 1788 | |
| 11685 | 42053 | B | 11756 | 1 | 1014 | |
| 11686 | 42054 | A | 11757 | 1 | 777 | |
| 11687 | 42055 | A | 11758 | 1 | 1029 | |
| 11688 | 42056 | A | 11759 | 1 | 2052 | |
| 11689 | 42057 | A | 11760 | 1 | 1392 | |
| 11690 | 42058 | A | 11761 | 1 | 993 | |
| 11691 | 42059 | A | 11762 | 1 | 1240 | PTDPAAEGPCLLDAKTNKRKGP STPILPFCPSPFIRGPKVDSTHGA WGQKQHR*TGIF*RSRAPSP\PA KEHGSSPATEQSWMENDFDEL REEGFRRI\NYSELKEEARTHGK EVINLEKK\LDEWITRITNAEKC LK\ELMELE\TKA\RELREECRS\ LRSRRNQLEERSVAMEDEMNE MK\QEEKFREKKNKKK*TKAL KELWDYVVKRPNLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QAN\VQIRGNRYRERPQRLPPRG RATPRTH//IIVRFTKVGNGREKM FKGQPGGKGRVTLKGKPIITLT ADLSAETSTSQKTEWGPIFNILE GKEFSNPEISYLSQT*AFISGREE LNSFYRTSQMLRDFCHHQASRL P*KSTRPALKELLKEEALKHGK GNNPVPSHLQKFIA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11692 | 42060 | A | 11763 | 1 | 1917 | |
| 11693 | 42061 | A | 11764 | 268 | 307 | AHHTHLCLLTESPPEGR*VCWG CGLGWGVVLSLVCP |
| 11694 | 42062 | A | 11765 | 2 | 349 | |
| 11695 | 42063 | B | 11766 | 1 | 1734 | |
| 11696 | 42064 | A | 11767 | 1 | 603 | |
| 11697 | 42065 | A | 11768 | 1 | 420 | |
| 11698 | 42066 | A | 11769 | 115 | 796 | EWSSVRRSLVEKRALRRPHPQC LCFRMKTILSNQTVDPENVDI TLKGRTVIVKGP/REGTLRRDFQ SPSMENFTFLERKKKRLRVDK WWGNRKE\LATVRTICSHVQN MIKGVTLGFRYKMRSV\YAHFP HQPLLSRGNGLSV\EI\RNFFG*K NISARVRMRP\GVA\CSV\SQAQ KGEF/ISLEGND\ELVSNSAALI QQATT\VKNKDIRKFLDGIYVFE KGTVQQADE |
| 11699 | 42067 | A | 11770 | 1 | 295 | ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETILSKLSQGGK TKHRMFSLVGGN |
| 11700 | 42068 | A | 11771 | 3 | 342 | |
| 11701 | 42069 | A | 11772 | 1 | 182 | |
| 11702 | 42070 | A | 11773 | 1 | 439 | |
| 11703 | 42071 | A | 11774 | 1 | 325 | |
| 11704 | 42072 | A | 11775 | 2 | 91 | |
| 11705 | 42073 | A | 11776 | 167 | 861 | IWAILADPRMAQGKLRMEIGTK LRCLIWTVHKGVHWVTFWWV ERSQTGNLEVRRLWLGLLTHL HSGVNSLFTRARIWNPSMIDW/I KKMWHIYTMYYAAIKKNQF MSFAGTWMKLSAPAAPT\VLFL ASFTNHYNLRASLLVESCLAPS YTSVEPRFSIPQSLTPARGSSDG HTCFHQSHDSSLICADSTHFW LSAHIWIQANAPPVPRAPSELSL KTRLKCSPQLNLRPP |
| 11706 | 42074 | A | 11777 | 1 | 660 | |
| 11707 | 42075 | B | 11778 | 1 | 2633 | |
| 11708 | 42076 | A | 11779 | 1 | 2985 | |
| 11709 | 42077 | A | 11780 | 398 | 605 | |
| 11710 | 42078 | A | 11781 | 204 | 585 | VTMCDRKAVIKNADMSEEMH QDSVECATQALEKYNIEKDIAA HIKKEFDKKYNPTWHCIVGEG TFGSLC*HIETKHFLTSYLGAK WAISFCFKFWFKRHGTVATHPV IPFQKQGIAALNFQLPED |
| 11711 | 42079 | A | 11782 | 1 | 810 | |
| 11712 | 42080 | A | 11783 | 188 | 534 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11713 | 42081 | A | 11784 | 1 | 1188 | |
| 11714 | 42082 | A | 11785 | 1 | 1137 | |
| 11715 | 42083 | A | 11786 | 19 | 428 | ERRNSGNMALRVERSVRAVLC SLHVVLAPAAPCLSRPWQLGM GAVWYCNLPEVGTKLNKQDE FGALERVKAASELYSPLSGEVT EINEALAENPGLVNKSRVEDG WLIKMTLSNPS*LDELMSEEAY EKYIKSIEE |
| 11716 | 42084 | A | 11787 | 66 | 631 | RRDPRTPANMALRVVRSVRAL LCTLRAVPLPA\APCPPRWQLG VGAVRTLRTGP\ALLSVRKFT KHEWVTENGIGTVG\SNFAQ\ EALGDVVYCSLPEVGTKI*TKP SWSLVLL\SVKAASELYSPLSG \EVTEIN\EAL\AENPGTCKTNFC Y\EDGWLIKMTLSNPSE\DELM SEEAYEKYIKSIEE |
| 11717 | 42085 | B | 11788 | 46 | 743 | |
| 11718 | 42086 | A | 11789 | 209 | 401 | MKPPVRSLSPPRSIIMGSSATEI EELNTTFKYLTGEQTEKMWQ RLKGMEIKKLN*G |
| 11719 | 42087 | A | 11790 | 135 | 313 | |
| 11720 | 42088 | A | 11791 | 1 | 624 | |
| 11721 | 42089 | C | 11792 | 81 | 299 | |
| 11722 | 42090 | A | 11793 | 5 | 166 | SPVMMSSFFLFVCLLT*RSPPSS SSSSSSSSSSSSSSSSSPSSSFS GSVV |
| 11723 | 42091 | A | 11794 | 3 | 173 | |
| 11724 | 42092 | A | 11795 | 169 | 291 | SCNSSILSFLSLSLVADPQIATYR /S*CSRLGHKGTLPGS |
| 11725 | 42093 | C | 11796 | 1 | 429 | |
| 11726 | 42094 | A | 11797 | 1 | 279 | |
| 11727 | 42095 | A | 11798 | 3 | 376 | |
| 11728 | 42096 | B | 11799 | 1 | 736 | |
| 11729 | 42097 | A | 11800 | 753 | 2455 | |
| 11730 | 42098 | A | 11801 | 1 | 312 | |
| 11731 | 42099 | A | 11802 | 48 | 397 | |
| 11732 | 42100 | A | 11803 | 51 | 286 | |
| 11733 | 42101 | A | 11804 | 1 | 420 | |
| 11734 | 42102 | A | 11805 | 11 | 537 | PDRPTRPCRQCARSFRRKLKAA VGVEGPSLSSGELGTRVPAAPS PTTRPRAMAFCLPSFAC\YSALI LHDDE\VT\VTEDK\NALIKSSR V*MLSPFWPGLFAKAL\ANVN\ MGLICNVGAGGPCCPASWVL QPAGRSLPPLLAASSLREKKV\ EAKKEGFRGSFD*LTWGFGSF |
| 11735 | 42103 | A | 11806 | 114 | 399 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11736 | 42104 | A | 11807 | 3 | 599 | AIRRLRJSAREEERENQPRLLPL SLGAGGGVGGFVQQWPRFKAR DLRGKKKEEL\LKQL\DDLKVE LVPSARRQKRQGAAS\KLSKI R\VVVRKSIAPCSPRLFTQTQKEN LRKFYKGKKYKPLADLRPKKTR AMRRRLNKHEEN\ARTKKQQR KERLYPLRKYAVKALGGALSIK HKENLTKKQQRKERLYPLRK YAVKA |
| 11737 | 42105 | A | 11808 | 226 | 370 | AGSP*FPQFSEA*RRGALGSGA DQDLSHPRITITLTSCRSLQTSS PR |
| 11738 | 42106 | A | 11809 | 3 | 7964 | RSGSGSKFEPRSRASVLAPSAL GPPNTSPRQLVAHCALPATRMP VTEKDLAEDAPWKKIQNTFT RWCNEHLKCVNKRIGNLQTDL SDGLRLIALLEVLSQKRMYRKY HQRPTFRQMQLENVSALEFL DRESIKLVSIDSKAIVDGNLKL LGLVWTLILHYSISMPVWEDEG DDDAKKQTPKQRLLGWIQNKI PYLPITNFNQNWQDGKALGAL VDSCAPGLCPDWESWDPQKPV DNAREAMQQADDWLGV |
| 11739 | 42107 | A | 11810 | 1 | 636 | |
| 11740 | 42108 | A | 11811 | 3 | 261 | QKKPLKQPKKQA*EMDEV RAGAEALAGAGALGDRPELNTLCLS P\EDKAFKQKQKEEQKKLEELK AKA\AGKGPLATGGIKKSGKK |
| 11741 | 42109 | A | 11812 | 1 | 621 | |
| 11742 | 42110 | A | 11813 | 1 | 1024 | |
| 11743 | 42111 | A | 11814 | 174 | 332 | SHCLANAPGDVKVRNDPESPRE L*HL*R*RINYTRWKRSI*EEWC QGHSWRG |
| 11744 | 42112 | A | 11815 | 1 | 1323 | |
| 11745 | 42113 | A | 11816 | 1 | 2322 | |
| 11746 | 42114 | A | 11817 | 1 | 336 | |
| 11747 | 42115 | A | 11818 | 22 | 391 | PPPPAAKTRRKVLATKVLGTV KWFNVRNGYGFINRNDTKEDV FVHQTAIKKNNPRK\YLRSVG\D GETVEFDV\VEGEKGAEAA\NVT GPDGVPV\EKGSRYAA\DRRR\Y RRCY\YDR\RRGPPPEYW |
| 11748 | 42116 | A | 11819 | 433 | 866 | PPPPAIDAEEKVLATKVLGTV KWFNVRNGYGFINRNDTKEDV FVHQTAIKKNNPRKY\LRSGD GETVEFDVVEGEKGAEAA\NVT GPDGVPVE\GSRYAADRRRYRR \GYYGKARWPPFANYAGGGRR RKGAQVEGFLPPLD |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11749 | 42117 | A | 11820 | 63 | 484 | |
| 11750 | 42118 | A | 11821 | 1 | 819 | |
| 11751 | 42119 | A | 11822 | 150 | 463 | |
| 11752 | 42120 | A | 11823 | 63 | 594 | FAKLPNPKGKGGEATRYMFSR PF*ENHGVVPLGHNN*RF\YKK GDIVDIQGEWGTLFQKGNC KVVTHGQNLGVLPMVTPAML VGHLL*TNQF*GKVFSKRINVR IEPIK\HSKSR\DSFLK\RVKEND QKKKEAKEKGTWVQLKRQPA\ PPREAHFVRTNGKEPELLEPIPY |
| 11753 | 42121 | A | 11824 | 2 | 1376 | |
| 11754 | 42122 | C | 11825 | 132 | 341 | |
| 11755 | 42123 | A | 11826 | 155 | 245 | |
| 11756 | 42124 | A | 11827 | 3 | 293 | |
| 11757 | 42125 | A | 11828 | 204 | 467 | LRAPHVACSRCNQGPCMENCL NTDQHTQTQRQG*EEKSSSSK/ PISSLMEYYKRSQCSVKSKARS VF*LKLRAQAQLLQETKKPVFR L |
| 11758 | 42126 | A | 11829 | 1 | 768 | |
| 11759 | 42127 | A | 11830 | 348 | 568 | REISYKERIGM*MPPSVILNSYV KSMLETYPHPLLRGVVAPGPLK KGFLTESLLALPDPSFSGRMTSF KITPV |
| 11760 | 42128 | A | 11831 | 1 | 840 | |
| 11761 | 42129 | A | 11832 | 2 | 216 | |
| 11762 | 42130 | A | 11833 | 1 | 726 | |
| 11763 | 42131 | A | 11834 | 3 | 3231 | PGGWLRRALPGRERLQSPVHA VPPQHGTSHSRLLVTWPAGAR DQDFSSPPLLLGETDHLHLDL PLSPLPTSDELFLPGICDPYVKL SLYVADENRELALVQTKTIKKT LNPKWNEEFYFRVNPNSHRLLF EVFDENRLTRDDFLGQVDVPLS HLPTEDPTMERPYTFKDFLLRP RSHKSRVKGFLRLKMAYMPKN GGQDEENSQDRDDMEHGWEV VDSNDSASQHQEELPPPPLPPG WEEKVDNLGRITYYVNHN |
| 11764 | 42132 | A | 11835 | 1 | 624 | |
| 11765 | 42133 | A | 11836 | 2 | 361 | |
| 11766 | 42134 | A | 11837 | 3 | 432 | NSRVDDFVAAQDAKGKKVAP APAVVKKQEAKKVVNPLFEKR PKNFGIGQ\QRLARAEEKKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVVIADVDPIELV VFLPALCRKMGPYCIK GKAR LGRLVHRKTCTTVAFT |
| 11767 | 42135 | A | 11838 | 1 | 684 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11768 | 42136 | A | 11839 | 9 | 247 | AVTSDEPKGKKAKAKKVAPAP AVVKNQEAKKVVDPLFEKRHK N\FGIGQDIQPKRASPRLCLEPR\ YIRLQRQRAILYKRLKGPFCDY PGFTRALDRQTV*SSLLKL\AHK YRP\ETKQEK\QRLFARAREEG VLAKGDPNERDPPVLRARSL TPFHHPWVEKQEKQLVNVNWH TDV\DP\NELVVLLALPLCREKW GVP\YCNYRREKARLWDRLP QERPCTTCPFTQGELRKTGG FWLKLGWKLIRTQFTIDQILMR SRRH\WG\GNVLG\PKSVGS*SP KLEK\AKAKELAH*TG |
| 11769 | 42137 | A | 11840 | 1 | 273 | |
| 11770 | 42138 | A | 11841 | 1 | 218 | |
| 11771 | 42139 | A | 11842 | 1 | 1522 | |
| 11772 | 42140 | A | 11843 | 136 | 441 | |
| 11773 | 42141 | A | 11844 | 24 | 274 | SRQAWHEAASASARRRGTRSP ALSPARAPAGPIWTNARRSARA NSVSPAAAPPPRRPVSLSDPGE SCTRDPRAPDPCGPFRC |
| 11774 | 42142 | A | 11845 | 194 | 365 | |
| 11775 | 42143 | A | 11846 | 1 | 782 | LLVVGTTVVVYFPNGRFKEFM SRHVHLMCYRICVRALTAITY HDRENRPNGGICVANHTSPID VIILASDGYAMVGQVHGGLM GVIQRAMVKACPHVWFERSEV KDRHLVVK\RLTEHVQDKSKLP ILIFPEGTCINNTSVMFMFKGSF EIGATVYPVAIKYDPQFGDAFW NSSKYGMVTYLLRMMTSWAIV CSVWYLPID*ERQIEDAVQFA NRVKSAIARQGGGLVDLLWDGG LKREKVKDTFKEEQQLYSKM |
| 11776 | 42144 | A | 11847 | 3 | 916 | |
| 11777 | 42145 | A | 11848 | 13 | 473 | DPPTDSLSPDGGSELEFYLAPE PFSMPSELLGAPPYSGLGVGDP YAPLMVLMCRVCLEDKPIKPLP CCKKAVCEECLKVYLSAQIQCP TCQFVWC*CAAGAWKTSPSSPC LAARRPCARSASKST/SSAQIQC PTCQFVWCFKCHSPWHEGVNC KEYKKGDKLLRHWASEIEHGQ RNAQKCPKCKIHIQRTEGCDH MT |
| 11778 | 42146 | A | 11849 | 92 | 1103 | |
| 11779 | 42147 | A | 11850 | 1 | 516 | |
| 11780 | 42148 | A | 11851 | 1 | 642 | |
| 11781 | 42149 | B | 11852 | 200 | 608 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11782 | 42150 | A | 11853 | 1 | 1856 | MEETGMCEGHGASPGMEASSG EREKRGTEASPGDREKRGTE ASSGEREKRRTEASSGDREKR GTGKASSGEREKRGTEASYG EREKRGGAAGGQESCAHCGG WLMPRAKPSTHRETNPRGTEA TAMAMDHVGQQADTTDSTDG SQWDPSEHSPNCGIREVGAGDP DTQQTGRHHCYYPACKETNEKT NTNRNSNTFIEQLLHAKQQRGN SGVPFKPGHVMRALTTNALSW AKLYPDPWCLRMGGTGNEVFE NEIKTGSCWIKQEQPRPQSP RSQVRPEADPGPSPLTKMSAEN EYRPPSPPKLAAERDKPSPRLRP RGVPWRRESRVAGRECALLR VAAEGARPPPAGMSYDRAITVF SPDGHLFQVEYAQEAVKIRGST AVGVRGRDIVVLGVEKKSVAK LQDHRPVRKICTLHDNVCMA FAGL/TPADARIVIQTGPGVEFQ\ SHRA*TVEGPRVTVE\YITPLTF ASLKASVYTQSKWGARPFGIS GPHRGFSTFDGTP*LYQTDPSG TYHAWKA\NSIGRGAKSSARS SWEKN\YTDKAIETDDL\TIKLV IKALLEVVQSGGKNIE\LAVMR RDQSLK\LNPEEIEKYVA\IEIK EKEENEKKKQKKAS |
| 11783 | 42151 | A | 11854 | 12 | 432 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11784 | 42152 | A | 11855 | 1 | 1775 | MSYPADDYESEAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIPEVIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVYEIQDIYENSWTKLTERFFK NTPWPEAEAIAPQVGNDVFLI LYKELYRHIYAKVSGGPSLEQ RFESYYNYCNLFNYILNADGPA PLELPNQWLWDIIDEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLLRHLHSL GDYYQAIKVLENIENKKSmys RVPRVPRSPTYYYVGFAYLMM RRYQDAIRVFANILLYIQRTKS MFQRTTYKYEMINKQNEQMH ALLAIAL\TMYPMR\IDESIHLQL REKYG\DKMLRM\QKGDQPQVY EELFSYSCPKFL\SPVVPNYDNI HPN\YHKE\PFQ\QLK\VSDEV Q\QQAQLSTIRSFLKLLHPPCLV AKPGLASLDLTEQEFRIQLLVF KHKMKNLRVDSAVSQALDGEF QSASEVDFY\NDKDMI\HIADTK VARRYGDFIRQ\HKFEELNPN P*RRMG\QRPWMIFTTHSGNLV |
| 11785 | 42153 | B | 11856 | 1 | 537 | |
| 11786 | 42154 | A | 11857 | 98 | 334 | WATERWKGRKNHEISWKCFFG KAIS*MRSSKQMKPNFPRCSSIT VLSVRGMVLFLTACPRFKMSS RTDFRFGNPQVT |
| 11787 | 42155 | A | 11858 | 4 | 422 | |
| 11788 | 42156 | B | 11859 | 1 | 2567 | |
| 11789 | 42157 | A | 11860 | 2 | 364 | |
| 11790 | 42158 | A | 11861 | 1 | 501 | |
| 11791 | 42159 | A | 11862 | 1 | 402 | |
| 11792 | 42160 | C | 11863 | 30 | 673 | |
| 11793 | 42161 | C | 11864 | 195 | 1263 | |
| 11794 | 42162 | A | 11865 | 3 | 648 | |
| 11795 | 42163 | A | 11866 | 200 | 420 | ILPSALRPPNPNWNVG/YVQTQ LVSKPLSLPTGIPCSTTSNLIKPV ITKDARLHRVIVHGWGIGGTIPI AKIAIS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11796 | 42164 | A | 11867 | 1 | 502 | MQLPGRGHSFVCKANAGSTQA RQGASAGVAGCRGWLNYAAS EQIVLRVPHMRCEIPHKCVRRK SRIRPHSPFRLRNCWKGRSVRA FSLLRQLAKGGCAARRLSWVT PGFSQSRRCKTTASAKLACLQV RAQSEDISTVPIHYAYNMTRVG RMQMLGKYNPQSAKLVREAIL PTKATLDLSNQNNEDFSAFQLG LAQALHIKVHTMTREVMSEDEL TKLLEGNLKPAIDMMVEFNTT GSLPENAVDVLNTALGDRKSF VALMALMEYSRYLVAEDKSAF VTPLYVEADGVTNGPINAMML MTGGLFTPDWIRNIAKGGL*FQ YTFTFNRSRSQCFHIFQETSKK FFSMCF*SSLLTKHCHSSRDVW VFSTSFQHIRHTLIDGISNRTNQ LTCNTTSTRTIDGNSQRVLSNTT |
| 11797 | 42165 | C | 11868 | 1 | 3831 | |
| 11798 | 42166 | A | 11869 | 1 | 5370 | |
| 11799 | 42167 | A | 11870 | 1 | 3999 | |
| 11800 | 42168 | B | 11871 | 1 | 12036 | |
| 11801 | 42169 | B | 11872 | 1 | 16395 | |
| 11802 | 42170 | A | 11873 | 1 | 19997 | |
| 11803 | 42171 | A | 11874 | 1 | 70 | |
| 11804 | 42172 | A | 11875 | 44 | 613 | AGTHLRPFSPSLSAAMALRYPM AVGLNKGHKVTKNVSKPRHSR RR\GRL\TKHTKFVRDMIREVCG FAPYERRAMELLKVSKDKRAL KFIKKRVGTHIRAKRKREELSN VLAAMRKA AAKKDLGPSPCPL PEIKDKLDRSPGSPAVRGWVW VCRGPAVPCLVPALSHTLSGCC LVVNQKPWPAHPSRGR |
| 11805 | 42173 | A | 11876 | 1 | 150 | FRGRCCVQRYRGCTLASA/CLL VGAEAEAPSPVDPLERSRPYAVL RGQNLE |
| 11806 | 42174 | A | 11877 | 447 | 725 | |
| 11807 | 42175 | A | 11878 | 2 | 206 | RPVAYLLLQGWGRCCVQRYRG CTLASA/CLLVGAEAEAPSPVDPL ERSRPYAVLRGQNLDQTLH*ST HQA |
| 11808 | 42176 | A | 11879 | 1 | 413 | |
| 11809 | 42177 | A | 11880 | 122 | 268 | |
| 11810 | 42178 | A | 11881 | 1 | 555 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11811 | 42179 | A | 11882 | 221 | 419 | LQTIHQGYSNQNSMVLVPKQR YRPMQNRALRNNAAYLQKSP *ADKQLQQ/ECQDTKSMCKNH KHSYTPITDKQRAKSRVNSHSQ LLQRE*NT*ESNLQGA*RTSSRR TTNHCSMK*KRIQTNGRTFHAH G |
| 11812 | 42180 | A | 11883 | 1 | 2464 | MDEFLNTYTLPRLNQEEVESLN RPITGSEIVAIINSLPRKKSPGPD GFTAEFYQRYKEELVPFLKLF QSIEKEGILPNSFYEASHILIPKPG RDTTIKENFRPISLMNIDAKILN KIILANRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAFFDKIQQP FMLKTLKKFGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKKWKNPSCSWVGRINIM |
| 11813 | 42181 | A | 11884 | 2104 | 2637 | MFQRGHISQWWVVVGALTVFT SVLDTDPMRDNKRSGSEILPFC REHGTSFTYNHAHSPSCSPSCL FSGALFSPENNSGFLCMTLPAS FTAGNRLFSSAGQPWWIQQGF KAHAKARRLILLAFHHYCCRPF LAVELKPSPVSTPTFLFA*LLPP CSVPGAILHESFGEAITWLDAE |
| 11814 | 42182 | A | 11885 | 69 | 417 | QTHSQHYTEWKGVESIPPENW NNTRMPIFTISIQHIIRSSSESNT RERNQGHPNG*RGSTVAFC*R YDRIPRKP*RLIQKTPRTASAAD TQANRVWSGPPASSNRPAEAGP DC |
| 11815 | 42183 | A | 11886 | 376 | 597 | ENKIPRNPTYKGCEGPLQGELO TAAQGNKRGHKHKMEKHSRLM DRKNQYPSAADTQANRVWSGP PANSNRPAEAGPD*PGQNFQYH VE |
| 11816 | 42184 | A | 11887 | 5 | 292 | LTVSCPCSRMLFLTDDVLLPLM FIKKLGANVASPSSKKPLFVIRL VITTLPLACGTLPTSSVSRRTFF RTMLPQA\PEFAPPSTGTESHYY CCIW |
| 11817 | 42185 | A | 11888 | 320 | 596 | YPGKQGLEWTSSKLQQTCKRY RERHKDTP/TRRATPR/RHNCQV HQS*NEGKNVKGSGRERSGYS QREAHQTNSRSLGRNSTSQKRV GASIQRS |
| 11818 | 42186 | A | 11889 | 3 | 239 | EASRGRIRQQHLPCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDK*KEN*QTERTSTPKPD LYITIHKDQSL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11819 | 42187 | A | 11890 | 3 | 278 | EASRGRIRQQHLPPFCNICCSAAS TGDTQANRVWVGPPANSNRPA AEGDC*KEN*QTERSTPKPD LYITIKDQRLIPGLFTSPWISARI |
| 11820 | 42188 | B | 11891 | 394 | 1213 | |
| 11821 | 42189 | A | 11892 | 856 | 1217 | VDRSRLQKVSNNKL VQAKGGC SNPLQGS*KLDNPKDANS/RQQ PERTWKWIFPQPHR*GAFGPRH C*ESHL YQFGLDLLNSAGSGIG KNEVQEQKRAEVGARAPEKE LPEALSWFLKVLW |
| 11822 | 42190 | B | 11893 | 1 | 894 | |
| 11823 | 42191 | B | 11894 | 93 | 938 | |
| 11824 | 42192 | A | 11895 | 149 | 508 | LLEGKLTNKKDIHIKTPSVRHH HQRPKPKISLS**ATSAKSQDTK SMCKNHHKHSYTTITDKQRAINH E*TPIHNCFKESKIPRNPTYKRC *G/RSSRRTANHCSRK*KRTQTN GRTFHTHG |
| 11825 | 42193 | C | 11896 | 1 | 1257 | |
| 11826 | 42194 | A | 11897 | 183 | 1065 | YWRCNGFLS*\YAEAAEEIVDCI TESLSILKTPPKKMNEEMLCQ EFGFGLASVKIMWPRTDEER ARERNCGFVAFMNRDAERAL KNLNATAFRPALSHFPSLPMDT TSQIPKH\PTVSSTNKLILIKTH FQAQSSLNQNIHPMDPSHGIQY SAFSPSTPNPSHPALP*PLAIQVH HAVCDGFHVGRMLNELQQYC DEWQRDKLEEILRGLTPRKNDI GDAMVFCLNNAEAAEEIVDCIT ESLSILKTPPKKMNEEMLCQE FGRFGLASVKIMWPRTDEERA RERNCGFVAFMNRDAERALK NLNATAFRPALSHFPSLPMDTT SQIPKHSSHRQFNKQAHSDHQD SLSGPVQSESKYP SHGSIPWDSI LSLLTLNTQPIPPSLALTHMEME SGLHFHCPFTASPPSAVPPPELE KTTLKFIWNQKRARIANSILSQ KNKAGGITLPDFKLYYKATVT KTAWTGSPTAIRQARTTRQEKE MKGIQIGKEEVKLSLFTDDVNL QVRENK |
| 11827 | 42195 | C | 11898 | 138 | 644 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11828 | 42196 | A | 11899 | 2 | 3088 | ADKTPGGSQKASSKTRSSDVHS SGSSDAHMDASGPSDSMPRT RPKSPRKHNRYRNESARESLCDS PHQNLSRPLENKLKAFSIGKM STAKRTLSKKEQEELKKKEDEK AAAEIYEEFLAAFEGSDGNKVK TFVRGGVVNAAKEEHETDEKR GKIYKPSSRFADQKNPPNQSSN ERPPSLVIETKKPPLKKGEKEK KKSNELEFKEELKQIQEERDER HKTKGRLSRFEPQSDSDGQRR SMDAPSRNRSSG |
| 11829 | 42197 | C | 11900 | 413 | 823 | |
| 11830 | 42198 | A | 11901 | 263 | 1246 | NPGKQGLEWTSSQTPADLQLR VLTVRRNTNKQKGHPHQNPICT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPVME DQMNEKQEEKFREKRMKRN EQSLQEIRDYVKRPNRLIGVPE SDGEKEPSWKTLCRILSRRTSP A*QGRPTFKFRKYRECHKDTPQ GEQLQDT*LSDSPKLK*RKKY* GQPERKKYRLPSANTKTSRLK* TRKSRRNG*ITGHIHPPKTKPGR S*IPE*TNRL*N*GNN**PANQK KSRTTRRIHSQILPEAQRGAGTIP SETIPINGKRGNNPPKLIL |
| 11831 | 42199 | B | 11902 | 67 | 2584 | |
| 11832 | 42200 | A | 11903 | 1 | 3793 | MSDAEDERFLQFQLRYRVYLT GDCRTVGAGQWVQRTREPKQ GEALPHPGSARGWGVFPFRDD GWHLENRVPTLILRFSHLSK QHTRRPYSAPGSEGPTPTPCSL LAQQSEIKLQDGSEAGGGPLLI PRQTGSGVDLRQTPDMQLRV LTVRRKTNKQKGQPHQNPICTS PSSKTKAPHHTYSKTDHIVGSK ALLSKCKRSEITNCLSDHSAIK LELRIKKRIQNRSTTWKLNLL LNDYCVHNEIKA EI |
| 11833 | 42201 | A | 11904 | 1 | 441 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11834 | 42202 | A | 11905 | 312 | 3705 | FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECLDRDEERAYVLYM KYVTVYNLIKRPDFKQQQDY FHSILGPGNIKKAVEEAERLSES LKLRYEEAEVRKKLEEKDRQE EAQRLQQKRQETGREDGGTLA KGSLENVLDSKDKTQKSNGEK NEKCETKEKGAITAKELYTMM TDKNISLIIMDARRMQDYQDSC ILHSLSPPEEAISPGVTASWIEA HLPDDSKDTWKKRGNV |
| 11835 | 42203 | A | 11906 | 1 | 609 | |
| 11836 | 42204 | A | 11907 | 3 | 755 | LRVDNAPAHASGLFFCAGAAG TVLFAMAPSRNGMVLKPHFHK DWQR\RVATWFNQPAR\KIRR\R RPRQAKARRIGPAPRGGGPIRPI VRCPTGRVHNGSWRPGRGFQP GRSSRVAGHSPRKVAPDPSGIS VDPK\RETSSHGSPLQAQRAS GLKE\YRSQTQSSSPRKPSAS/PL *GDSSAEELKL\ATQ\LTGPVMP VRNVYKKEKARV\ITEEV\KNF KAFASLRMARA\NARLFGIRAK RAKEAAEQDVEKKK |
| 11837 | 42205 | A | 11908 | 1 | 327 | |
| 11838 | 42206 | A | 11909 | 1 | 756 | |
| 11839 | 42207 | A | 11910 | 1 | 219 | |
| 11840 | 42208 | A | 11911 | 2 | 227 | |
| 11841 | 42209 | A | 11912 | 1 | 567 | |
| 11842 | 42210 | B | 11913 | 99 | 799 | |
| 11843 | 42211 | A | 11914 | 61 | 342 | |
| 11844 | 42212 | B | 11915 | 1 | 945 | |
| 11845 | 42213 | A | 11916 | 92 | 133 | DPPSQKLKTLRKD*TNG*LQ*P MKRSP*MT*WS*KP*HENYVTH AQASVPDSINWKKGYQ*LKIK* MK*SKKRSLEKKE*KETNKASK KYGTM*KD |
| 11846 | 42214 | B | 11917 | 1 | 368 | |
| 11847 | 42215 | B | 11918 | 1 | 106 | |
| 11848 | 42216 | A | 11919 | 1 | 705 | |
| 11849 | 42217 | B | 11920 | 1 | 834 | |
| 11850 | 42218 | B | 11921 | 1 | 1305 | |
| 11851 | 42219 | A | 11922 | 1 | 1187 | |
| 11852 | 42220 | A | 11923 | 228 | 619 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11853 | 42221 | A | 11924 | 1499 | 2238 | KGKKKVINQISLGQRMRLSQSS HGKVQACQVPFHPNAPPVQF QSRELQSGSRPRSCGEKATRCL RQGPREVPLPKNAWA*QRKQE KKRSRKGS/GREPGLRRPPNAQ ARDRSSRAPATHRKELKPEREH ISCSRSHIRYQEWSVLRDTHVR NLVLDTKRHPALILVEYKERTS SPATEQSCMENDFDELREEGFR RSVITNFSELKEDVQTHHKEAK NLEKRLDKWLTRINSVEKSLND WMELKTMA |
| 11854 | 42222 | A | 11925 | 699 | 796 | |
| 11855 | 42223 | A | 11926 | 1029 | 1223 | ERELPDPLRFPSEGNASALLSAS RTVRASTDRLPLSGTP*RDEPGT SDGNAEITRLLRRSGWEL |
| 11856 | 42224 | A | 11927 | 186 | 1597 | |
| 11857 | 42225 | A | 11928 | 1 | 1200 | |
| 11858 | 42226 | A | 11929 | 1 | 600 | |
| 11859 | 42227 | A | 11930 | 1 | 663 | |
| 11860 | 42228 | A | 11931 | 908 | 1331 | GDMRGRREGGFGLGRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLT MPLAPATFL RVNCWAG/RGR/C*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEEQLAPSPEKRDPL RVKDQGRHPCVV |
| 11861 | 42229 | A | 11932 | 1 | 1707 | |
| 11862 | 42230 | A | 11933 | 1 | 1012 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLIDIYGTLHP KSTEYTTFSAPHHTYSKIDHILG SKALLSKCKRTEIITSYLSHSAI KLELRQNLTQNHSTTWKLNNL LLNDYWLHNEMKAEIKMFFET NENKDTTYQNLWDAFK/RSV*R EIYSTKCPQEKAGKIQN*HPNID QQN**TTSKANKEKKREDSNRC NKK**RGYHHRSHRNANYHQR ILQ/YTSMQIN*KI*KKWINSSTH TLSQD*TRKKLNL*IDQ*QELKL WQ*SIAYQPKRVQDQMDSQPN STRVASKRIKYLGIQLTRM*RTS SRRTTNHCSMK*KRIQTNGRTF HAHG |
| 11863 | 42231 | C | 11934 | 1 | 1788 | |
| 11864 | 42232 | A | 11935 | 550 | 827 | DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLQLL PQEHTRKTLPLQQTSAWTYRLF HTSCEI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 11865 | 42233 | A | 11936 | 584 | 1094 | NWIPSLHLTQKLIQDGLKT*ML DLKP*KP*KKT*AIPFRT*AWAR TSCLKHQKQWQQKPKLTNGI*L N*RVSA/PAKETTISMN/EATYR MGENFCNLLI*QRANIQLQ*T QTNLQEKKNQPHQKVGKGHEQ TLLKKRHLCSQKTHEKMILIITG HQRNANQNHNEMPFHTS |
| 11866 | 42234 | A | 11937 | 797 | 1044 | EESIS*KWPYCP*FVDSMPSPS SYR*VSSQNWKLL*SSYGTKQ EPTLPSQS*AKRTKLEASHYLT NYTTRLQ*PKQHGT |
| 11867 | 42235 | A | 11938 | 176 | 374 | LTNQKKSRTRWIHSQILSEVQR GADKQPNRE*TPIHNCFKENKIP RNPTYKGCEGPLQGEQTAAQ |
| 11868 | 42236 | B | 11939 | 1 | 1843 | |
| 11869 | 42237 | A | 11940 | 3227 | 3391 | DPLPGQRQLLLQKQRRP*TQAG LLSFQPGPQPHGSVPPTLSQPW LPGGWPELSG |
| 11870 | 42238 | B | 11941 | 1 | 1479 | |
| 11871 | 42239 | B | 11942 | 1 | 2097 | |
| 11872 | 42240 | A | 11943 | 654 | 1341 | KNRNYNKLSLRPQCNOQTRTQD *ESHKPLNYMETEQPAPE*LL GT*RNEGRNKDVL*NQREQRH HIPESLGRIQSSV*REIYSTKCLQ E//MQERSKIDTLTSQLEKEKQ EQTHSKASRRQE/DN*NQSRTE GNRDTKNPSKNQ*IQELVF*KD QQN**TASKTNKEKKREESNRH NKK**RGYHHRSHRNTNYHQRI LQTPLRK*TRKSRNGYIPRHH SPKTKTGRS |
| 11873 | 42241 | A | 11944 | 471 | 611 | |
| 11874 | 42242 | A | 11945 | 1 | 585 | |
| 11875 | 42243 | A | 11946 | 3 | 1029 | GRQHGGSQRMGGTASARASSG RLAPRGRGAFRRRCPSRRW RLTCGPAAVEHSFCHNVGPGV RATADKYTCMFTYASQGGTNE QWQMSLGTSEDHQHFTCTIW RPPRGKSYLIYFTQFKAEVAGR LRFYRHGLTFKAA/SLKRES VPLENLRNFEVNQNSSGLTRPG GISKAELSKLVIVGQGIRALSCD QQPLLRRGGTFSSPVKLKGACVP ERAQHITGFLGGTLKFSTWADV ALSRRGFSGWLKPWGREQRVQ GPPGSQQLFRFPLPVKLFWTQD RRSRGTKRVGNMGAMLGKAA MLPPTSSRASFMSLQNCFPMT QGTSFQMNWEEMKCFIFK |
| 11876 | 42244 | A | 11947 | 1 | 1206 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11877 | 42245 | A | 11948 | 1 | 654 | |
| 11878 | 42246 | A | 11949 | 849 | 1089 | SPEGKHYRCYLVHMPSDTERSS L*MRPRAGRSSAEGPGCRQRSL ALDHMVQQAQRCWRYQWWR RFSKEFNQWWRRFSEEL |
| 11879 | 42247 | A | 11950 | 5 | 1376 | |
| 11880 | 42248 | A | 11951 | 2 | 278 | VPQPDTRKGSVLKWISKRGKPL AVEIEESHCLVCLPLRTECLGIKP IVHLFSCTRPVIVPSLELNVDV DSIAHMFVADLLLMITLPSYDIP |
| 11881 | 42249 | A | 11952 | 3 | 267 | |
| 11882 | 42250 | A | 11953 | 1152 | 1338 | FKRGQYGRLLRPRFHHGQILYA RRQGAEP LAIQVHHAVCDGFH VGRMLNELQQYCDEWQGGA |
| 11883 | 42251 | A | 11954 | 394 | 615 | ASDPLRGLLCGPSLLDERHPLL HGAQSHRPPKG*GVRANNAGL AGSSIYLQPRCGIHEVKPSGLLS REGLQLQS |
| 11884 | 42252 | C | 11955 | 114 | 362 | |
| 11885 | 42253 | A | 11956 | 1 | 211 | |
| 11886 | 42254 | A | 11957 | 395 | 547 | |
| 11887 | 42255 | C | 11958 | 412 | 641 | |
| 11888 | 42256 | A | 11959 | 3 | 905 | SNNSPTSASRVAGITGVRHCVR NWWVLGLTDFKNEAVDPRAW TTKSKTPPQNKTQENKNEDV GRDQRVEWLVTTEEVSLSLKG EKLHWKEKEVQSTGKETDARS SMRNYLMLLGPEVQEKEPVKR RLARGKAFVELAEPTRAPGNSG FPVSGGVFTPSLGALTWICKFR VKSWAILNSQLLLDTMKGIV YKNGDRIQGNRSADNRNNGVP LTGARDMQPAMPEPPTHSMGS CAARAFPMASASCFRAPSPIDH PKAEE\WGARRGTGGQPTCSP GAGIHWVKPAGLLSREGLQLH |
| 11889 | 42257 | C | 11960 | 482 | 709 | |
| 11890 | 42258 | A | 11961 | 1 | 734 | MRLESD/KHLVQFVPIHKSKGL EYPIGPWLPFITNSRVQEAFYH DRHSFEAVLDLNAAPESVDLAE AERLAEDLRLLYVALTLSAFAP LVRRRGDKKGD TDVHQSA LGR LLQKGEPQDAAGLR TCIEALCD DDIAWQTAQTGD NQPWQVND VSTAELNAKTLQRLPGDNWRV TSYSGLQQRGHGIAQDLMPRL DVDAAGVASVVEEPTLTTHQF PAGASRGTFWHSLFEDLDFTQ PVDPNWRL |
| 11891 | 42259 | A | 11962 | 21 | 898 | |
| 11892 | 42260 | A | 11963 | 1 | 1962 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11893 | 42261 | A | 11964 | 1 | 313 | MRFYGQLAEDPGQKAGETTR HTEDYISQLPLQRQGIPELALQK DLFINKIYGKEFNVCSTLEDPR VHVLCRDMDEAGNHHSQTIA RTENQTPHVLTHRRELNNT WTQGGEHHTPEPVMGWG*RPR AAKSWGNNKAY*RLYFSAFA ETRDPRTPCPSERSFY*QDLWK/ MSSMSAGRL*RIPEFMSFVGTW MKLETIILSKLLQGQKTKHRMF SLIGGN |
| 11894 | 42262 | A | 11965 | 47 | 178 | QQLVHTAFVIRLIRGTTEGAWR NCKQMAR*QSI SLECKFMPRT |
| 11895 | 42263 | A | 11966 | 2 | 223 | |
| 11896 | 42264 | A | 11967 | 2 | 133 | |
| 11897 | 42265 | B | 11968 | 179 | 6003 | |
| 11898 | 42266 | A | 11969 | 1 | 1125 | |
| 11899 | 42267 | A | 11970 | 1 | 360 | |
| 11900 | 42268 | A | 11971 | 677 | 1238 | |
| 11901 | 42269 | C | 11972 | 193 | 471 | |
| 11902 | 42270 | A | 11973 | 17 | 280 | |
| 11903 | 42271 | B | 11974 | 1 | 654 | |
| 11904 | 42272 | B | 11975 | 526 | 597 | |
| 11905 | 42273 | A | 11976 | 1 | 1261 | |
| 11906 | 42274 | A | 11977 | 170 | 998 | |
| 11907 | 42275 | A | 11978 | 1 | 1130 | |
| 11908 | 42276 | A | 11979 | 1 | 369 | |
| 11909 | 42277 | A | 11980 | 1 | 300 | |
| 11910 | 42278 | C | 11981 | 207 | 451 | |
| 11911 | 42279 | A | 11982 | 1 | 348 | |
| 11912 | 42280 | A | 11983 | 2 | 469 | RGIREGEEFDVDLAGMEVAVG GWGRGLWLHRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFLLSSNTTCQQFRDPGFR GRYPASPHTLSLPPETAHL*LLL CLPAAGVLPHTWPLLDRQGW RGHAR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11913 | 42281 | A | 11984 | 1 | 937 | MAAPLVVLVAVTVRAALFR SSLAEFISERVEVVSPLSSWKRV VEGLSLDLGVSPYSGAVFHER QYIPVKMKSKAFWIFSWEYAM MYVGS/HSGNHLPLLLPSQLLG FHPRSL/VALYFLFQISLQTLVIF WYFFAEMFEHFSLFFVCVFQIN VFFYTIPLAIKLKEHPIFFMFIQI AVIAIFKSYPTVGDVALYMAFF PVWNHLYRFLRNIFVLTCHIVC SLLFPVLWHLWIYAGSANSNFF *GITLTFNVGQRPHRLKAPRASS AARSDRGPAASPASPGDAARPV SGRRPWDAPPHNYLNAVPPPSR |
| 11914 | 42282 | A | 11985 | 1 | 521 | |
| 11915 | 42283 | A | 11986 | 1 | 207 | |
| 11916 | 42284 | A | 11987 | 1 | 867 | |
| 11917 | 42285 | C | 11991 | 1 | 225 | |
| 11918 | 42286 | A | 11992 | 72 | 425 | |
| 11919 | 42287 | A | 11993 | 1 | 354 | |
| 11920 | 42288 | A | 11994 | 460 | 752 | |
| 11921 | 42289 | A | 11995 | 93 | 401 | PQKKYIHIFLDSLALLPRLECSG AISAHCKLHLLVSSDSPASASQ VAGITGARHHAWLIFVFLVEM GFHH/VGQAGLELLTSGDPPAL ASQRAGVSIFIYLFIF |
| 11922 | 42290 | A | 11996 | 2 | 315 | |
| 11923 | 42291 | A | 11997 | 615 | 1180 | |
| 11924 | 42292 | A | 11998 | 3 | 151 | |
| 11925 | 42293 | A | 11999 | 2126 | 2241 | |
| 11926 | 42294 | A | 12000 | 1 | 765 | |
| 11927 | 42295 | A | 12001 | 924 | 995 | |
| 11928 | 42296 | A | 12002 | 1 | 789 | |
| 11929 | 42297 | A | 12003 | 2 | 132 | FFFFFLVEMGFHHVGQAGLKLL TSSDRPPWPPKVLGLQARAT |
| 11930 | 42298 | A | 12004 | 504 | 755 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11931 | 42299 | A | 12005 | 1 | 1322 | MAILPKVIYRFNAIPIKLPVTFFT ELGKTTLRFIWNQKRACIGKSV LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT ESSEIMLHIYNHLIFDKPDKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLTSHTKINSRWIKDL NVRPKTIKTLEENLGNTIQAIG MGKDFMTKTPKAMATKAKID KWDLIKLKSFCTAKETTIRLLG RPPALFTASSSVLKQLALEGILI LDSRALLGFLYEARHSHSNSPN HDAQNATSKKNIRDGYDKIYR QEQVLARMEEKTITAGGNVK WCSHFRKQIGGQWLTLETCTK TPQPFSSTSQISTDKDKGLNPQL LKMDPGHMGWCPPGMGIPWQ LSSDDR VVWVLAAGSGRHPGS GFKSL/PGLLHEGSYGH****S*I *GGNS*GSSGGPQCISGEERVFR |
| 11932 | 42300 | A | 12006 | 12 | 143 | |
| 11933 | 42301 | A | 12007 | 1 | 534 | |
| 11934 | 42302 | A | 12008 | 1 | 591 | |
| 11935 | 42303 | A | 12009 | 2 | 353 | |
| 11936 | 42304 | A | 12010 | 1 | 1923 | |
| 11937 | 42305 | A | 12011 | 1 | 465 | |
| 11938 | 42306 | A | 12012 | 1 | 784 | PGWEKMSRSSVNTQEALPT AAIPRDAKGRVYYFNHITNASQ WERPSGNSISSGGKNGQGEPAR VRCSHLLVKHSQSRPSSWRQ EKITRTKEEALELINGYIQIQS GEEDFESLASQFSDCKHQPKA RG\DLGAFQKKVRLQKPF*RTP RFALADGGR*AGPCFTD\SGIHII LPHLSEGWGAQAWPRGRAGRL GRPAPPCPPASGRTPHSLPPSHSI YCSHNGWEGALPDWGPFTQGG PGVPHSLSVPSWGC DLQTLH |
| 11939 | 42307 | A | 12013 | 1 | 319 | PRERAPRGSVGAGGEICHTSVC CCQPSWTRL LLLITWMLL/YYS ECKPFHCSREEPDNHILLKI*EF GPPSTQQQHAAPLSRSRYSCCP DRYLLRKLGCQEHQLL |
| 11940 | 42308 | A | 12014 | 1 | 1058 | |
| 11941 | 42309 | A | 12015 | 1 | 861 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 11942 | 42310 | A | 12016 | 1 | 431 | IVLGGVATTVCQLNEFIMTDNA VPADVLVLTKPLGTQVAVAVH QWLDIPEKWNKIKLVVTQEDV ELAYQEAMMNMARLNRTGGL LICLPREQAARFCAEIKSPKYGE GHQAWIIGIVEKGNRTARIIDKP RIMEVA\HKWPLKM |
| 11943 | 42311 | A | 12017 | 1 | 1020 | |
| 11944 | 42312 | A | 12018 | 247 | 1436 | GERGPRTMSTRESFNPESEYELD KSFRLTRFTELKGTGCKVPQDV LQKLLESQENHFQEDEQFLGA VMPRLGIGMDTCVIPLRHGGLS LVQTTDYIYPIVDDPYMMGRIA CANVLSDLAMGVTECDNML MLLGVSNNKMTDRERDKVMPLI IQGFKDAAEEAGTSVTGGQTVL NPWIVLGGVATTVCQPNFIMP DNAVPGDVLVLTKPLGTQVAV AVHQWLDIPEKWNKIKLVVTQ EDVELGLPGRRLMNMARLNRT AAGLMHT\FNAHAAT\DTG\FG ILGHAQNLGQASRRNDVSFVIH NLPGAWPRWLAVSKACGNMF GLMHVTCPETSGGLLICLPRIE QAARFCAEIKSPKYGEGHQAWI IGIVEKGNRTARIIDKPRIIEVA\ HKWPLKM |
| 11945 | 42313 | A | 12019 | 219 | 380 | RPLQIRSHSELLGVWTPTESEF*E DTTQSVTAGLLEVSWGRVVLC SKSFPALQS |
| 11946 | 42314 | A | 12020 | 1 | 516 | |
| 11947 | 42315 | A | 12021 | 1 | 228 | |
| 11948 | 42316 | B | 12022 | 56 | 656 | |
| 11949 | 42317 | A | 12023 | 1 | 488 | |
| 11950 | 42318 | A | 12024 | 3 | 419 | |
| 11951 | 42319 | A | 12025 | 1 | 348 | |
| 11952 | 42320 | A | 12026 | 1 | 708 | |
| 11953 | 42321 | A | 12027 | 25 | 213 | |
| 11954 | 42322 | A | 12028 | 1 | 1165 | |
| 11955 | 42323 | A | 12029 | 1 | 411 | |
| 11956 | 42324 | A | 12030 | 1 | 996 | |
| 11957 | 42325 | B | 12031 | 1 | 744 | |
| 11958 | 42326 | A | 12032 | 1 | 444 | |
| 11959 | 42327 | A | 12033 | 1 | 555 | |
| 11960 | 42328 | A | 12034 | 1 | 2241 | |
| 11961 | 42329 | A | 12035 | 1 | 408 | |
| 11962 | 42330 | B | 12036 | 1 | 423 | |
| 11963 | 42331 | B | 12037 | 1 | 507 | |
| 11964 | 42332 | A | 12038 | 3 | 529 | |
| 11965 | 42333 | A | 12039 | 191 | 319 | |
| 11966 | 42334 | A | 12040 | 1 | 660 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11967 | 42335 | A | 12041 | 1 | 579 | |
| 11968 | 42336 | A | 12042 | 1 | 2940 | |
| 11969 | 42337 | A | 12043 | 1 | 4280 | MEYYAAIKKDEFMSFVGTWM MLETIILSKLSQGRKPKRRMLSL IGSQLLTNKGTSMWENEFDELT EVGFRRTLHPKSTTEYTFFSAPH CTYLLKIDHIIASKTLLSKCKRTEI ITNGLSDHSVIKLELKIKKFTQN CTTTWKLKNLLNDYWVNNEI KAEIKMFFETSENEEDTMYQNL WDTFKPLCRGKFIALNAHKRK QRRSKIDIQTAQLKELEKEQQT NSKASRRQEITKIRAEKVTETR KTLQKINESRSW |
| 11970 | 42338 | A | 12044 | 1 | 645 | |
| 11971 | 42339 | A | 12045 | 3 | 362 | LDQLLDMSYE/QLMQLYSCAQ RRRLNPGLRRKQHSLLK\RLRK AKK/EAPMEKPEVVKTHLRD MIILPEMVGSMVGVYNGKTFN QPEMIGHYLGEFSITYKPVKH/G RPGIGATHSSRFIPLK |
| 11972 | 42340 | A | 12046 | 1 | 519 | |
| 11973 | 42341 | A | 12047 | 2 | 599 | PPRSEDPAKMAEVEHEEGSG PFRKFTLPAAVDL\DQ\LLDIVPT KQFDAAVQVAAQRRRLEPGGL RRKQ\HSPA*KRLRKAKKGGPA PWRKPEVVKT/HTLRDYDHSYP EMVG\SMVG\IVYNGK\TFNQV GDQGVCGRPCRLGWAGVA*CR RDQLTPSFALGLPQPEMIGHYL GEFSITYKPVKHGRPGIGATHSS RFIPLK |
| 11974 | 42342 | A | 12048 | 8 | 224 | RTASYPRRFPWDHLLICPCQQL LICFLSLWIRLVFTKVSCT*NHN NMFSCVWLLLLSMIFLRFTHIA CIRNI |
| 11975 | 42343 | C | 12049 | 65 | 163 | |
| 11976 | 42344 | A | 12050 | 3 | 187 | |
| 11977 | 42345 | A | 12051 | 3 | 689 | HASDQKEIIIEPFQAVDEVERVP EDYYTGPPVYLTEVTTLQQRLLQ PDFQPVCASQLYPRHKHLLIKR SLRCRKCEHNSKPEFNPTSIF KIQLVAVNYIPEVRIMSIPNLRY MKESQVLLTLNPNVENLTHVTL LECEEGDPDDINSTAKVVVPPK ELVLAGKDAAAAYDELAEPQD FQDDPDIIAFRKANKVGIFIKVT PQREEGEVTVCFMKHDFKNL \AAPISP |
| 11978 | 42346 | A | 12052 | 1 | 882 | |
| 11979 | 42347 | C | 12053 | 152 | 404 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11980 | 42348 | A | 12054 | 3 | 398 | LRKIKIDLGKFSDNPDGYIDVLQ GLRQSFDLTWRDIMLLLDQSLT PNEKSAAKTAAREFGDLWV/S FQN*SCKTTNRSSNGAPDAVHD *D/PTADPWTGPLAHMLMTL KAPLTRKSQLHDPYYAPIQQA V |
| 11981 | 42349 | A | 12055 | 2 | 286 | |
| 11982 | 42350 | C | 12056 | 261 | 482 | |
| 11983 | 42351 | B | 12057 | 1 | 1133 | |
| 11984 | 42352 | A | 12058 | 438 | 575 | NKTRMPSLTTPLOHSTESPSQSS QTREGNKGYPNW*RGSHTVTV C |
| 11985 | 42353 | B | 12059 | 50 | 309 | |
| 11986 | 42354 | A | 12060 | 1 | 870 | |
| 11987 | 42355 | A | 12061 | 148 | 368 | ELSSCSLMSHRAIHPSEERATT T/NQQSEPGSW*GWVGANRWC HKMSSGSLGTEPCGSCCLACSA WTVTVQAQ |
| 11988 | 42356 | A | 12062 | 405 | 707 | RLSLQTAGCSDVPVFPSAPSGPP SPA*AP*SGSAASPWPPFAPSAA HVAMPAPPRHWPQLSLKMPPW PPDSPVPPGCLA*AEAPPHCPV HLPASRSALS |
| 11989 | 42357 | A | 12063 | 90 | 470 | KSVHSLPPSFSSLLPWTCNRTLS KPPALPSPSRQPECRRLLHCSG SRHSSCPSSSSSPSFSSSPSSSS SASASPPPPSPSPAPP*LWLQPL FCSQ*QLCHCQELVHLESRLTY PYHSSNQPF |
| 11990 | 42358 | B | 12064 | 1 | 474 | |
| 11991 | 42359 | A | 12065 | 1 | 383 | MEYYAAMKNDEFMSFVGTWM KLETIILSKLSQGQKPNTACSHS WMDPQRRGKRQSLISEAGAN QFPKSVFRFFGLGDSKVGSKWS ATCACEPIHTSEYCGDRVICKTT SSLRGASFAWCSSNGE*WFPA SSMSLQRT |
| 11992 | 42360 | A | 12066 | 1 | 384 | MIITGLEDYEMGLRMEGTLEIP GHYQKDKFLAQSTPDLLLPKTS LTNPFSINQILAERQIVTFTVYP DTERDRETRNLADLKQIKIDLG KFSDNPDGYIDILRGLRQSFDLT WRDIMLLLNQTLAPN |
| 11993 | 42361 | A | 12067 | 152 | 238 | |
| 11994 | 42362 | A | 12068 | 89 | 544 | |
| 11995 | 42363 | A | 12069 | 62 | 199 | SWKPSFSANYHKDRKPNTACS HS*DPAFLAPSPVP*SRPLRPPQ D |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 11996 | 42364 | A | 12070 | 1 | 655 | SVSGLVEKVTFEQRLKGGEGDS TVGSSGNEIFRQWPCWELSNGC SLQGDAGCSCLVVHVTFPAGSL SGDGLPTAQWLQSLVLAGGR RVNSTQGHRCHHWGSVAEPCV LVKRHHAAQEGLCSFQKTPRS QVPFHLFWDPGHHTLLCSYCPS VGVAGTQPAVQAVSTAV*TAAE GEPLPMSNMRLVFCPCDSLL RMMVSSFIRVPTKDMNSSFFM |
| 11997 | 42365 | A | 12071 | 1 | 987 | MLVLGYNRKNTEGTQKQKGT NASDFHFLSQVLEQVSPKGSK EAQCCVLRHLGCESSESAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLKGKERR QREGERRERKRERERERESQR KERKREKKGKKREREDRSDL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYYL TWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPIN*SMISTI TQGKEENPTAFLERLREALRKH |
| 11998 | 42366 | A | 12072 | 1153 | 1379 | CLASWKEKSLHCPQRKQRLR GEELEKLKKWKETATQIKRSYC WI*PSKSPHYLTS*KR*WNY**L GNYNSIPAS |
| 11999 | 42367 | A | 12073 | 1 | 864 | |
| 12000 | 42368 | B | 12074 | 8 | 441 | |
| 12001 | 42369 | A | 12075 | 62 | 332 | TDSPHCTDPPSRPTVPASCLKRK CCGSTMPTARPIMPTLMETR*M PISPRVSWAGPRPTSWPALISST LFPRMANHWRD*SRITWFQGG A |
| 12002 | 42370 | A | 12076 | 34 | 409 | TRAAGIRHEGKPEKTGLKRNFT N/DCRKS*TSG*RSTTSSRSRSPS PAPRSRSCSR\RDLPAPPPLSRSG DRPQTAPSCPMWRARLPSCPGS AIPIPRPAWTRSACCGAastrLR PFSGSSTSPQWM |
| 12003 | 42371 | A | 12077 | 1054 | 1368 | |
| 12004 | 42372 | A | 12078 | 298 | 514 | PNWFKHDVSKSESFSNMWIA KILKA/ARPAPLTQCV/RNSCFL QCRHLSSVSASDLT*DNVKRQF CVSPHTES |
| 12005 | 42373 | A | 12079 | 2 | 1613 | |
| 12006 | 42374 | A | 12080 | 2 | 106 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12007 | 42375 | A | 12081 | 42 | 305 | YNTVLPKACLCGSLICWMN*SH SDQNMQVSVERSINLRVRLYAC CGLLLCTAYPQHFAHRYVDKIP GYPSRAGTLTGLHPMQVCRCR |
| 12008 | 42376 | A | 12082 | 206 | 6038 | |
| 12009 | 42377 | A | 12083 | 1 | 4316 | MQWEEAEKDPGSCVFQRPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGT QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSDN |
| 12010 | 42378 | A | 12084 | 393 | 991 | |
| 12011 | 42379 | A | 12085 | 324 | 438 | |
| 12012 | 42380 | B | 12086 | 528 | 598 | |
| 12013 | 42381 | A | 12087 | 52 | 574 | |
| 12014 | 42382 | A | 12088 | 1235 | 1366 | |
| 12015 | 42383 | A | 12089 | 1 | 1800 | |
| 12016 | 42384 | A | 12090 | 1 | 513 | |
| 12017 | 42385 | A | 12091 | 3 | 77 | |
| 12018 | 42386 | A | 12092 | 1923 | 2171 | GAFCPFTLLHGYQVLQWPGSSL PHKEGPAPALEGGHVYPRWI*A SADSQSTEAGRIGPASTG*RQYP GGEEHACCLPALLHS |
| 12019 | 42387 | A | 12093 | 1 | 360 | |
| 12020 | 42388 | B | 12094 | 21 | 3636 | |
| 12021 | 42389 | A | 12095 | 1 | 936 | |
| 12022 | 42390 | A | 12096 | 1 | 599 | |
| 12023 | 42391 | A | 12097 | 1 | 248 | VGKSSIVCRFVQDHFHDHNISPTI GASFMTKTVLCGN/ELHKFLIW DTAGQER/SRQIPPLDPHENGNN GTIKVEKPTMQASRRCC |
| 12024 | 42392 | A | 12098 | 1426 | 1572 | |
| 12025 | 42393 | A | 12099 | 367 | 513 | |
| 12026 | 42394 | A | 12100 | 31 | 661 | APALPGCEHMMAIKRELKVCLL GDTGVGKSSIVCRFVQDHFHDH NISPTIGASFMTKTVPCENDFT KFLIWDTAGQERFYS LAPMY RGSGAAVIVYDFTEAGFH FHPL KKWVKRLKELGPEINIVMAIA GNKCDLSDIREVPLKGC*RNTA ESIGAIVVETS AKNAINIEELFQ GMSRPDPHPWTPHENGNNGTIK VEKPTMQASRRCC |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12027 | 42395 | A | 12101 | 1 | 487 | MDKFLDITYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAIFYQRLISNFSKVSQYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNW KKLL |
| 12028 | 42396 | A | 12102 | 1 | 1563 | |
| 12029 | 42397 | A | 12103 | 1 | 1449 | |
| 12030 | 42398 | A | 12104 | 3 | 1606 | |
| 12031 | 42399 | A | 12105 | 2 | 402 | |
| 12032 | 42400 | A | 12106 | 172 | 329 | |
| 12033 | 42401 | A | 12107 | 1 | 720 | |
| 12034 | 42402 | A | 12108 | 97 | 206 | |
| 12035 | 42403 | B | 12109 | 1 | 1248 | |
| 12036 | 42404 | A | 12110 | 1 | 1419 | |
| 12037 | 42405 | A | 12111 | 1 | 1387 | MDKFLDITYTLPRLNQEEVESLN RSITGSEIVAIINSLPTKKSPGPD GFTAIFYQRYKEELVLLLKL QSIEKEATLPNSFYEASIIIPKP GRDTTKKENFRPISLMNIDAKIL SKILANQIQQHIKKFVHHDEVG FIPRMQGWFNHKSKNVIQYIN RTKDKNYMIISIDAEKAFDKIQ QLFMLKTL SKLGIDGTYLKIIRA IYDKPTVKIILNGQKLEEFPLKT GTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGILLGKEEVKLSLF ADDMIVYLENPIVSAQNLALKLI SNVS\KV*GYKINVQKSQAFLY TTNRQTESQIMSELPFTIASKRI KYLGIQFTRDVKD LFKENYKPL LNEIKEDTNKWK NIPCSWVGRI NIVKMAILPKPLLIPRQTGSGV DLQQTPTDLQLSVLTVRRKINK QKGHPHQYLIWTSPPSKTKGRQ LLASNRTKLDGE |
| 12038 | 42406 | B | 12112 | 1 | 711 | |
| 12039 | 42407 | A | 12113 | 1694 | 4489 | IYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIAKAIRSQKNKS GGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYNYLIFDKPEKNEQWGKDSLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLIVRPKTIKT LEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTKWEKTFA TYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDM |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12040 | 42408 | A | 12114 | 1 | 115 | |
| 12041 | 42409 | A | 12115 | 58 | 414 | |
| 12042 | 42410 | A | 12116 | 6 | 389 | VMTTGTNSRVEPRVRGRVYKK KMDKKRQEKITEAKSKDKSQM DEEKTD/DEKPKLQVELEQEYQ DKFKRLPLEILEFVQEAMKGKI SEDSNHGSAPLSLSSDPGKVNH KTPSSEELGGDIPGKEFDTP |
| 12043 | 42411 | B | 12117 | 50 | 5137 | |
| 12044 | 42412 | A | 12118 | 1 | 1194 | |
| 12045 | 42413 | A | 12119 | 1 | 2559 | |
| 12046 | 42414 | A | 12120 | 3 | 406 | |
| 12047 | 42415 | A | 12121 | 119 | 423 | TSSCSSEK FVITHLLKPTSVNSS KSFSFQLCSIG/VQGAAILWRRR GSLVFRIFSFSALVSPHLCGFIYL WSLTMVTYFSLNNGRPSPCQA AAPQVNLGLLC |
| 12048 | 42416 | A | 12122 | 3 | 597 | ISASASDNVFMVSSPSCSSCFF TLRYRLWKSEKPLYYSFVDKP VAYKKREMVVN LQKQFKHTG RVQ/SSN LLEKKAPSSFQFNWT EEDTDRTCFHGHSLQGV LKEK GQSLLTKNSLYWLSTQKF*RCY GHHVPPYEESIYFLSNR FN LNF SFLLRIKTSFLHEEVSLVEK\KL FEEKIQCKERNQDPRKVRTTL |
| 12049 | 42417 | A | 12123 | 1 | 883 | |
| 12050 | 42418 | A | 12124 | 23 | 362 | FAFNMPEPGKIVPAP*KGSKKA VTKAQNKDGEKRMLSRKESYS VYVYKVLKQVHPDTGVSSKG MGIMNSFVDDILERIAGEAFRL AHYNKRSTITSREIQT D VRLLLT REMVK |
| 12051 | 42419 | A | 12125 | 2 | 405 | |
| 12052 | 42420 | A | 12126 | 1 | 398 | LHSAMPEPAKSAPAPKKGSKK AVTKAQKKDGKKRKR SRKESY SIYVYKVLKQVHPDTGISSKAM GIMNSFVNDIFERIAGEASRLAH YNKRSTITLPREIQTAVRLLLP GELAKHAVSEGTKAVTKYTSA K |
| 12053 | 42421 | A | 12127 | 1 | 401 | |
| 12054 | 42422 | B | 12128 | 48 | 424 | |
| 12055 | 42423 | A | 12129 | 3 | 462 | DAWVSGRLTELPSSCFFPPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKKDGKKRKR SRKESYS VYVYKVLKQVHPDTGISSKAM GIMNSFVNDIFERIAGEASRLA HYNKRSTITSREIQTAVRLLLP ELAKHAVSEGTKAVTKYTSSK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12056 | 42424 | A | 12130 | 74 | 504 | FAFNMPEPAKSAPAPK\KGSKK AVTKAQKKDGKKRK/RSRQGR AYSVYVYKVLKQVHPDTWHL LLRPWGIMELLSFNDFRNGIAG LRVSRLGRI*QQGVSTIHLPGEI HDGPLRLACLPGGVWPSKAVF RGAPRPFNQVNTSV |
| 12057 | 42425 | A | 12131 | 53 | 471 | |
| 12058 | 42426 | A | 12132 | 1 | 241 | FKDTCTRMFIAALFTIAKTWNQ PKCPTMWHIYTMEEYAAIK/SD EFMSFVGTWMKLETITLSKL*Q GQKTKHRMFSLLIGGT |
| 12059 | 42427 | A | 12133 | 1 | 244 | |
| 12060 | 42428 | B | 12134 | 1 | 2142 | |
| 12061 | 42429 | A | 12135 | 1 | 1962 | |
| 12062 | 42430 | A | 12136 | 3 | 393 | IWMKLETIILSKLSQG*KTKHR MFSLTGGNLTMRITLGHRLPSL PHRLRPCARLHLRCPWPSPSR RRCARSTTPTATPPSTATSRWSS TPPTCTCLWPSTSTGTTWPWRT SSATSCACRTTKWSMPRS |
| 12063 | 42431 | A | 12137 | 2 | 87 | |
| 12064 | 42432 | A | 12138 | 1 | 270 | |
| 12065 | 42433 | C | 12139 | 1 | 214 | |
| 12066 | 42434 | A | 12140 | 1 | 684 | |
| 12067 | 42435 | C | 12141 | 1 | 333 | |
| 12068 | 42436 | A | 12142 | 1 | 189 | |
| 12069 | 42437 | A | 12143 | 215 | 310 | |
| 12070 | 42438 | A | 12144 | 2 | 91 | |
| 12071 | 42439 | C | 12145 | 1 | 229 | |
| 12072 | 42440 | A | 12146 | 1 | 268 | |
| 12073 | 42441 | A | 12147 | 1 | 278 | |
| 12074 | 42442 | A | 12148 | 2 | 274 | WMKLETIILSKLSQRQKTIHHLF SLIALFTIAKKWKPPRYLSVDK WIKKLWY/HTYTMEYYSAFKK EAILPIAIAWMGLKDIMLSEISQ TWP |
| 12075 | 42443 | A | 12149 | 2 | 136 | |
| 12076 | 42444 | A | 12150 | 2 | 95 | |
| 12077 | 42445 | A | 12151 | 1 | 233 | |
| 12078 | 42446 | A | 12152 | 377 | 484 | |
| 12079 | 42447 | A | 12153 | 2 | 91 | |
| 12080 | 42448 | A | 12154 | 1 | 891 | |
| 12081 | 42449 | A | 12155 | 1 | 1194 | |
| 12082 | 42450 | A | 12156 | 785 | 892 | |
| 12083 | 42451 | A | 12157 | 191 | 317 | |
| 12084 | 42452 | A | 12158 | 410 | 520 | |
| 12085 | 42453 | A | 12159 | 683 | 796 | |
| 12086 | 42454 | A | 12160 | 830 | 927 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12087 | 42455 | A | 12161 | 18 | 539 | PTDP*LGIIYQKEYKSCYYKDICT/RVVCVPAALFTIANTWNQPKCTSMIDWVKKMWHIYTMEEYAAIKTDEFMSFAGTWMKLETIILRKLSQGQKTKHRMYSLIGGNLTMRFTFGHSAGSHHTPGPIMRCGAGGGIALGEIPNVNDELMGTANQHGTICIPMQQNCTLCTCTLKLKV |
| 12088 | 42456 | A | 12162 | 1 | 108 | ASTAGVSYYVAQAGLKLLGLSLSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFMYFAGTWMKLETIILSKLSQGQKTKHRMFSL*GVSYYVAQAGLKLLGLSLSKCRDYRCEPPCPE |
| 12089 | 42457 | A | 12163 | 1 | 701 | |
| 12090 | 42458 | A | 12164 | 274 | 435 | |
| 12091 | 42459 | A | 12165 | 1 | 3658 | |
| 12092 | 42460 | A | 12166 | 749 | 856 | |
| 12093 | 42461 | A | 12167 | 1 | 598 | |
| 12094 | 42462 | A | 12168 | 538 | 664 | |
| 12095 | 42463 | C | 12169 | 1 | 873 | |
| 12096 | 42464 | B | 12170 | 177 | 325 | |
| 12097 | 42465 | B | 12171 | 1 | 1245 | |
| 12098 | 42466 | A | 12172 | 1 | 3313 | |
| 12099 | 42467 | A | 12173 | 1940 | 2060 | |
| 12100 | 42468 | A | 12174 | 1 | 1213 | |
| 12101 | 42469 | B | 12175 | 155 | 559 | |
| 12102 | 42470 | A | 12176 | 2 | 321 | PAPRGGAYRGRQTSLSGGLHPV*ASWLLCLPKQAWAM/VGRP PQASLLPCSLISDCCASNQRDSVGVPSEPCAGYNLLLCRFLSQSEKHSIRVGAVDCSCSYLAIL |
| 12103 | 42471 | A | 12177 | 1 | 519 | |
| 12104 | 42472 | A | 12178 | 1 | 477 | |
| 12105 | 42473 | A | 12179 | 119 | 375 | KRTQT*AIAGAPPPASLPPCSLISDCCASNE*GSVGIGPSKPGAGYNLLLCHLISPSISPTSSPKSDTCPI ADFSNKSPDRSSAGDILLAMQSLGSMALFLILPTREHGKFFHLFVSSFISLSSGL |
| 12106 | 42474 | B | 12180 | 1 | 363 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12107 | 42475 | A | 12181 | 1 | 1309 | MAEGEEGTSYMAAGERVVAIA LIDGFRPLTLESTFFNSGSCSKL EQHSTYLGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVPEP KQHGIGPKQKYRSTGPNRALR NNAAYLQFLIFGNLEKTKPWG KDSLLIKVFEAAVLWIECFAFIF YDARGVLIVVQVDSCSKLEQHS TLSRALLIYKGFRCFRNHHQTG FSPAGANQRGPLAATLSGPGGE GQSAVARLTGEKKNHPGAQYA NRLSPRVGRFINAAGTTGFPTG KRAVSATQLMDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGHLISDCCASNQPDVGVG PSEPGAGYNLVVRHFLSPSEKH SIRVGVTFRSRCRPSPLPLTQKG NSLTPCASQLRQCLALLRLR*R AISCCPSHW*KEKPPWRPIRKPP LPARWPIH*CSWHDRFPD/CESG HLISDCCASNQPDVGVGPSEP GAGYNLVVRHFLSPSEKHSIRV GVTRFSRCRPSPLPLTQKGNSLT PCASQLRQCLALLRLRH |
| 12108 | 42476 | B | 12182 | 1 | 1335 | |
| 12109 | 42477 | A | 12183 | 1 | 1675 | |
| 12110 | 42478 | B | 12184 | 57 | 1530 | |
| 12111 | 42479 | A | 12185 | 1 | 1419 | |
| 12112 | 42480 | A | 12186 | 1 | 574 | RVDDFVRQTRPSAQAALAEKM AANQPPPLMMKHSQTDLVSRL KTRKILGVGGEDDDGEV/HRSP ISQALGTEIKFTIREPLGLTVWQ FVSAVLFSGIAIMALAFPDQLY DAVFDGAQVTSKTPIRLYGGAL LSISLIMWNALYAEKVIRWTL LTEACYFGVQFLVVTATLAETG LMSLGIRLTRSSRRGR |
| 12113 | 42481 | B | 12187 | 79 | 387 | |
| 12114 | 42482 | A | 12188 | 1 | 908 | |
| 12115 | 42483 | A | 12189 | 2 | 70 | |
| 12116 | 42484 | A | 12190 | 1 | 1158 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12117 | 42485 | A | 12191 | 2 | 611 | FVSVPSVLLGLQFWRSERD/TARLQSARWRVERGRLEKLLSRQRPRRREEVVVGREVCRTMEV RASLQKIVSNGDEQLEKAMEEI LRDFEKRPSLLVDCQSSSEISD HSFGDIPASQTNKPSLQILDP NTEISTPRPSSPGGLPEEDSVLF NKLTYLGCMKVSSPRNEVEAL RAMATMKSSSQYPPVTLVYP |
| 12118 | 42486 | A | 12192 | 3 | 497 | |
| 12119 | 42487 | A | 12193 | 1 | 804 | |
| 12120 | 42488 | A | 12194 | 1 | 1243 | MAPVEHVADAGAFRLHAAL QDIGKNIYTIREVVTEIRDKATR RRLAVLPYELRFKEPLPEYVRL VTEFSKKTGDYPSLSATDIQVL ALTYQLEAEFVGVSHLKQEPQ KVKVSSSIQHPETPLHISGFHLP YKPKPPQETEKGHSACEPENLE FSSFMFWRNPLPNIDHELQELLI DRGEDVPSEEEEEENGFEEDRK DDSDDGGGWITPSNIQIQQE LEQFDVPEDVRVWLA*PPDFA MQNVLLQMGLHVLAVNCMLI REARSYILRCHGCFKTTSDMSR VFCSHCGNKLKVSVTVSDD GTLHMHFSRNPVLPNPRGLRY SLPTPKGGKYAINPHLTEDQRF PQLRLSQKARQKTNVFAPDYIA GVSPFVENDISSRSATLQVRDS TLGAGRRRLNPNACRKKFVKK |
| 12121 | 42489 | C | 12195 | 164 | 350 | |
| 12122 | 42490 | A | 12196 | 1 | 378 | |
| 12123 | 42491 | B | 12197 | 265 | 1539 | |
| 12124 | 42492 | A | 12198 | 1 | 2511 | |
| 12125 | 42493 | A | 12199 | 1 | 1077 | |
| 12126 | 42494 | B | 12200 | 38 | 1451 | |
| 12127 | 42495 | A | 12201 | 1 | 207 | |
| 12128 | 42496 | A | 12202 | 1 | 197 | |
| 12129 | 42497 | A | 12203 | 1 | 216 | |
| 12130 | 42498 | A | 12204 | 1 | 335 | |
| 12131 | 42499 | A | 12205 | 1 | 174 | |
| 12132 | 42500 | A | 12206 | 1 | 1309 | |
| 12133 | 42501 | A | 12207 | 1 | 1266 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12134 | 42502 | A | 12208 | 1 | 590 | IDRFDAPCGLEELEDHEDEFNE EDERAIEMYRRRLAEWKATK LKNKFGEVLEISGKDYVQEVTK AGEGLWVILHLYKQGIPLCALI NQNL SGLARKFPDVKFKAISTT CIPNYPDRNLPATILVYPGVDIN G\QFIGPLSV\GGMNLTRDELEW KLSSEGAIMTDLEENPKKPIEDV LLSSVRRSGPHEEGQRFGR |
| 12135 | 42503 | A | 12209 | 291 | 416 | SHYDKIAEKLSEYDQISPPNSQ PDKENPVLST**SIQRRHMTLFK MNLKIILKYRKPEA*SQRLVSK R*KHSIRGSGINLSFVPTGFQIVP FHLFETSLWL |
| 12136 | 42504 | A | 12210 | 437 | 773 | DYTITGELKTAIQRSKINFCPIH SHSSHNAKSFVI*TVTLLHRHLL *KVSVNKVQSLFIQCGIFSEAGA GVYNYCPPPRQRRQPGDKPRW RWRRGRNNRCSANSHGLQLYA |
| 12137 | 42505 | A | 12211 | 1 | 1183 | |
| 12138 | 42506 | A | 12212 | 1 | 459 | |
| 12139 | 42507 | A | 12213 | 1 | 513 | |
| 12140 | 42508 | A | 12214 | 91 | 1168 | |
| 12141 | 42509 | A | 12215 | 323 | 429 | |
| 12142 | 42510 | A | 12216 | 870 | 1305 | SPGLPHCWQPCRARSRGTDVW NVLVS\GSGSGAYKEPAILVGPE NLTLTVHQTAVLECVATGNPRP IVSWSRLGWPPNPTAKEQEQRRA KTESQRKQPRDKARENQPKAA RPKRAAPKSHEAARKTNPPTAS TKRQAAPTNTPKESS |
| 12143 | 42511 | A | 12217 | 1 | 2695 | |
| 12144 | 42512 | A | 12218 | 1 | 258 | |
| 12145 | 42513 | A | 12219 | 1 | 624 | |
| 12146 | 42514 | A | 12220 | 247 | 425 | |
| 12147 | 42515 | A | 12221 | 31 | 858 | LLEIVNSSIQPEKQAGWLSQAV HGAPDGNRPMLHPETSPGRG HLLAVLLALLGTTWAEVWPPQ LQEQAPMAGALNRKESFLLLSL HNRLRSWVQPPAADMRLDW SDSLAQLAQARAALCGIPTPSL ASGLWRTLQVGWNMQLLPAG LASFVEVSLWFAEGQRYRHA AGE*ARNATCTHYMQLVWATS SQLGCGRHLCSAGQAAIEAFVC AYSPRGNWEVNGKTIVPYKKG AWGSLCTASVSSLLKAWDHAR GLLGGPRETLGKEPTEPWTALK |
| 12148 | 42516 | A | 12222 | 1 | 1519 | |
| 12149 | 42517 | A | 12223 | 1 | 789 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 12150 | 42518 | A | 12224 | 1 | 505 | ATEDPGVAMGRRPARCYRYCK NKPYPKSRFCRGVDAKIRIFDL GRKKAKVDEFPLCGHMSDEY EQLSSEALEAARICANKYMKVS CGKDGFHVRVRLHPFHVIRINK MLSCAGAD/RIHISKKWGFTKF NADEFEDMVAEKRLIPDGCGV KYIPSRGPLDKWRALHS |
| 12151 | 42519 | A | 12225 | 135 | 828 | RFWVSPHGPAAAPARCYRYCKN KPLPKVLRFCR\GVP\DAKIRIFD PGAERQKVE*VFRFCGHMVS DE\YNQLSS*ALEAARNLCPIS TMVKS\CGKDGFHVRVRLHPF HVIPHQTRCCSCAGADRLQTG MRG\AFGKPGQTVARVHIGQVI MS\RTKLQNKHEV\IDALRRAK \FKFPGRQ\KIHISKKWGFTKFN ADEFEDMVAEKRLIPDGCGVK YIPSRGPLDKWRALHS |
| 12152 | 42520 | A | 12226 | 2 | 367 | |
| 12153 | 42521 | A | 12227 | 2 | 376 | QTYSLRRATPRHIIVGFTKVM KEKVLRAA/NKPIRLTVDLSAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW |
| 12154 | 42522 | A | 12228 | 1 | 714 | |
| 12155 | 42523 | A | 12229 | 122 | 939 | YPGKQGLEWTSNKIQQTCS*GS SLLEGKLTNRKDIHTKTPSVRH/ RSSKAKERSVIEDQMNETKRE EMFREKRVKRNEQSLQEIWEY VKRPNLRLIGVPESDGDNGTKL ENTLQDIIQQYFPNLRQANIQI QEIQRMPQRCSSRAAPRHIIVR FTKAEMKEKMLRAARGKGRV THKGKPIRLKVDVLAETLQARR EWGPIFNILKEKNFQPRISFPAK LSFISKGEIKSFTDKEMLRDFVT TRPALQELLKEALNMERNRY QPQQKHAKL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12156 | 42524 | A | 12230 | 1 | 1043 | MGDFLHSTDRNYLIKFWAKLS AKKTPANSSSPLGDHQPCHTK NLQIPEKWLIGLLLPLKADLLK EDAGTHCKEAKNLDERLDEWL TRINSVEKFLNDLMELKTMAQE LHYACTSFSSQFDQLEERVSVIE NQMSEMKREEKFREKRVKRNE QSLQKIWDYVKRPNLRLTGVPE SDWENGTKLENSLQDIIQENFP NLARQANIHIQEIQRMPQRYSS RRATPRHLIVRFTKFEMTEKMY RAAREKGQVTHKGKPIRITADI SAETLQARREWGPIFNILKEKN FQPRISYPAKLSFISEGEIKSFTD KQMLRDFVTTRPTLQELLKEAL /NMERNNQYQPLQKHAKL |
| 12157 | 42525 | B | 12231 | 1 | 1275 | |
| 12158 | 42526 | A | 12232 | 1 | 1584 | |
| 12159 | 42527 | B | 12233 | 1 | 1023 | |
| 12160 | 42528 | A | 12234 | 1 | 2052 | |
| 12161 | 42529 | A | 12235 | 5160 | 6183 | VSKHPQASAGDTQTNRVWSGP PANSRPAAGPDC*KEN*QTE RTSINQNPICMSPSSKTKEAKNL DKRLDEWLTRINSIEKTLNDLM ELNTMARKLRDACTSFSSQFDQ VEERVSVIEDQMNMKREEKF REKRIKRNKQSLQEIWDCVKRP NLRLIGVPESDGNGTKLENTL QDIIQENFPNLARQVNIQIQEIQ RTPQRYSSRRGTPRHIVRFTKV EIKEKILRAAREKGRVTHKGKPI RLTAVLLAETLQARREWGPIFN ILKEKNFQPRVSYPKLSFISEG EVKSFTDKQMLRDFVTTRPAL QELLKEALNMERNNRYQLLQK HATLSRPSMLG |
| 12162 | 42530 | A | 12236 | 1 | 975 | |
| 12163 | 42531 | A | 12237 | 3 | 1186 | |
| 12164 | 42532 | A | 12238 | 1 | 906 | |
| 12165 | 42533 | A | 12239 | 1 | 1882 | |
| 12166 | 42534 | A | 12240 | 1 | 1394 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12167 | 42535 | A | 12241 | 1 | 4935 | MGPGARLAALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLLRRYLRGEEARLRDL TRCNDETITYLLDKRLTVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLRSRWAVGGATG SWVLSKGDRA SLGERVV TGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLSPSTRQRGQ SERSQDANGRRKQKT |
| 12168 | 42536 | B | 12242 | 88 | 1014 | |
| 12169 | 42537 | A | 12243 | 686 | 1920 | IKPQRWGKKQNRKTGNSKKQS ASPPPKERSSSPATEQSWTENDF DELREEGFRRSVITNFSELKEHV VTHRKEAKNLEKKALDEWITRI TNAEKSLKDLMEKTTAQELR NECTNLSNRCDQLEETVSAME DQIN/EMNEMKQEGKFREKRIK RNEQSFQ\EIGDYVKRPNLH\LI GVPESDGQNGTKLENTLQDIIQ ENFPNLARQANIQIE\QRT PQ RYSLRRATPRHIIVRFTKVEMK EK\MLSAAREKGR\VTHKGKPIR LTTADLSAETLQAQKTEWG\PIF NIL\KEKNFQPRISYPK\LSFIS EGEIKYFTDKQMLRDFCHHQG LPLKELLKEEALKHWKGTTTRY QPLAKTLPKYRSTRQKVNKDT QELNSALHQADLIDIYRTLHTK STEYTFQHHHTPIPKLTT |
| 12170 | 42538 | A | 12244 | 1 | 633 | |
| 12171 | 42539 | A | 12245 | 3 | 109 | |
| 12172 | 42540 | A | 12246 | 2 | 575 | |
| 12173 | 42541 | A | 12247 | 1 | 237 | |
| 12174 | 42542 | A | 12248 | 1 | 1065 | |
| 12175 | 42543 | A | 12249 | 2 | 338 | |
| 12176 | 42544 | A | 12250 | 1 | 1319 | |
| 12177 | 42545 | A | 12251 | 1 | 744 | MQKALCAAPDLGTFVTVLT PPP GAQIGSRRRERSKVPYIVRQCVE EIERRGMEEVGIYHVSGR\VA DIQALKA AFDVN/NRTMHSSWE ESDELLKARDDPHSGQHSRDG ALAKAGMADKKDMSVMMSET DMNAIAGTLKLYFRELPEPLFT DEFYPSFAEGIDRLERVAEKEA VNKMSLHNLATVFGPTLLRPSE KESKLPANPSQPITMTDSRSLEV MSQVEVLLYFLRLEAIPALDSK RQSILFSTDV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12178 | 42546 | A | 12252 | 1 | 507 | |
| 12179 | 42547 | A | 12253 | 1378 | 4280 | STPMAVAGPLGRPWSTSPTRAS TSGASWKGRARARSCAARAPL SRRSALPGPAGPTPPGVLRIAEA AIPRTAAPMRTSPPARRTSPLAS PAACPQAPPPTACSGTKAALPR RTRNSPSTA AVPPRRSAISGTGT ARLSCPRPPSWASARPGRS GPT MTRAPSMETQMARSEHHLDTA ALQTGQRSSAGTKMGCPTLMT RPPHRPTSAARAGAAGMRWSR EP*SPLK/RSELDLEKGLEMRK WVLSGILASEETYL |
| 12180 | 42548 | A | 12254 | 1 | 1109 | MRTPYKTSPMRMLYMTSLMTP TRHANEDAVDDIAYKDTVQDI TSEDVYDIANEDVYDIANED ALQDIANEVAVYDIANEDIVYD IANEDALYDITNEDAVYNIANE DAVYGIANEDAVYEFANKHAV YDIANEDTVQDICKKEDAANK CYFPGFFPIRCRHEHLPVCIIDVI CSLIKCRHEHLPSSLIGQDRLGA QASRRERSKVPYIVRQCVEEIER RGMEEVGIYRMSGVAADIQAL KAAFNVSECRPAQDGMEVWA VVSAMRSQSAPRPRHVTFSVS FLHLSGSSRRPLHFRALS\NNKD VSVMMSSEMDVNAIAGSLKLYF RELPEPLFTDEFYPNFAEGIGEH WRPWP HGRLLHVHCCPQRL |
| 12181 | 42549 | A | 12255 | 1351 | 4308 | WKGRARARSCAARAPLSRRSA LPGPAGPTPPGVLRIAEAAIPRT AAPMRTSPPARRTSPLASPAAC PQAPPPTACSGTKAALPRRTRN SPSTA AVPPRRSAISGTGTARLS CPRPPSWASARPGRS GPTMARA PSMETQMARSEHHLDTAALQT GQRSSAGTKMGCPTLMTTRPPH RPTSAARAGAAGMRWSREPWS PLK/RSELDLEKGLEMRK WVLS GILASEETYL SHLEALLPMKPL KAAATTSQPVLT SQ |
| 12182 | 42550 | B | 12256 | 1 | 1017 | |
| 12183 | 42551 | A | 12257 | 2310 | 2834 | EEKYNMQTRLRRAEDVFPVIG VAAHKG GYKTSVSVHLAQDL ALKGLRVLLVEGNDPQGTASM YHGWVPDLHIHAEDTLLPFYL MLRLAIETVAHDYDVIVIDSAP NLGIGTINVCAADV LIVPTPAE LFDYTSALQFFDMLRDLLKNV DLKGFEPDVRILLTKYSNSNGW |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12184 | 42552 | A | 12258 | 106 | 108 | NFLFVLRRQLWVGGLCW*AAE LNKVCL |
| 12185 | 42553 | A | 12259 | 1 | 901 | |
| 12186 | 42554 | A | 12260 | 23 | 482 | KPRELGPISPVWLPPDRLPERPQ RRRPSGVDPGSWLGSGSCGSTG CSALMSCSCGSTPLLSLALKVT PGGVLGAPSGSEDGS*PNRKAC GSEMEICLTTRGVWGPEVALG VGGGLQQSCRAPCGGLPKLLRS WSQSSLSPNSPGRGASSGEAA |
| 12187 | 42555 | A | 12261 | 1 | 1938 | |
| 12188 | 42556 | A | 12262 | 1 | 2235 | |
| 12189 | 42557 | A | 12263 | 43 | 1827 | THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLPLPAAGR VVVRRL AVVRSGSRSLSTADMTKGLVL GIYSKEKEDDVPQFTSAGENFD KLLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDPCG DAQAAAEGAVLGLYEYDDLK QKKKMAVSAKLYGSGDQEA WQKGVLFASGQNLARQLMETPA NEMTPTRFAEIIKLNLSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFGVGKITFDSSGGISIKASA NMDLMRADMGGAATICS AIVS AAKLNLPINIIGLAPLCENMP SGKANKPGDVVRKNGKTIQVDN TDAVEGRLILADALCYAHTFNP KVILNAATLTGAMDVALGSGA TGVFTNSSWLWNKLFEASNET GDRV*RMPLFDHYTRQ\VVDC QLAD\VNNIGKYRSAGIACTAA AFVKEFVTHRKAHLDIAGVM TNKDEVPOSTGKA*LGRPTRTL I\EFLLRFSQDNCLVQILKNVFH SVLNWTVELKKVFE |
| 12190 | 42558 | A | 12264 | 1 | 405 | GIRSAEVGKHLAHILLSRQQGR RPVTLIGFSLGARVIYFCLQEM AQEKDCQGHIEDVILLGAPVEGE AKHWSLSGRVVSGRINGYCR GDWLLSFVYRTSSVQLRVAGL QPVLLQDRRVENVDLTSVVSG |
| 12191 | 42559 | A | 12265 | 1 | 1072 | |
| 12192 | 42560 | A | 12266 | 105 | 514 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12193 | 42561 | A | 12267 | 44 | 872 | NARPWVRGLLIEFRRRGSCLCRE RAREMEMGRRIHLELRNRTPSD VKELVLDNSRSNEGKLEGLTDE FEELEFLSTINVGLTSIANLPKL NKLKKLELSDNRVSGGLEVL EKCPNLPWHLI*GGNKIKDLSTIE PLEKLENLKS LDFNCEVTNLN DYRENVFKLLPQLTYLDGYDR DDKEAPDSDAEGYVEGLDDEE EDEDEEEYDEDAQVVEDEEDE DEEEEGEEEDVSGEEEEEDEKGY NDGEVDDEEDEEELGEEERGQ KRKREPEDEGEDDD |
| 12194 | 42562 | A | 12268 | 1 | 388 | KRGAAMDGRVQLIKALLALPIR PATRRWRNPIFPETFDGDTDR LPEFIEQTGSYMFVDENTFSSDA LKTALPQSLPSIASHRQTAAPS DLDSPRRYLGWPSLSDSDS WPPPKGSVTFSETYFLPTP |
| 12195 | 42563 | A | 12269 | 1 | 127 | |
| 12196 | 42564 | A | 12270 | 5 | 434 | ISLRYLDGLAGPTHASAATEAS DRSEDLRWTVCAQLIQALLAL PIRPATRRWRNPIFPETFDGDT DRLPEFIVQTCSYMI\VDENTFS SDALKVTFLITRLTGPAL\QWVI PYIKKESPLLNDYRGFLAEMKR VFGWED\DEDF |
| 12197 | 42565 | A | 12271 | 515 | 1137 | |
| 12198 | 42566 | A | 12272 | 1 | 762 | |
| 12199 | 42567 | A | 12273 | 1 | 468 | |
| 12200 | 42568 | A | 12274 | 2716 | 3411 | KREEETKKKSKREMEVVKKKQ CTYSFKSQGKFLSTHARQFSIGS QPISASQTVEEIMKSILTLQSQI\ NSLAAVTLQNR*GLDLLTAEKG GLCTFLGEECCFYTNQSGIA*D ATQRLQEKASEIRRLSNSYTNL WSWATWLLPFLGPVAAILLLL AFGPRIFNLLVKFVWSRIEAIKL QMV LQIEPQMSSTNNFYRGPLD *PAGTSPGLESSLKDTTTAKPL LRPYPAGSS |
| 12201 | 42569 | A | 12275 | 8312 | 9221 | |
| 12202 | 42570 | A | 12276 | 74 | 471 | |
| 12203 | 42571 | A | 12277 | 4043 | 4159 | LFCQSGFHSLLTPSTATCSTIR* VATSRLRPVFTCRRS |
| 12204 | 42572 | A | 12278 | 1 | 1332 | |
| 12205 | 42573 | B | 12279 | 29 | 1316 | |
| 12206 | 42574 | A | 12280 | 1 | 580 | |
| 12207 | 42575 | A | 12281 | 2 | 710 | |
| 12208 | 42576 | A | 12282 | 1 | 1559 | |
| 12209 | 42577 | A | 12283 | 1179 | 1490 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 12210 | 42578 | A | 12284 | 2 | 313 | |
| 12211 | 42579 | A | 12285 | 599 | 743 | GALART*PPQQRWVSCPR/GVP/ GAL*REFTMFLSLQAENSIDFVS RELCAHSIRKLQAHVLLIK*VFI K |
| 12212 | 42580 | A | 12286 | 208 | 398 | |
| 12213 | 42581 | A | 12287 | 716 | 1069 | |
| 12214 | 42582 | C | 12288 | 326 | 577 | |
| 12215 | 42583 | A | 12289 | 188 | 590 | |
| 12216 | 42584 | A | 12290 | 860 | 1121 | VPFLTSWVNVGFKSSALHSSAL LQFWLTLWE*LPAWARCCCL PNGSFWGRSSRLDVAWERPV APGWREVSPLLSELWTAASGP YG |
| 12217 | 42585 | B | 12291 | 1 | 1614 | |
| 12218 | 42586 | B | 12292 | 1 | 1080 | |
| 12219 | 42587 | A | 12293 | 3 | 219 | |
| 12220 | 42588 | A | 12294 | 890 | 1094 | VESGTHLGQYKIYFGFLYQKKF SLQSHGYILFGCPQYW/ITSTDC PSIPCMWYSRTL*VTWSKKQVT SE |
| 12221 | 42589 | C | 12295 | 1 | 3912 | |
| 12222 | 42590 | A | 12296 | 881 | 1151 | |
| 12223 | 42591 | A | 12297 | 1 | 1323 | |
| 12224 | 42592 | A | 12298 | 1817 | 2284 | VWDGSILYQKLGALDGLSS*VI PLASSLQSLQYPLPSSFIQRILNT YSVKGLRSWTVNEDRVDVSS GGIWLQVEASLVLY*MLYFSIIT LLILGLVHVNFKILDSSSELITD KLCGGLGFTLYTGSKLI*SDVTF PRAFSASTQTSMLTKYTVE |
| 12225 | 42593 | A | 12299 | 1 | 1109 | |
| 12226 | 42594 | A | 12300 | 1 | 367 | |
| 12227 | 42595 | A | 12301 | 1 | 531 | |
| 12228 | 42596 | C | 12302 | 1371 | 1746 | |
| 12229 | 42597 | A | 12303 | 1 | 645 | |
| 12230 | 42598 | C | 12304 | 387 | 680 | |
| 12231 | 42599 | A | 12305 | 655 | 2498 | |
| 12232 | 42600 | A | 12306 | 1 | 528 | ENLGNTIQDTGMGKDFMTETP KAMTTKAKIDKRDILKLSFCT AKETTIRVNRQPTWEKIFAVY PSDKGPISRIYKQLKQIYKKKSN NPIKKWAKNRNRHFSKEDIYV AKKHMEKSSSSLVIRKMHKTT VGYHLM PVRMAIIKKSGNNRC WRGCGE\C*WEGQLVQPLWKT VWQ |
| 12233 | 42601 | A | 12307 | 1 | 1359 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12234 | 42602 | A | 12308 | 1968 | 2648 | TQTNLQEK NKQLHQKVGKGYE QTLKRRHLCSQQTHMQPTDT WKNAAHHQLAIREMQIKTTMRY HLTPLRMAIIKKSNNSCWRGC GEIGTLLHCWWDCCLVQPLWK TVWRFLKDLESEIPDLAIPLLCI YPKDYTSFCYKDTCTCMFIAAL FTIAKTWN*PKCSSVIDWIKKM WHIY/TTMEYYGAIKRNKIMSF AGTWMKLDAILSKLTQKQKT KLRMFLLISRS |
| 12235 | 42603 | A | 12309 | 1 | 403 | |
| 12236 | 42604 | A | 12310 | 3 | 264 | FFYAHIMFIAALFTIAKTWNQS KCTSMIDWIKKMWHIHTMEY YAAIKR\RGFMSFTRTWMKLEA IILSKLTQEQKTK\HHMFSLIRGS |
| 12237 | 42605 | A | 12311 | 79 | 432 | |
| 12238 | 42606 | A | 12312 | 1 | 933 | |
| 12239 | 42607 | A | 12313 | 70 | 675 | |
| 12240 | 42608 | A | 12314 | 1 | 339 | |
| 12241 | 42609 | A | 12315 | 3 | 422 | |
| 12242 | 42610 | A | 12316 | 1 | 471 | |
| 12243 | 42611 | A | 12317 | 1 | 963 | |
| 12244 | 42612 | A | 12318 | 375 | 542 | ENDKARRSDTPSML*WVEGMK *SVKAPHTLHLASDYVLEPWG GESATFIPASWDC |
| 12245 | 42613 | C | 12319 | 1 | 2148 | |
| 12246 | 42614 | A | 12320 | 1 | 1881 | |
| 12247 | 42615 | B | 12321 | 1 | 1074 | |
| 12248 | 42616 | C | 12322 | 143 | 439 | |
| 12249 | 42617 | C | 12323 | 123 | 362 | |
| 12250 | 42618 | A | 12324 | 474 | 603 | NHKNPRRKPRQYHSGHRHGQG LHV*NTKNNGNKSQNGQMGSN |
| 12251 | 42619 | A | 12325 | 5169 | 5756 | CPSLPPPHGKPAAACPRSPGGC CTPRSARTVPRGLSENSQTKCH SADLPPEGPRVFWTPPGTGAAP APPAPAPGPARGPARRCHAWPP QRRSSGAGRSPPPRHFAEFLKM VAFLRILILRAVSLRLSLDLEIS* G*RP*GPSWGGPPQSTPSAASA ASKTSSPRRWSTPAWAFLARA HPRWVAPSTAAQCTAAP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12252 | 42620 | A | 12326 | 21 | 98 | ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMRDSCPLDCKVY VGNLGNNNGNKTELERAFGYG PLRSVWVARNPPGFAFVEFEDP RDAADAVRELDGRTLACG\CRV R\VELVRMGEK\RSRNRGPPPS\ WGRRPDDYRR\RSPPPRRRSP R\RRSFS\RSRSRSL*ERVGWC WAGGKREDSSERV DLSRRIF |
| 12253 | 42621 | A | 12327 | 919 | 1043 | |
| 12254 | 42622 | A | 12328 | 460 | 657 | CFSPGMWQKTHSRKHSPGAICP INPVGECLVRKIKQLD*ITWINA I*LPLRDGLFYFLNFPFCCRG |
| 12255 | 42623 | A | 12329 | 1 | 2235 | |
| 12256 | 42624 | A | 12330 | 1 | 255 | |
| 12257 | 42625 | A | 12331 | 2 | 429 | CRADLNSRIDDFVPNPSVAVSG ASYAVAAVTMAHYKAADSKR EQFRKYFEK\SGVLDLT\KVLV ALYEEPEK\NSALDFLKHHLG AATP\ENPEIELRLLEAEMKEK YEAIVEENKKLKAKLAQYEP\P QEEKRAELGFFSV |
| 12258 | 42626 | A | 12332 | 670 | 860 | |
| 12259 | 42627 | A | 12333 | 2 | 450 | VNKAGGLIYQLDSYAP/RAEAE KTFSYPLDLLLKLHDERVLVAF GQRDGIRVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANYP VSIRFGRPRLTSNEKLMLASMF HS\IKFVVLADP\RQAGIDSLLRK IYEIYSDFALKNPFYSLEMP |
| 12260 | 42628 | A | 12334 | 1 | 2034 | |
| 12261 | 42629 | A | 12335 | 1 | 324 | |
| 12262 | 42630 | A | 12336 | 2 | 694 | FGTRGKAAMAFSVYVVVNKAG GLIYQLDSYAPRAEAEKTFSYP LDLLLKLHDERVLVAFGQRDGI \RVGHAVLAINGMDVNGRYTA DGKEVLEYLGNPANYPVSIRFG RPRL\TSNEKLMLASMFHSLFAI G\SQLSPE\QGSSGIEMLETDTFK LHC\YQTLTGIFVVL\ADP\RQ AGIDSLLRKIYEIYSDFAL\KNPF \YSLEMPIRCELFDQNLKLALEV AEKAGTFGPGS |
| 12263 | 42631 | A | 12337 | 2 | 1658 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12264 | 42632 | A | 12338 | 3 | 997 | VQKPNRQWRLVQDLRIINEAV VPLYQAVRNPTYLLSQIPEETG WFTVLDLKDALFCIAVHPDSQF LLAFEDPLNPTSQTLTWTVPQG FRDSPHLFGQALAQDLSQFSYL DTLVRLRYVDDLLLAAPSETLCH QATQVLLNFLATCGYKVSLLK AQICSQQVKYLGKLSKGTRAL SEERIQPILAYPHPKTRKQLRGL LGITGFCQIWIPRYSEIARPLHTL IKKTQKANTHLVRWTPEAEAA FQVLKKALTQAPVLSLPTGQDF SLYVTEKTGIALGVLTQHYGE ERNS*LPTEYLSNIRKPLGDYY WLYRNLKRWQSYTARVIRKER |
| 12265 | 42633 | A | 12339 | 3 | 421 | |
| 12266 | 42634 | A | 12340 | 3 | 4804 | KRLNIQKTLEVAFSEAVWMQ PSVVLDDLDLIAGLPAVPEHE HSPDAVQSQRALAHALNDMIKE FISMGSVALIATSQSQSLHPL LVSAQGVHIFQCVQHIQPPNQE QRCEILCNVIKNKLDKCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAIHSRLSRQSISTREKLVL TTLDFQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL |
| 12267 | 42635 | A | 12341 | 1 | 2223 | |
| 12268 | 42636 | A | 12342 | 1 | 3864 | MQWEEAEKDPGSCVFRPPV ALVFPLHSKWTLVNPPSSGDP YVGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNNPSLTSIYRSEV FCAHRHLHPPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSGQTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLKGFSDN |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12269 | 42637 | A | 12343 | 204 | 963 | DCACTFHCRSATKIVKDLKAQ GLVKPCNSPCSTPILGVQKPNG QWRLVQDLRIIDEVVVYVDDL LLAARSKTLCHQATQALLNFLI TCDYKVSKPKAQLCSQKVLYL GLKLSKGTRVLSEERIQUIPAYP HPKTPKQLRGFLGITGFCRIWIP RYSEIARPLYTLIKKTQKADTH LVEWTPAEVAFQALKEALTQ APVLSLPMGQDVPLYVTEKTI ALGVLGVLTQVRG/LSLQPMAY LSKEMDVVAKGWPH |
| 12270 | 42638 | A | 12344 | 1 | 1178 | MPESPTLLGRDILAKAGAIHL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFPYQRQYPLRPEAQQGLQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPVNPYTLSSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQQECHQATQV LLNVLATCGYKVSKQKAQLCS QQVKYLGVKLSKGTRAL/QQ*R TDRT*LSTSNCSNLRHSRGPARG SLD*SQPQLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIRRRKKGL IRIYMLPLILSAPYDHLH |
| 12271 | 42639 | A | 12345 | 1 | 841 | |
| 12272 | 42640 | A | 12346 | 3 | 1428 | |
| 12273 | 42641 | A | 12347 | 2 | 268 | |
| 12274 | 42642 | A | 12348 | 1 | 897 | |
| 12275 | 42643 | B | 12349 | 1 | 1650 | |
| 12276 | 42644 | A | 12350 | 232 | 1002 | TPGSTVHAPEADQGLQKIVKDL KAQGLVKPCNSPCSTPILGVQK PNGQWRLVQDLRIIDEVVVYV DDLILLAARSKTLCHQATQALL NFLITCDYKVSKPKAQLCSQKV KYLGLKLSKGTRVLSEERIQUIP AYPHKTPKQLRGFLGITGFCRI WIPRYSEIARPLYTLIKKTQKAD THLVEWTPAEVAFQALKEAL TQAPVLSLPMGQDVPLYVTEK TGIALGVLTQVRG/LSLQP MAYLSKEMDVVAKGWPH |
| 12277 | 42645 | A | 12351 | 1 | 2217 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12278 | 42646 | A | 12352 | 1 | 6530 | MWGSDDLRLAGAGGGGA AVTVAF FTNARD CFLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSDQGENVAEINRQVGQKL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFFVWVDQQT YIFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADA EYKKLHS YGRDQKGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSIFS FQSEKKQETSWG LTEINAFKNMQSKVVPL |
| 12279 | 42647 | A | 12353 | 1734 | 4349 | MPNRACFQCGLQGHFKKDCPS RKPQVCLTIESQEVNCLLDAGA AFSVLLSCPGQLSSRSVTIRGVL GQPVTRYFFQPLSCDWGALPFS HAFLIMPESLTPLLEREILVKAG AIIHLNIGEGTPICRLLFEEGISPE VWATEGQYGQAKNAHFVQVK LKDSTSFYQRYPLRPEAQQR LQKIVKDLKAQGLVKPYSSPCN TPILGVQKPKRQWRLVQDLRII NEAVFPLYPAIPSPYTLLSQIPEE AEWFTVLDLKD AFFCIPVHPDS QFLFAFEDPSNPTSQLTWTVLP QGFRDSPHLFGQALAQDLSQFS YLDTPVLQCMDDLLAARSET LCHQATQALLNFLTTCGYKVS KPKAQLCSQQVKCLGLKLSKV TRALSEERIQPILAYPYPKTLKQ LRGFLGITGFCRIWIPRYGKIAR PLYTLIKETQKANTHLVRWTPE AEAAFHALKKALMQAPVLSLL TGQDFSSYVTKNKQTKKKKAT* IALRVLALV*GTS LQPVA YL/SK EIDVVAKGQPHCLRVVAVAV LVSEAVKIIQGRNLTVWTS HDV NGILTAKGDLWLSDNHLLKYQ ALLLEGPMRLRLCTCAALNLDTF LPHNEEKIEHNCQQVIAQTYAT RGDHLEVPLTDPNPNLYTDGRS FVEKGLQKVG YAVVSDNGILES NPLTPGTSAQLAKLTRAELGE GKRVNIYTDSKYAYLVLHAHA |
| 12280 | 42648 | A | 12354 | 5 | 138 | |
| 12281 | 42649 | A | 12355 | 1 | 909 | |
| 12282 | 42650 | A | 12356 | 3 | 245 | |
| 12283 | 42651 | A | 12357 | 1 | 1080 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 12284 | 42652 | A | 12358 | 3 | 955 | VPRKSVHSGDAEYHKVLKEEA SDSRENKVGTTWLQILSGSFAS RVTEHITQPLQESVSLWISSEQN IPPKFMGRNLNKLKATYKRKYS AAKSKVEKKKKEKVFATVTKP VGVDKNGGTNRVVQTRKLP YHPTEDVPRKIVEPPQKNLFSQ HVRKTAKTALPPGTILILTGRH RGKRVVFLK\QLASGLILVTAP LVLNRVPLRRTHQKFVIATSTKI DISNVKIP\KKKKDKTPLLTDAYL \KKKKLRLKPR/HPRKGEIFDTVK RGNMRITE\QRTIDQKA VDSQIL PKIKAIPQA/LQGYLRILCLL*RN GIYPHKL VF |
| 12285 | 42653 | A | 12359 | 1 | 555 | |
| 12286 | 42654 | A | 12360 | 1 | 300 | |
| 12287 | 42655 | A | 12361 | 1 | 588 | |
| 12288 | 42656 | A | 12362 | 1 | 264 | |
| 12289 | 42657 | A | 12363 | 1 | 870 | |
| 12290 | 42658 | C | 12364 | 239 | 400 | |
| 12291 | 42659 | A | 12365 | 9 | 98 | SWKPSFSAN*HRNRKPNTTCSH SQVGVDL |
| 12292 | 42660 | A | 12366 | 9 | 81 | |
| 12293 | 42661 | A | 12367 | 3 | 169 | |
| 12294 | 42662 | A | 12368 | 134 | 481 | GCCGGTIKNSFSFPPLPNWPRFV MFPSLCVLIVETCETWICTLIVQ LPLMSENMRCLIFCSCVSLLRM MVSSFVHVHDHKVKSHSRPS/G NLRKSKEASPSPKTSKVGKLT VQ PSVCG |
| 12295 | 42663 | A | 12369 | 41 | 388 | SYGQMMKCQPFTFPSPGYGAG VFSSDKIGQMTFMERT*RMCK EAAQDHTAREKEKVELKFPSLP FRRKELL*PCTWLGSPISLVTL D FPWPQGSGRLSMPVLWTCLIPG SLEIG |
| 12296 | 42664 | B | 12370 | 1 | 909 | |
| 12297 | 42665 | C | 12371 | 295 | 2025 | |
| 12298 | 42666 | A | 12372 | 14 | 260 | |
| 12299 | 42667 | A | 12373 | 1 | 142 | TCTCVFIAALFTIAKTWN*SKCP SMRDWIKKNVAHTHHGILCSH KKE |
| 12300 | 42668 | A | 12374 | 1 | 395 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12301 | 42669 | A | 12375 | 2 | 976 | REHLAEGMAVGTASADLNISA CWLRRQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQRK EQAAIFAVLQPPLVIPRKTGSGV DLEQTPADLQKRGLTVTRKTN KQKAIASSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSPAR EQNWMENEFDELTEVGFRRW VITNSSELKKHVLTQCKEAKNL EKRDMD EAGNHHSQQTNTGTE NQTPHVLTHKWELNNENTRTRI YKKHGAACLASGIYHSVDLPF WGLDLPFDLED SGSTILSGGG QWPSSHSSTRQCTSVDSVWGL |
| 12302 | 42670 | B | 12376 | 1 | 111 | |
| 12303 | 42671 | A | 12377 | 34 | 346 | |
| 12304 | 42672 | A | 12378 | 1 | 585 | |
| 12305 | 42673 | A | 12379 | 3 | 14703 | |
| 12306 | 42674 | A | 12380 | 1 | 636 | |
| 12307 | 42675 | A | 12381 | 1 | 1626 | |
| 12308 | 42676 | A | 12382 | 1 | 3246 | |
| 12309 | 42677 | C | 12383 | 62 | 202 | |
| 12310 | 42678 | A | 12384 | 1 | 286 | |
| 12311 | 42679 | A | 12386 | 1 | 1176 | |
| 12312 | 42680 | C | 12387 | 1 | 942 | |
| 12313 | 42681 | A | 12388 | 785 | 892 | |
| 12314 | 42682 | A | 12389 | 2 | 91 | |
| 12315 | 42683 | A | 12390 | 1 | 708 | |
| 12316 | 42684 | A | 12391 | 3 | 96 | TWMKLETIILSKL*QRQKTKHR MFLGIGN |
| 12317 | 42685 | B | 12392 | 1 | 1954 | |
| 12318 | 42686 | A | 12393 | 1550 | 1830 | DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKKMW HIYTM EY YAAIK/SDEFMCFW TWMKLETIILSKLSQEHTKHH MFSLTSGS |
| 12319 | 42687 | A | 12394 | 3 | 553 | |
| 12320 | 42688 | A | 12395 | 1 | 1428 | |
| 12321 | 42689 | A | 12396 | 642 | 753 | |
| 12322 | 42690 | B | 12397 | 1 | 759 | |
| 12323 | 42691 | B | 12398 | 1 | 900 | |
| 12324 | 42692 | A | 12399 | 623 | 775 | |
| 12325 | 42693 | A | 12400 | 992 | 1156 | |
| 12326 | 42694 | A | 12401 | 86 | 349 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12327 | 42695 | A | 12402 | 1 | 2521 | MNIDAKILNKILANRIQQHIKKL IHHDQVGFIQGMQGWFNIRKSI NIVQHINRTNDKNHMIISIDAEK AFDKIQQRFMLKTLNKLIGDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAJRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGILQTRDVKDLFKEN YKPLLNDIKEDTNKWKNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMFTFFTELEKTTLKFIWN QKGARIAKSILYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKWGND LFNKWCWENWLAICRKLKLD FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNTIQDIAMGKDFMS KTPKAMATKAKIDKWDLINLK SFCTAKETTIRVNRQPIEWKIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSLAIREMHI KTTMRHHLTSVRMAIHKKLGN DWCWRGCGEIGRLLHCWWDC KLVQPLWKSVMRFLRDLELET PFDPASPLLGIIYQKE\YKSCYYK DICT/RVCVPAALFTIANTWNQP |
| 12328 | 42696 | B | 12403 | 80 | 5612 | |
| 12329 | 42697 | B | 12404 | 68 | 505 | |
| 12330 | 42698 | A | 12405 | 1 | 471 | |
| 12331 | 42699 | A | 12406 | 194 | 430 | IAIMRLLLQISIIILSSCLREVKSM QAYRKALRKLKLADVKRYQKS LVVQKRS*ER*SLVLILPARTF QSYLAPIC |
| 12332 | 42700 | A | 12407 | 1 | 546 | |
| 12333 | 42701 | A | 12408 | 2 | 418 | |
| 12334 | 42702 | A | 12409 | 302 | 746 | ETSHQVMDRSNPVKPALDYFS NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGGQLKV LGANLWWPYLMHEHPAYLYS WEDGDCFTPALDPLPACDLC DQLHLRSRQGGSVCGCDPCEQ LLLLVSQLQAPAISSAAAGRPV |
| 12335 | 42703 | A | 12410 | 83 | 552 | |
| 12336 | 42704 | A | 12411 | 1 | 459 | |
| 12337 | 42705 | A | 12412 | 34 | 588 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12338 | 42706 | A | 12413 | 1 | 466 | |
| 12339 | 42707 | A | 12414 | 950 | 1230 | CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ |
| 12340 | 42708 | A | 12415 | 497 | 847 | |
| 12341 | 42709 | A | 12416 | 1 | 337 | MGVVPEELFLEELNLSGLKWD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQHPEFAPP SHGD |
| 12342 | 42710 | A | 12417 | 716 | 961 | |
| 12343 | 42711 | A | 12418 | 1 | 1218 | |
| 12344 | 42712 | A | 12419 | 1 | 1104 | |
| 12345 | 42713 | A | 12420 | 548 | 1078 | |
| 12346 | 42714 | B | 12421 | 83 | 345 | |
| 12347 | 42715 | A | 12422 | 1 | 681 | |
| 12348 | 42716 | A | 12423 | 1 | 1431 | |
| 12349 | 42717 | A | 12424 | 566 | 871 | |
| 12350 | 42718 | A | 12425 | 145 | 980 | |
| 12351 | 42719 | A | 12426 | 2 | 702 | |
| 12352 | 42720 | B | 12427 | 1 | 1156 | |
| 12353 | 42721 | A | 12428 | 188 | 584 | |
| 12354 | 42722 | A | 12429 | 1 | 1194 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12355 | 42723 | A | 12430 | 170 | 1855 | LLEGKLTNRKDIPHQNPICSTSPS SKTKGILPISEPPSNRIFACWGK PAWTACCN/FSQGGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQINHTPNSF HIGAGGSWCLSESPCVVLNYK YPLVCGYTDGNAEVSKFGNFFL DLSRTRCLAEGNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGT ENGYQGEESLFNKAYYGGGTN FFRKESQKLQQSACKRDAELA NGALGIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKMNGKW YLFTDSRGSKMTIDGINSNDIY MLGYVSNLTGPYKPLNKTGL VLQMGLDPNDVTFTYSHFAVP QAKGNNVVITSYMTNRGFFED KKATFAPSFLMNIKGNKTSVVK NSIRREGFCFRNHHQTGFSPA GANQRGPLAATLSGPGGEGQS AVARLTGEKKNHPGAQYANRL SPRVGRFINAAGTTGFPTGKRA GFCFRNHHQTGFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGTTGFPTGKRAV |
| 12356 | 42724 | A | 12431 | 851 | 2237 | |
| 12357 | 42725 | A | 12432 | 2 | 2346 | |
| 12358 | 42726 | B | 12433 | 329 | 479 | |
| 12359 | 42727 | B | 12434 | 656 | 2404 | |
| 12360 | 42728 | B | 12435 | 486 | 834 | |
| 12361 | 42729 | A | 12436 | 1 | 693 | |
| 12362 | 42730 | A | 12437 | 1 | 114 | |
| 12363 | 42731 | A | 12438 | 152 | 391 | AGGWALPSLGLPSWTSRCPWR RGSAGLLLEASVPVQQ*PKLLD RLSRRWPGEHPRPARVRSCM ALGPRRLGVLCQEPS |
| 12364 | 42732 | A | 12439 | 1 | 1707 | |
| 12365 | 42733 | A | 12440 | 1 | 897 | |
| 12366 | 42734 | A | 12441 | 36 | 420 | |
| 12367 | 42735 | A | 12442 | 2 | 217 | |
| 12368 | 42736 | A | 12443 | 1 | 903 | |
| 12369 | 42737 | A | 12444 | 1 | 1626 | |
| 12370 | 42738 | B | 12445 | 107 | 757 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12371 | 42739 | A | 12446 | 1 | 1655 | MGTVPRSAGQETWVLCEHIIGG ERSFTEYSLCHRIESSTSSIKLEL GGNNVEPLESSRVFDSTVQNEE ADAVSTGEEGVTHEGTQGCKV IPQMHHMGSGLQPKSFSQNRSQV NNDMIVTDNNGAVKFPQLCKF CDVRFSTCDNQKSCMSNCSITSI CEKPQEVCAVVCWMSEEICTN VMYSPLPCKFLHLSPIEVLPIRS PVNQSGRCKIRHIGSNRLQRS TCQNTGWESAHVMKTPGFREY NTSNPDLLLVIQVVTGISLLPPL GVAISVIIIIFYCYRVNRQKLLSS TWETGKTRKLMEFSEHCAIILE DDRSDISSTCANNINHNTPELLPI ELDTLVGKGRFAEVYKAKLKQ NTSEQF*DSGQFKILFPIEYAS WKTEKDIFSDINLKHENILQFLT AEERKTELKGQYWLITAFHAK GNLQEYLTRHVISWEDLRKLGSL SLARGIAHLHSDHTPCGRPKMP IVHRDLKSSNILVKNDLTCCCLC DFGLSLRLDPTLSVDDLANSQG CYEVCSSGRFLVTIFKGNRLRE RTEKNTRITPRDWVYEWLW |
| 12372 | 42740 | A | 12447 | 1555 | 3277 | RAAGSAMGRGLLRGLWPLHIV LWTRIASTIPPHVQKSVNNDMI VTDNNGAVKFPQLCKFCDVRF STCDNQKSCMSNCSITSICEKPQ EVCVAVWRKNDENITLETVCH DPKLPYHDFILEDAAAPKCMK EKKKPGETFFMCSCSSDECNDN IIFSEEYNTSNPDLLLVIQVVTGI SLLPPLGVAISVIIIIFYCYRVNRQ QKLSSTWETGKTRKLMEFSEH CAIILEDSDISSTCANNINHNT PELLPIELDTLVGKGRFAEVYK AKLKQNTSEQFETVAVKIFPYE EYASWKTEKDIFSDINLKHENIL QFLTAEERKTELKGQYWLITAF HAKGNLQEYLTRHVISWEDLR KLGSSLARGIAHLHSDHTPCGR PKMPIVHRDLNSSNILVKNDLT CCLCDFGLSLRLDPTLSVDDL ANSQGVTARYMAPEVLESRMN LENAESFKHTDVYSMALVLWE MTSRCNALGEVKDYEPFPGSK VREHPCVESMKDNVLRDRGR EIPSWLNLHQGIQMVCELTTEC CDHDPYARLTAQCVAERFSELE HLDRLSGRSCSEEKIPEDGSLNT |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12373 | 42741 | A | 12448 | 3 | 1354 | |
| 12374 | 42742 | A | 12449 | 1 | 168 | |
| 12375 | 42743 | A | 12450 | 2 | 147 | |
| 12376 | 42744 | A | 12451 | 3 | 523 | LQFFRRSEVKMKNHLLFWGVL AVFIKAVHVKAQEDERIVLVDN KCKCARITSRIIRSEDPNEDIVE RNIRIVVPLNNRENISDPTSP\LR TRFVY\HLSDLCKK\CDPTEVEL\ DNQIVTAT\QSNICGWMTPVQS TCYTLSTGNKCYTAVVPL\VYG GETK MVETALTPDACYPD |
| 12377 | 42745 | A | 12452 | 3 | 274 | |
| 12378 | 42746 | A | 12453 | 1 | 120 | |
| 12379 | 42747 | A | 12454 | 119 | 461 | PVPQDLQA AVLGRTTALFK\AV KTGTLQVCKRLLLSFVCL/CPA PRGRQASLSCGGLHPVRASWLL CLPKQAWAMAGAPPPAWLPPC SLISDCCASNQRDSVGV RPSEPG VGYSLV |
| 12380 | 42748 | A | 12455 | 2 | 370 | |
| 12381 | 42749 | A | 12456 | 1 | 3135 | |
| 12382 | 42750 | A | 12457 | 1 | 942 | |
| 12383 | 42751 | A | 12458 | 1 | 462 | |
| 12384 | 42752 | A | 12459 | 1 | 297 | |
| 12385 | 42753 | A | 12460 | 935 | 1338 | CTDGFLVWMSFLFVSFPLPPCS LISDCSASNERDSVGVGPSEPG AGYNLVVRRFLSPSEKRSIRV* VTRFSRCRPSPLSLTRKGNSLTP CASQVRQCLALFRLAHGVRTH SPAPTVWHSLPKVGPFLNSVP |
| 12386 | 42754 | A | 12461 | 1 | 268 | |
| 12387 | 42755 | A | 12462 | 3 | 479 | |
| 12388 | 42756 | A | 12463 | 1 | 262 | |
| 12389 | 42757 | A | 12464 | 1 | 304 | MAGAPAPASLPPCSLISDCCAS NQRDSMGVGPSEPGAGYNLVP VIEKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLALL QLAHGRGSPNPRP |
| 12390 | 42758 | A | 12465 | 1 | 512 | |
| 12391 | 42759 | B | 12466 | 1 | 1257 | |
| 12392 | 42760 | A | 12467 | 1 | 705 | |
| 12393 | 42761 | A | 12468 | 1 | 3039 | |
| 12394 | 42762 | B | 12469 | 66 | 467 | |
| 12395 | 42763 | C | 12470 | 360 | 747 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12396 | 42764 | A | 12471 | 3771 | 4703 | SFQFFCSVFSPSLWFYLLLVFDD GDVQMRFRGCGPCFLLVFLLED RTLSCRSVGIPCRVRCQCALLG GASQLGCSGVKGSRDPLEEAV CPFS\DL\QLRAGGNTALFKAVR QGHLSLQRLLSFVCLCPAPRG GAYRGGQASLSCGGLHPV*AS\ RLLCLPKQAWAMAGAPPPASL L\PCILISDCCASNQRDSVGVP S/ERPGVGYSLVVRRFLSRSEKR NIRGGVTRFSRCRPSPLSLTRK GNSLTPCASQSEGNAIGPAFGF AHGARTHVALRPTVWHSLE MNPVPQMEMQKSPVFCVAHA GGCRPEL |
| 12397 | 42765 | A | 12472 | 1 | 1038 | |
| 12398 | 42766 | A | 12473 | 27 | 428 | LADRSAIPGFAIFAVTFLLALVG AVLYLYPWTLKPC*SHY*GIN LVVAV*VKTT*GKNCKMV*L IL*RVTLPS*RFGLRLEKAF*M GHLIKT*LGKNNMKMPSCNWS LF*GTS*KNEKEGTSVNIFSLTP |
| 12399 | 42767 | A | 12474 | 107 | 362 | NKPCEEFYFLAALIYLLYHGRK KADTKIPP*ISRFFLILYPSHETI FIVIHIMCDLGCTWAICFLTSE EVQKKLYEEINQVFG |
| 12400 | 42768 | A | 12475 | 193 | 637 | TSSEVVKKQIAQVHNFAVIMQL ARENIILSS/EDLLVIKVPY*GV NENMLTEVPSFSFFYDVP*NRL QLHEGIFILFFPSHVFIK*PI*KAF SNLRPNCAMILLEANDFLIFKC TTHYHLCNRLHSKTKHMLAEG HVLGLWVGEPFI |
| 12401 | 42769 | A | 12476 | 1 | 1930 | |
| 12402 | 42770 | A | 12477 | 1 | 362 | |
| 12403 | 42771 | A | 12478 | 58 | 160 | GVSLQSTSEEGRGMRQE*TERE IKVTCTSHYRLA |
| 12404 | 42772 | A | 12479 | 3 | 410 | |
| 12405 | 42773 | A | 12480 | 1 | 807 | |
| 12406 | 42774 | A | 12481 | 154 | 375 | |
| 12407 | 42775 | A | 12482 | 2 | 512 | |
| 12408 | 42776 | C | 12483 | 29 | 455 | |
| 12409 | 42777 | A | 12484 | 209 | 433 | |
| 12410 | 42778 | A | 12485 | 1 | 1546 | |
| 12411 | 42779 | A | 12486 | 3 | 931 | |
| 12412 | 42780 | A | 12487 | 1 | 363 | |
| 12413 | 42781 | A | 12488 | 1 | 351 | |
| 12414 | 42782 | B | 12489 | 82 | 263 | |
| 12415 | 42783 | A | 12490 | 1 | 1878 | |
| 12416 | 42784 | A | 12491 | 24 | 242 | |
| 12417 | 42785 | A | 12492 | 1 | 3558 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 12418 | 42786 | A | 12493 | 2 | 478 | HNSLKSDENKENSFSADHVTTA VEKSKESQVTADDLEEEKAKA ELIMDDDRTVDPLLSKSQSILIS TSATASSKKTIEDRNIKNKKSTN NRASSASARLMTSEFLKKSSSK RRTPTTTTSSHVLGTLKVLDQK PFTETEA*EPDRADNIRGSCLFR |
| 12419 | 42787 | A | 12494 | 1 | 1047 | |
| 12420 | 42788 | A | 12495 | 1 | 1055 | |
| 12421 | 42789 | A | 12496 | 212 | 611 | |
| 12422 | 42790 | A | 12497 | 2 | 195 | YVMGRNDGGYLMIDSKTAEIK FVKNMNRDSTFIVNKITAEVL AID\RYSGKNCLLISWSYICG |
| 12423 | 42791 | A | 12498 | 1 | 429 | |
| 12424 | 42792 | A | 12499 | 1 | 503 | |
| 12425 | 42793 | A | 12500 | 3 | 825 | GTTKWQTVRRQKREWIKFAAA CREGEDNSKRNPiAK*SDLQNS LLPALY*KH\IRSDCESNQKITY RISGVGIDRPPYGVFTINPRTGEI NITSVVDREITPLFLIYCRALNS RGEDLERPLELRVKVMDINDN APVFSQSVYTASIEENS DANTL VVKLCATDADEENHLNSKIAY KIVSQEPSGAPMFILNRYTGEV CTMSSFLDREQHSMYNLVVRG SDRDGAADGLSSECDCRIKVLD VNDNFPT/FRENFQKNSRFSNS LLSSFDQWRKL |
| 12426 | 42794 | A | 12501 | 986 | 4030 | KQRLTWTFS PGKSETMMGLFP RTTGALAI FVVVILVHGELRIET KGQYDEEEMTMQQA KRRQKR EWWKFAKPCREGEDNSKRNPiA KITSDYQATQKITYRISGVGIDQ PPFGIFVVDKNTGDINITAIVDR EETPSFLITCRALNAQGLDVEKP LILTVKILDINDNPPVFSQQIFM GEIEENSASNSLV MILNATDAD EPNHLNSKIAFKIVSQEPAGTPM FLLSRNTGEVRTLTNSLDREQA SSYRLVVSGA |
| 12427 | 42795 | B | 12502 | 1 | 3572 | |
| 12428 | 42796 | A | 12503 | 1 | 594 | |
| 12429 | 42797 | A | 12504 | 1 | 612 | |
| 12430 | 42798 | B | 12505 | 200 | 532 | |
| 12431 | 42799 | A | 12506 | 2 | 735 | |
| 12432 | 42800 | A | 12507 | 5 | 400 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12433 | 42801 | A | 12508 | 2 | 1260 | GQAASPASPASPAMAWAA LLGLLVALLLLLLSRRRTRRP GEPPLDLGSIPWLGALDFGKD AASFLTRMKEKHGDIFTILVGG RYVTVLLDPHSYDAVVWEPR RLDFHAYAIFLMERIFDVQLPH YSPSDEKARMKLTLLHRELQAL TEAMYTNLHAVLLGDATEAGS GWHMGLLDF/CLQLPAQSRLP DSLRLN*GAATHP*KPGPGPRPLS *CLPHLSPARPAAPQTGPWLPV SGGQGPVHVQCQKSPVEAAIPSQ AGQAGPPEQMAGELPAAPGGD GCVRGDAGTGPAAAVGHTGE YGSRCLLAPALPSQES*SPGCCP RRAREYPLASGAACLADDSPT EGSRQHTC/DLIAC*VRASGLQL PPSSPARLGGPGHAHGRRERI PATW*PPPPLPLPEPPERPRNLH RPRGI |
| 12434 | 42802 | A | 12509 | 3 | 466 | |
| 12435 | 42803 | A | 12510 | 1 | 1134 | |
| 12436 | 42804 | A | 12511 | 2 | 1211 | |
| 12437 | 42805 | A | 12512 | 2 | 405 | HEMLLASEIKHLPRRLIGQERE TQTSELKIKRRGNEEAPS/PPPSS AYERGTRPDDRYDTPTSKKK VRIKDRNKLSTEERRKLFEQEV AQREAAKQQQQMQNLGMTSP LPYDSLGYNAPHHPFAGYPPGY PMQA |
| 12438 | 42806 | A | 12513 | 191 | 898 | |
| 12439 | 42807 | A | 12514 | 1 | 270 | |
| 12440 | 42808 | A | 12515 | 2 | 1328 | |
| 12441 | 42809 | A | 12516 | 1 | 2868 | |
| 12442 | 42810 | A | 12517 | 1 | 1254 | |
| 12443 | 42811 | A | 12518 | 1 | 576 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12444 | 42812 | A | 12519 | 1919 | 3044 | HQGPSTPPSWAMSGPPTPLSRE DWHQGPSTPPSWAMSEPPT/SSI QGLASGAVHTILLGDVRATYTS IQGVTSQVSQVSRAAQMVPSS RILQLSKPKAPATLLEWDPVP KPKPHVSDHNRLHLAKVPRK EGSGKKVGAFPEIKGPEAFRDK ARAMESQSNMPFDELLALYG YEASDPISDRESEGGDVPNLP DMTLDKEQIAKDLLSGEEEEET QSSADDLTPSVTSHEASDLFPN RSGCLLAGEAESSRGLLPRAQP VPRGAGLADNSRGALLRAHGT VRVGTTATVKPADAPPESPRDR RSRNDSHRPTGPSESERQPQSN QPTLLLRGHGTIRVRTTATVKP ADAPAESPRDRSRNDSHGQSS |
| 12445 | 42813 | A | 12520 | 413 | 1412 | |
| 12446 | 42814 | A | 12521 | 293 | 412 | NHLSVAGNGSSPCGL*AGALGL LLWLLASSGHRVLSGMI |
| 12447 | 42815 | A | 12522 | 2 | 181 | |
| 12448 | 42816 | A | 12523 | 1 | 277 | |
| 12449 | 42817 | A | 12524 | 1 | 739 | |
| 12450 | 42818 | A | 12525 | 1 | 326 | |
| 12451 | 42819 | A | 12526 | 3 | 566 | |
| 12452 | 42820 | A | 12527 | 1 | 465 | |
| 12453 | 42821 | A | 12528 | 1 | 1167 | |
| 12454 | 42822 | A | 12529 | 260 | 395 | EVATATPTLSNHYPDQSAAIN/D QG*PLHQKDHILQKAQMNISI F |
| 12455 | 42823 | A | 12530 | 209 | 958 | FRCVLISFWSHKLHLWYHEGRI VPSDRIVPPHGIVSSHGVALPQR ILMRQFTLLEGLNKDGRFLIQLS GTAPWSSYFNSVAKFGVIHRIH SFFLSHNGHKA VAPLDLLSNVG GSCLCGDASSFTTPSRITMTSK SWLARSVAEMSYR/WTALVNH VADDQRGHQKNVIALDWVINR NVQLVNRNHLPRCSCFLDHLD AHRGTNDHAFPPQVTHSEHEAQ LAISDGNHSMMAAENQSFCSVS LSCFHENAA |
| 12456 | 42824 | A | 12531 | 1 | 1965 | |
| 12457 | 42825 | C | 12532 | 520 | 684 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12458 | 42826 | A | 12533 | 701 | 1307 | GRHLTTNHTAAVVVFPRPLCS SFFRYSGFRGVAGATASGRGQG PAG*DNCQRAWRGAFYKFQAT LSAGAGTRAEEGSDGDGEAAE PGAGTAREPARLRGYRSRRFVL DGRRCCLCYFKNPHDPLPLGHL DIAEACFSYQRADEAAEQPAHF QVRSAGAATVLEVGTALRGV HLLRAHRGIWAQAWSPVSFLQ AVLPAWLL |
| 12459 | 42827 | A | 12534 | 1 | 1356 | |
| 12460 | 42828 | B | 12535 | 1 | 1449 | |
| 12461 | 42829 | A | 12536 | 3 | 2449 | |
| 12462 | 42830 | A | 12537 | 1 | 3327 | |
| 12463 | 42831 | A | 12538 | 1 | 1359 | |
| 12464 | 42832 | A | 12539 | 1 | 672 | |
| 12465 | 42833 | A | 12540 | 1 | 1281 | |
| 12466 | 42834 | A | 12541 | 1 | 399 | |
| 12467 | 42835 | A | 12542 | 1 | 399 | |
| 12468 | 42836 | A | 12543 | 171 | 426 | PVSCATGEEEDNVLPKGGDLP R**PGKLWCEFHASSISQALGQ HPRRSVLDTDQSHVPLVRRKTT CFSQRAMISPDDPSQEAGALS RNNLLAPYSALTFMENGNCCLL QLFQLGKLLVQASHLHGQLLV FVQKIIISM |
| 12469 | 42837 | A | 12544 | 1 | 988 | |
| 12470 | 42838 | A | 12545 | 3 | 129 | LFHPCQDSQQHH*CVCCRLTGH GAA*VHGPCQAVQTYRASH |
| 12471 | 42839 | C | 12546 | 532 | 1101 | |
| 12472 | 42840 | A | 12547 | 197 | 355 | |
| 12473 | 42841 | A | 12548 | 1 | 1275 | |
| 12474 | 42842 | A | 12549 | 3 | 131 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12475 | 42843 | A | 12550 | 1746 | 3504 | ESDPSNSTTSM DRTLL/MSSIVP RLPSACRILPTGFTIPE*SCVHRT ASLIPPLPPGSRKYSPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTSPDISHQQAALLRTY LKNLSPYINSTPPIFGPLTTQTTI PVAAPLCISWQRPTGIPLGNLSP SRCSTLHLRSPTTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCISLHPWLSSPCSSDSP PRPSSCLLIPSPENNSERLLVDT RRFLIHENRTFPSTQLPHQSPL QPLTAAALAGSLGVVWQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAGISTSVMTFRSLSNDFS ASITDISQTL SVLQAQVDSLAA VVLQGQLRGLDLLTAEGGLCI FLNECCFYLNQSGLVYDNIKK LKDRAQKLANQASNYAESPWA LSNWMSWVLPVSPLIPIFLLLL FGPCIFRLVSQFIQNRIQAITNHS IRQMFLLTSPQYHPLPQDLPSA |
| 12476 | 42844 | A | 12551 | 2 | 394 | |
| 12477 | 42845 | A | 12552 | 1 | 882 | |
| 12478 | 42846 | A | 12553 | 45 | 409 | |
| 12479 | 42847 | A | 12554 | 1 | 1035 | |
| 12480 | 42848 | A | 12555 | 118 | 312 | |
| 12481 | 42849 | A | 12556 | 1 | 1083 | |
| 12482 | 42850 | B | 12557 | 1 | 1122 | |
| 12483 | 42851 | A | 12558 | 97 | 439 | |
| 12484 | 42852 | A | 12559 | 1 | 450 | |
| 12485 | 42853 | A | 12560 | 1 | 471 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12486 | 42854 | A | 12561 | 2 | 1407 | WGKNRAEKLETLKSRVPLLLQ RNAVPHQQWNKAGRRMTLTS* EKKASDD/PNYSKLQEEIQTKG KEVKHFEKNLDECITRITNREK CLKELMELKAKARELREECRSL RSQCDQLEERVSVMEEIQTIRE YYKHL YENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPTGSE IVAIINSLPTKKSPGPDGFTAKF YQRYKEELIPFLKLQFSIEKEGI LPNSFYEASIIIPKQGRDTTKK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQG WFNICKSRNVIHHINRTKDKNH MIISIDAEKAFDKIQPFMLKTL NKLGIDETYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIVLEVLAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNL FELISNFSKVSGY KINVQISQAFLYTNYRQSAKS |
| 12487 | 42855 | A | 12562 | 1 | 846 | |
| 12488 | 42856 | A | 12563 | 1 | 1281 | |
| 12489 | 42857 | B | 12564 | 1 | 274 | |
| 12490 | 42858 | B | 12565 | 1 | 2265 | |
| 12491 | 42859 | A | 12566 | 1 | 2742 | |
| 12492 | 42860 | A | 12567 | 1 | 1272 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12493 | 42861 | A | 12568 | 222 | 2130 | RKKNKKK*TKPPRNMGLREKT KSMSDWCT*K*RGewnQV/AK TLCRILSRRT/YPNLARQADIQI EIQRTPQRYSSRRATPKHII VRF TKVEMKEKMLRAAREKGRVT HKGKPIRLTADLSAETLQARRE WGQIFNILKEKNFQPRISYPAKL SFISEGEIKPFTDKQMLRDFVTT RPALKELLKEVLNMERNNRKK LNRPI TGSEIVAII NSLPTKKSPG PDGFTA EFYQRYKEELVPFLK LFQSKEKEGIHPNSFDEASIILIP KAGRDTT TKDNFRPISLMNIDA KILNKILANQIQQHKKLIHHDQ VGFIPGMQGWFNICQSINVIQHI NRTKDKNHVIISIDAEKAFDKIQ QRFMLKTLNKL GIDRMYLKIIR AIYDKPTANIILNGQKLEAFPLK MGTRQGCPLSPLLFNIVLEVLA RAIRQEKEIKHIQLGKKEVILSL FADDMIVYLENSIVSAQNLLKLI SNFSKVSGYKINVQKSHAF LHT NNRQTESQIMSELPFTIASKRIK YLG IQLTKDVKDLFKENYKPLL NEIKEDTKKWKHIPC SWVGRIN IVKMAILPKVIYRFNAIPIKLPM TFFTELEKTTLKFIWNQKRAHT AKSILSQKNKAGGITLPDFQLY CKATVTKTAWY |
| 12494 | 42862 | A | 12569 | 1 | 474 | |
| 12495 | 42863 | A | 12570 | 1 | 1197 | |
| 12496 | 42864 | A | 12571 | 1 | 1518 | |
| 12497 | 42865 | A | 12572 | 1 | 3189 | |
| 12498 | 42866 | A | 12573 | 1 | 2199 | |
| 12499 | 42867 | A | 12574 | 3 | 2820 | ENKDTTYQNL\WDAFKAVCRG KFIALNAHKKRKQERSKIDTLTS QLKELEKQEQT HSKASRRQEIT KIRAE LKEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKREK NQIDTIKNDKGDITDPTEIQT TI REYYKHL YANKLKNLEEMDKF LDYTYL PRLNQEEVESLNR PITG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLKLFQSIEKE GILPNSFYEASIILIPKPGRD TTK KENFR |
| 12500 | 42868 | B | 12575 | 1 | 1593 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12501 | 42869 | A | 12576 | 1 | 3549 | MGDFNTPLSTLDRSRRQKVNK DTQELNSALHQVDLIDYRTLH HKSTEYTFPSAPHHTYSKIDHIV GSKALLSKCKRTEITNYLSDHS AIKLELRKLNLTQNRSTTWKLN NLLLNDYWIHNKMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLELEKQEQTHSKASRRQ EVTKIRAELEIETQKTLQKINE SRSWFFERINKIDRMLARLIKK KREKNQIDTIKNDK |
| 12502 | 42870 | A | 12577 | 1 | 2724 | |
| 12503 | 42871 | A | 12578 | 1 | 3567 | |
| 12504 | 42872 | B | 12579 | 709 | 2064 | |
| 12505 | 42873 | A | 12580 | 1 | 3370 | |
| 12506 | 42874 | A | 12581 | 1 | 2024 | MGFYHVGQAGTELLTSNDPLT SASQSARITGKALQKPTEVPVP YEKMLQDQSALIVQGLPEGVA FKHPENYDLATLKWILENTAGI SFIINSATIEPPAAQPMSTHMG HSLCVLVVETHAKPVAVQSSSF TRNPEVISLEVAAVTVKEESED PDYDYITFKDLPGLAYETKAYV LWPQLSKICKSKNGDKNKAYRG QQCRLRQQNPLAALTGKISVSV YVSHPSLRVSIGWTRQVARQT MQKDRDGPLKNEGEKNCAGSE KNTLTSQLELEKQEQTHSKAS RRQEITKIRAELEIETQKTVEK INESRSWFFERINKIDRPLARLIK KKREKNQVDAIKNDKGDITDP TEIQTTIREYYKHL YANKLENV EEMDKFLDTYTLPRLNQEEVES LNRPIGSEIVAIINSLPTKKSPG PDGFTAIFYQRYKEELVPFLK LFQSIEKEGILPNSFYEASIIIAK PGRDTTKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHIN RAKDKKHMIIISIDAEKAFDKIQ QPFMLKSLNKL/DIGKNYFKVH MGPKKSPCRQVNPKEQSWR HHST*LQTILQGYSNQNSMVLV PKQRYRSMEQNTALRNNATYL QLSDL*QT*EKQAMGKGFP** |
| 12507 | 42875 | A | 12582 | 722 | 4214 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12508 | 42876 | A | 12583 | 228 | 1152 | KNRDYNKLSLRPQCQNQTRTQN *ESHKPLNYMETEQPAPE*LL DT*RMKAEIKMFFETNENKDT TYQNLWDAFKATASKTNKEKE KNQIDTIKNDKGDITTDPTIEQT TIREYYKHL YANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGAEIVAIINSLPTKKSPGPDGF TAEFYQRYKEELIGWLRESVSK ICLKFDHQVQVITGRLLIRFQIAF GTVVLCQLTRHIDV FVGKRLA NARFAPSLGGAPDLFTLKPCFV AVETQGDLPQATTVVDIDGCL GKPANVQVALDL DVKGFQQW |
| 12509 | 42877 | A | 12584 | 1 | 2028 | |
| 12510 | 42878 | A | 12585 | 2 | 2264 | |
| 12511 | 42879 | A | 12586 | 1 | 2130 | |
| 12512 | 42880 | A | 12587 | 1 | 2900 | MENDFDELREEGFRQSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERV SAME DEMNMKGEGKFREKRIKRNE QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQT TISEYYKHL YTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNR PITGAE |
| 12513 | 42881 | A | 12588 | 1 | 2745 | |
| 12514 | 42882 | B | 12589 | 1 | 3288 | |
| 12515 | 42883 | A | 12590 | 1090 | 2526 | |
| 12516 | 42884 | A | 12591 | 1 | 3242 | |
| 12517 | 42885 | A | 12592 | 3862 | 8976 | RAKSPANIIMTGSNSHITLTN VNGLSNPIKRHRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTTFSAPHHSYSKIDHILGSEA LLSKCKRTEITNYLSHSAIKL ELRIKNLTQSR |
| 12518 | 42886 | A | 12593 | 1 | 1000 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12519 | 42887 | A | 12594 | 1 | 979 | MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFGVDLQQPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGRNQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRLVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDLMEL KTMARELRDSCTSFSRQFDQVE ERVSVIEDQMNMKREEKFRE KKMLEVLPAIRQEKEIKGIQL GKEEVKLSLFADNMTVYLENPI IS\PKISLS**ATSAKSQDIKSMC KNHKHSYTPITDKQRAKS |
| 12520 | 42888 | A | 12595 | 1140 | 2210 | KPWHKNFVTHAQASIADLIKW KKG YQ* LKIKLMK*SKKTRNTN YHQNTINISMQIN*KI*KKWRNS WHTLSQY*TRKKLNL*IDQ*Q ALKL/QAIIYSLPTKNVQGMQD SQSNTTRVWGILARAIRQEKEI KDIQLENEEVKLSLFADDMTVY LENSIVSAQNLLKLRIKYLGIQL TTDVKDLFKENYKPLLNIKED TNKWKNIPCSWIRGINIMKMAI LPKLIYRFNAIPIKLPMFTFFTELE KATLKFIWNQKRAHIAKTILSK KNKAGGIMLPDFKLYYKATAT KAAWYWYQNRDIDKKLTQIYK KKTNNPIKKWAKDMNRHLSKE DIYGANRHMKKCSSSLVIREKQ IKTTMR |
| 12521 | 42889 | A | 12596 | 520 | 697 | GLCSVPLLCISVLVPVPCCFGYC SLVV*FEVR*SDASSFVLLA*DF LGNAVSFLVPYEL |
| 12522 | 42890 | A | 12597 | 1 | 1410 | |
| 12523 | 42891 | A | 12598 | 1 | 1461 | |
| 12524 | 42892 | A | 12599 | 77 | 457 | QALKLRQ*LIAYQPKRVQDQM DSQTNSARGTKRSWYHSF*NYS N/PTEKEGILLNSFYEAGIILPKP GRDTTKKENFRPISLMSINAKIL NKILANRILQHIKKLINTIKSASS LGCKAGSTYANQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12525 | 42893 | A | 12600 | 1 | 919 | MGDFNTPLSTLDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNCSTTWKLNN MLLNDYWEHNKMKAEIKMFF ETNKNKDTTYQNLWDTLKA VC RGKFKALNAHKRKKERSQIDTL TSQLKELEKQEQTTHSKASRRQE ITKIRAELEKETETQKTLQRLMN PGAVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIVYLENP MSQPKISLS**ATSAKSQDIKSIY KNHQHSYTPIRDKQRAKS |
| 12526 | 42894 | A | 12601 | 1 | 1264 | MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLPTQKSSGPD GFTAIFYQRYKEELVPFLKLKLF QSIEKEGILPNSFYEASILIPKPG RYTHKKNNFRPISLMNIDAKIL NKILANRIQQHIKKLIHQDQVGI IPGMQSWFNIHKSINVIQHINRT KDKNHMIIISIDAEKAFDKIQQPF MLKTLNKLLENKIPKNPTYKGCE GPLQGELQITAQRNKGHRHKQM EEHPMLMDRKNEYHKNIGHTPK VIYRFNVIPIKLPMTFSELEKST LKFIWNQKRARIAKTILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEM TPHIYNHLIFDKPDKNKQWGK DSLFNKWCWENWLAIGRQLKL DPFLTPYTKINSRWIKDLNVRP KTIKTLEENLGNTIQDISMGKDF MSKTPKAMATKAKMDKWDLI KLKSFACTAKETTIRQSWPEMTK FTFSSNTDVKNWKHGKNNIGR HKTSVNTCKMDSGLVLERWM EWNPGFPLSIDAKCHKDLPRDI QFDSEKGVDFVLNYSKANMR WAGSMFL*FIESF*HEWLLNFV KGLFCIY*DNHVVFVFGSVYML |
| 12527 | 42895 | B | 12602 | 1 | 1827 | |
| 12528 | 42896 | B | 12603 | 13 | 1377 | |
| 12529 | 42897 | A | 12604 | 557 | 664 | KTPLSQPKISLS**ATTAKSQDT KSVYKNQQHSYT |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12530 | 42898 | A | 12605 | 77 | 1866 | QAPKLRQ*LIAYQPKKVQDQTD SQPNSTRGTTKSWYHSF*NFSN/ PIEKEGIFPNLFYEANILIPKGR DTTKKENFRPISLMNVNAKILN KLLANQIQQHIKKLIHNNQVGFI PGMQGWFNICKSINVIQHINRT KDKNHRISIDA EKA FNKIQQPF MLKTLNKLDDMIVYLENPIVSA KNLLKLISNFSKVSGYKINVQK SQAFLYTNNRQAESQIMSAVSF TIASKRIKYLGIQLTRDVKDLFK ENYKPVLNKIKEDTNKWKNI PSLWIGRVNIMKMAILPKVIYRFN AIPKLPMTFFTELEKTTLKFIW NQKRAHIAKTILSKKNKAGGIT LPDFKLYYKATVTKTAWHWY QNRDIDQWNRTEPSEIIPHIYNH LIFDKLDKNKTLGKDYL FNKRC WENWLAICRKLKLDPFLTRYT KINSRWIKDLNIRPKTIKTLEEN LGDTIQDIGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWENIFAIPSDK GLISRIYKELKQIYKKKSNNPIK KWAKDMNRYFSKEDIYAANR HMKKCSSLALREMQIKTTMR YHLIPVRMAIHKSGNNRCW |
| 12531 | 42899 | A | 12606 | 67 | 243 | GLCCVPLIYISVLVPVPCCFGYC SLVV*FEVR*HDASSFVLLA*D* LGDVGSFLVPYEL |
| 12532 | 42900 | A | 12607 | 1554 | 1692 | |
| 12533 | 42901 | A | 12608 | 640 | 816 | GLCSVALVCISVLVPVPCCFGY CSLVV*FEVR*HDASSFVLF A*D *LGNVDSLLVPYEL |
| 12534 | 42902 | A | 12609 | 1626 | 1739 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12535 | 42903 | A | 12610 | 1 | 2014 | MKREGSLEKKRIKRNEQSLQEI CDYVKRANLRLIGGPESDGENG TKLENTLQDMQEKFPNLARQA NIQIQEIQRTPQRYSSRRATPRHI IVRFTKVEMKEKMLRAAREKG QVTHKGKSIRLTADLSAETLQA RREWGPFIENILKEKNFQPRISYP GKLSFISEGEIKSFTDKQMLRDF VTRPALKELLKEALNMEKNK QYQPPQKHAKLTREARANTFK PSRRREITKIRAEKKEIETPKTAQ KINESRSWFSEIRINKIDRPLARL RKKKREKNQIDTIKNDEGDITT HPTEIHTIIREYYKHL YANKLEN LEEMDKFLDTYTLPRPNQEEVE SLNGPIAGSEIQAINSLPTKKSP GPDGFYQRYKEELVPFRLKLFQ SIEKEGILPNSFYEASIIIPKPGR DTTKKENFRPISLLNINAKILNKI LANRIQQHIKKLMHHDQVGFIP GMQGWFNIRKSINVIQHINRTK DKNHMIISIDAEKAFDKIQQPF MLKTLNKLIGDGYHKIIRANY DKPTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLARAIR QEKETEGIQLGKEEVKLSLFAD DMIVYLENPMSQPKISLS**ATS AKSQDTKSMCKNHKYSYTPIT DKQRAKSSVNSPFTIASKRIKYL GIQLTRYVKDLFKERSMK |
| 12536 | 42904 | A | 12611 | 1 | 700 | MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLSTKKSPGPD GFIAQFYQRTKDKNHMIISIDAE KAFDKIQQHFMKTLNKLIGD TYLKIIRAVYDKPTASIIILNGQK LEAFPLKTGTQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLGKE EVKLSLFADDMIVYLENPMSQ PKISLS**ANSAKSQDIKSMCKN LKHSYTLITDKQRAKSSVNSHS QLLQRE |
| 12537 | 42905 | A | 12613 | 1 | 1765 | |
| 12538 | 42906 | A | 12614 | 1 | 2310 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12539 | 42907 | A | 12615 | 1 | 836 | MENEFDELTEVHFRRWVITNSS ELKEHVLVTQCEEAKNLARRNK LENLEEMDKFLATYTFPSLNQE EVESLNRPITSSEIEAAINSLPTK KHPGPDGFTAKFYQRYKEELHI NRAKDKNHMIIISIDAEKAFDKI QHPVKLKILNKLIDGTYLKIIIR AIYDKPTANLILNGQKLEAFPL KTGTRQGCPLSPLLNFIVLEVLA RAIRQEKEIKGIQLGKEEVKLSL FADDRLYI*GTPLSQPKISLS** ATSAKSQDTKSMYKNHKHSYT PTTDKQRAKS |
| 12540 | 42908 | A | 12616 | 355 | 4502 | QSARFRGRRTLRRPGVGYSLVV *FEVR*CDASSFVLLA*DCLGN AGSFLVPYEL |
| 12541 | 42909 | A | 12617 | 248 | 362 | |
| 12542 | 42910 | A | 12618 | 529 | 680 | YYTRCSKWWNCVSLP*YIYINF HLPHGKLNKTDYIKKKLHDFFF KNSKHI |
| 12543 | 42911 | A | 12619 | 1 | 641 | |
| 12544 | 42912 | B | 12620 | 36 | 48 | |
| 12545 | 42913 | A | 12621 | 1 | 326 | |
| 12546 | 42914 | A | 12622 | 1 | 444 | PGSTHASAHACERLQTRTLRAF SSQRRFPATASRASLSSNMAKIS SPTETERCIESLIAVFQKYAGKD GYNYTLSTKTEFLSFMNTELAAF TKNQKDPGCP*PHDGRKLGQPT VDGQLDFSEFLNLIGG\QAMAC HDSFLKAVPSQKRT |
| 12547 | 42915 | A | 12623 | 2 | 6008 | |
| 12548 | 42916 | A | 12624 | 530 | 856 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 12549 | 42917 | A | 12625 | 1 | 952 | MAARGTGDKVKPGCEEAGAAF ELPPSVYAAALHESHQHQPCPA GGARAQRVPGGI VTEPLTCTPP KDMVFLSDDGDDDDDDNDND GGGDDNDGNDNDGDNNDNGD DDDGDDNDDGGDDNDGNG NDGDNDNDGDNDDSNNGND GDGDDDGVDNDDNSDGNNDG DDDDSDDDGDSNGYDDDG GNDDDDGDSDDDDSDNGDGD NGDGDDDGDDDDNDGHDD DGDMMMMIVMMVMVMVMV MMVMVMVMVVVQLRKRAEA SVSEAKCSINVSDNDGDN DGDDDDSDGDDDDGGGDDGD SELTNQFPTNHSGMKASKLRK DSDHREW*W**WWWCN*GR EQRPVFLKQSAQLMSVMIMMM VMVMVMVMVMVMVMVMTMV VVMVVIVNSPINSRLITQA |
| 12550 | 42918 | A | 12626 | 3 | 380 | |
| 12551 | 42919 | A | 12627 | 5 | 765 | RQWEVGRWSGTTIFSCFKKTL YFTNPSPSSSLVTILRREVTH/ CGGAPEQRYQIIPVCVAARLPT RAQDVLD AHLSEVNAVRFGN SSLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDFDPS VRNSAPVAWDCALSDLHTGQG YQVLAATYNQAAQLWKVGEA QSKETLSGHKDKVTAAKFKLT RHQAVTGSRDRTVKEWDLGRA YSPKRQRPSRTGHDDGGFVE KKRGKCGEKRDQIVTVSV |
| 12552 | 42920 | B | 12628 | 1 | 2802 | |
| 12553 | 42921 | A | 12629 | 458 | 708 | QNRHRHHGPFMSMAVSSQLLD TPAERLSLHTWKIAQRPGRGTP HFPDGA V/QAETLPQTGRPGR GTPHFPDGAASSFGYCSLVA |
| 12554 | 42922 | A | 12630 | 2300 | 6491 | EGLEALIHQERLSYWANQVSED RPVCKAIIQGKQFEGLVDTGAD VSIIALNQWPKNWPKQKAVTG LVGIGTASEVYQSMEILHCLGP DNQESTVQPMITSIPNLWGRD LLQQWGAEITMPAPLYSPTSQK IMTKMGYIPGKGLGKNEDGIK VPVEAKINQEREGIGYPFLGAV TVEPPKPIPLTWKTEKPVWVNQ WPLPKQKLEALHLLANEQLEK GHIEPSFSPWNSPVFVIQKKS GK WHTLTDLRAVNAV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12555 | 42923 | A | 12631 | 1 | 434 | MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDVSDGFKG GLIEIPDSIGKDKEACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF |
| 12556 | 42924 | A | 12632 | 1 | 642 | |
| 12557 | 42925 | A | 12633 | 260 | 534 | |
| 12558 | 42926 | A | 12634 | 1 | 438 | |
| 12559 | 42927 | C | 12635 | 391 | 750 | |
| 12560 | 42928 | A | 12636 | 199 | 451 | |
| 12561 | 42929 | A | 12637 | 120 | 992 | RDRIPGPVCKGKWKNKERILIFS SRGINFRTRHLMQDLRMLMPH SK\HDTNMARSDNLSVINEGCE MNNWLRCIYFEAKKKQDLYM WLSNSPDGPSAKFLVQNIHTLA ELKMTGNCLKGSRPLLSFDPAF DELPHYALLKELLIQIFSTPRYH PKSQPFVDHVFTFTILDNRIWFR NFQIIEEDAALVEIGPRFVLNLIK IFQGSFGGPTLYENPHYQSPNM HRRVIRSITAACYREKQQVKDV QKLRRKEPKTLLPHDPAADV VTPAEEKPIEQWVKPETKVDL KASV |
| 12562 | 42930 | A | 12638 | 1 | 342 | |
| 12563 | 42931 | A | 12639 | 1 | 580 | PGWEKRMSRSS/GVNTQEALPT AAIPTDAKVRVYYFNHITNASQ WERPIGNSSSGGKNGQGEPARV RCSHLLVKHSQSRPSSWRQEK ITRTKEEVALELINGYIQIKSGE EDFE\SLASQFSDCSSAKA\RGD LG\SFSRGQMOKPF*RTPRFAL\ RTGGDERGPCFTD\SGIHILPHL SEGGKPRPGLGAGQGG |
| 12564 | 42932 | A | 12640 | 3 | 116 | |
| 12565 | 42933 | A | 12641 | 2 | 253 | |
| 12566 | 42934 | A | 12642 | 3 | 512 | EDYLERKRQ/VPTECQTHSKLG GPMTLKREVKP/KVDVSPSKKG PL\QHHTLLVCHVRIFYPGSIQ/ VRWFLNGRKKTAGVVPNLIR NGDWT/FQILVMLEM/TPQQGD VYTCQVEHTSLDSPVTVEWKA QSDSARSKTLTGAGGFVLGLIIC GVGIFMHRRSKK\FNEDLHKQG |
| 12567 | 42935 | A | 12643 | 1 | 363 | |
| 12568 | 42936 | B | 12644 | 70 | 1229 | |
| 12569 | 42937 | A | 12645 | 1 | 430 | |
| 12570 | 42938 | B | 12646 | 1 | 1321 | |
| 12571 | 42939 | A | 12647 | 3 | 446 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12572 | 42940 | A | 12648 | 1 | 417 | |
| 12573 | 42941 | A | 12649 | 269 | 452 | TILRSFGYFFRRINIMLTEEKIKS DHRKISQLIFLQKLCQTLQSENV SQGGMLYRAKA*H*T*TLVWV *HVMSYPHKGLGLMLSLCSVK HSTLRDVFTL |
| 12574 | 42942 | A | 12650 | 83 | 1385 | |
| 12575 | 42943 | A | 12651 | 1 | 974 | MNPLECVDRSSQPWGNPTWTS SGMRSVTFLVGFKLTFLALAQT LNAAASLTGQELLAGFPPGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGII LCILMNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDL FKANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCVIGLQMGTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGFLPPCLGPSQE |
| 12576 | 42944 | A | 12652 | 1 | 1103 | MNPLECVDRSSQPWGNPTWTS SGMRSVTFLVGFKLTFLALAQT LNAAASLTGQELLWNFLLMF AWKIAPALCCGNTTVIKPAEQT PLSALYMGALIKEAGFPPGVINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGII LCILMNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDL FKANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCVIGLQMGTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGFLPPCLGPSQE |
| 12577 | 42945 | A | 12653 | 1 | 729 | |
| 12578 | 42946 | A | 12654 | 259 | 390 | SFCSANFEVFRLTAQQ*FVR*H ALSHIF*G*V*SFPKSTKRVNF |
| 12579 | 42947 | A | 12655 | 68 | 735 | |
| 12580 | 42948 | A | 12656 | 1 | 825 | |
| 12581 | 42949 | A | 12657 | 3 | 470 | |
| 12582 | 42950 | A | 12658 | 1 | 1683 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12583 | 42951 | A | 12659 | 1 | 1748 | MNKPYIRNLSENAAPLDLEGIL KDAKIPVSGPFLVKIGYAFVDC PDEIWALKAIEALSGKIELHGKP IEVEHSVPKRQRIRKLQIRNIPPH LQWEVLDS*LVQYGVVESCQQ VNTDSETAVVNVITYSSKDQAR QALDK/LLDKLNGFQLENFTLK VAYIPDEMATQQNPFLQPRGRR GLGQRGSSRQSGSPGSVSKQKPC DLPLCLLVPTQFVGAIIGKEGAT IRNITKQTQSKIDVHRKENAGA AEKSITILSTPEGTSAACKSILEI MRKETQDVKFTEEIPLKILAQN NFVGRLLIGKEGRNLKKIEQDTD TKITISPLQELMQYNPEHTITAK GNVETCAKAEIEIMKKIRER*E NDITSM/N/LQAHLPGLNLNAL GLFPPTSGMPPPTSGPPSAMTPP SPQSESESETVHLFIPALSVRA LISKQGQHIKQLSRFAGASSKIA PVEAPDAKVRMVMIAGSPEAR FKAQGRIYGKIKEENFVSPKEE VKLEAHIRVPSFAAGRVIGKGG KTVNELQNFSSAEVVVPRDQTP DENDQVVVKITGHFYACQVAQ RKIQEILTQVKQHQQQKALQSG |
| 12584 | 42952 | A | 12660 | 3 | 803 | |
| 12585 | 42953 | B | 12661 | 1 | 330 | |
| 12586 | 42954 | C | 12662 | 127 | 342 | |
| 12587 | 42955 | A | 12663 | 324 | 491 | |
| 12588 | 42956 | A | 12664 | 1 | 891 | |
| 12589 | 42957 | B | 12665 | 1 | 1869 | |
| 12590 | 42958 | A | 12666 | 2 | 136 | |
| 12591 | 42959 | A | 12667 | 108 | 355 | |
| 12592 | 42960 | A | 12668 | 2 | 811 | FGMRGSRGGWAGEMAASGES GTSGGGGSTEEAFMTFYSEVKQ IEKRDSVLTSKNQIERLTRPGSS YFNLNPFEVLQIDPEVTDEEIKK RFRQLSILVHPDKNQDDADRA\ QKAFAVDKAYKLLLDQEQQK RALDVIQAGKEYVEHTVKERK KQLKKEGKPTIVEEDDPELFBKQ AVYKQTMKLF AELEIKRKERE AKEMHERKRQREEEIEAQEKA KR/EEREWQKNFEES\RDGRVD SWRNF\QAQFRRGKKEKKNRTF LRPPESKNGSNE |
| 12593 | 42961 | A | 12669 | 731 | 850 | |
| 12594 | 42962 | A | 12670 | 201 | 377 | LMTLPCKIPSPGSSWLKISPIEHL MTPTPASQRTTPFDCNFPLPTQI L*NGPTPISLH |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12595 | 42963 | A | 12671 | 742 | 2982 | KIFPFDASFLPCLHKFNLKGKG NSKGFKMAEFESLMNIHGFDL GSRYMDLKPLGCGGNGLVFSA VDNDCDKRVAIKKIVLTDPQSV KHALREIKIIRRLDHDNIVKVFE ILGPSGSQLTDDVGSLELNSV YIVQEYMETDLANVLEQGPLE EHARLFMYQLLRGLKYIHSAN VLHRDLKPANLFINTEDLVKI GDFGLARIMDPHYSHKGHLSE GLVTKWYRSPRLLSPNNYTK AIDMWAAGCIFAEMLTGKTLF AGAHELEQMQLILESIPVVHEE DRQELLSVIPVYIRNDMTEPHK PLTQLLPGISREALDFLEQILTFS PMDRLTAAEALSHPYMSIYSFP MDEPISSHPIHIEDEVDDILLMD ETHSHIYNWERYHDCQFSEHD WPVHNNFDIDEVQLDPRALSD VTDEEEVQVDPRKYLDGDREK YLEDPAFDTNYSTEPWCQYSD HHENKYCDLECSHTCNYKTRS SSYLDNLVWRESEVNHYEYPK LIIDLSNWKEQSKEKSDKKGKS KCERNGLVKAQIALEEASQQLA GKEREKNQGDFDFSFIAGTIHL SSQHEPTDVGDKLNDLNSSVS QLELKSLISKSVSQEKQEKGMA NLAQLEALYQSSWDSQFVSGG EDCFFINQFCEVRKDEQVEKEN TYTSYLDKFFSRKEDTEMLETE PVEDGKLGGERGHEEGFLNNSGE |
| 12596 | 42964 | A | 12672 | 826 | 1041 | WKITVKGGVFLWWAGVGDTK VLSGGAF*ARMSQEEDFHKVM SSVKARTGHLHFFCGGMSSVK AGQGPFVLL |
| 12597 | 42965 | A | 12673 | 1 | 1482 | |
| 12598 | 42966 | A | 12674 | 3 | 488 | |
| 12599 | 42967 | A | 12675 | 2 | 114 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12600 | 42968 | A | 12676 | 1 | 897 | MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSITRRIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDEDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSDFCHWGQRFR YSYYDESQGEIY*SIEHLDKMG MSIIEQLDPVSFSNYLKKYHNTI CGRHPIG\VLLNAITELQKNGM NMSFS\FLNYAQSSQC\RNWQD SSVSYAAGALTVH |
| 12601 | 42969 | A | 12677 | 2 | 114 | |
| 12602 | 42970 | A | 12678 | 1 | 897 | MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSITRRIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDEDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSDFCHWGQRFR YSYYDESQGEIY*SIEHLDKMG MSIIEQLDPVSFSNYLKKYHNTI CGRHPIG\VLLNAITELQKNGM NMSFS\FLNYAQSSQC\RNWQD SSVSYAAGALTVH |
| 12603 | 42971 | A | 12679 | 1 | 912 | |
| 12604 | 42972 | A | 12680 | 1 | 156 | |
| 12605 | 42973 | A | 12681 | 112 | 1120 | |
| 12606 | 42974 | A | 12682 | 33 | 415 | NMNKPITPSTYVRCLNVGLIRK LSDFIDPQEGWKKLAVAIKKPS GDDRYNQFHINDAVPKTANTLP SKEAITVQQKQMPFCDKDRTL MTPVQNLEQSYMPPDSSSPENK SLEVSDTRFHSFSFYELKN |
| 12607 | 42975 | A | 12683 | 3 | 311 | |
| 12608 | 42976 | A | 12684 | 1 | 1125 | |
| 12609 | 42977 | A | 12685 | 1 | 1365 | |
| 12610 | 42978 | A | 12686 | 3 | 141 | VVSTVVPDS/AHKLFIGGLPNYL NDDQCHGLSKGYAFCEYVDIN VTV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 12611 | 42979 | A | 12687 | 1 | 1255 | GTRSTSSLRRQMKNIVHNYSEA EIKVREATSNDPWGPSSSLMSEI ADLTYNVVFASFSEIMSMIWKRL NDHGKNWRHVYKAMTLMEYL IKTGSERVSQCKENMYAVQT LKDFQYVDRDGKDQGVNVRE KAKQLVALLRDEDRLREERAH ALKTKEKLAQTATASSAAVGS GPPPEAEQAWPQSSGEEELQLQ LALAMSKEEADQEERIRRGGDL RRRWQSRRARGRLGARRSRPS WTLTSSSRPQLLPRPQTGGGAQ HPWLLPSPRLPPRTPGAAPLSL QLLIPGEVQPPRRPLGTPGGLLP LQDPQLTLGVGPQPLQLGRGPR LIHGEVPMVGSRVSGPQPPIPGH RPRPSQIPGEGHLPSPAPMAQQ QPGDSTRSPTSSLTLTDSARHCR PPGAAQESWSCWQERCPEAL |
| 12612 | 42980 | A | 12688 | 116 | 1541 | |
| 12613 | 42981 | A | 12689 | 3 | 415 | |
| 12614 | 42982 | A | 12690 | 1 | 1440 | |
| 12615 | 42983 | C | 12691 | 117 | 314 | |
| 12616 | 42984 | A | 12692 | 3 | 120 | |
| 12617 | 42985 | A | 12693 | 1 | 729 | |
| 12618 | 42986 | A | 12694 | 79 | 870 | EWSSVRRLVEKRALRRPHPQC LCFRMKTILSNQTCRPFPE\NVD VTLKGRP/VIV*GPAEGTLR\DF VHLQW*NLSLSWKEKKRGRSR VDK\WWGNRKGNWPTVVRTYL VVHVQNMKGVLPLGLPVTKD EGLVYA\HFPHPTLVIPGRNGSS LLKSRNFLGVKNTSRRVSG*RP GVACSVSSSPRKDEFNPLKGN DIGACFQISAGFGFQQAPHTCL KTRDIQGNFWDGYPMVLWKK GTVSARAGWNKDLKEFTWATE RKMPG |
| 12619 | 42987 | A | 12695 | 2 | 293 | |
| 12620 | 42988 | A | 12696 | 1 | 273 | TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFGVSLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS |
| 12621 | 42989 | A | 12697 | 1 | 1308 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12622 | 42990 | A | 12698 | 124 | 1135 | DKNSMGLPGVIPSCAAVLWSSI HLSSSALSPTISACRHPMEDSM DMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTV SLGAGAKDELHIVEAEAMNYE GSPKVTLATLKMSVQPTVSLG GFEITPPVVLRLKCGSGPVHISG QHLVAVEEDAEESEDEEEEDVK\ LLSISGKRSAPGGGSKVPQKK\ KLAADVEDDDDDDEEDDDDED \DDDDFDDEEAEEKAPVK\KSI\ RDTPAKNAQKSNQNGKDSKPS STPRSKGQESFKKQEKTPKTPK GPSSVEDIKAKMQASIA/EKGGG LPKVEAKFINYVKNCFRMTDQ EAIQDLWQWRKSL |
| 12623 | 42991 | A | 12699 | 201 | 416 | |
| 12624 | 42992 | A | 12700 | 2 | 678 | |
| 12625 | 42993 | A | 12701 | 3 | 2149 | |
| 12626 | 42994 | A | 12702 | 1 | 219 | |
| 12627 | 42995 | A | 12704 | 267 | 437 | |
| 12628 | 42996 | A | 12705 | 507 | 845 | |
| 12629 | 42997 | A | 12706 | 426 | 704 | SRRWGGVHSCPPSPPTAGHWT LLILCAKARRSEAMVLASRRR RPGPRPRRRRLPVLGSRGGAG PARGRGPSWPGPLRAAPSP*P SSTV |
| 12630 | 42998 | A | 12707 | 195 | 892 | |
| 12631 | 42999 | A | 12708 | 1 | 893 | |
| 12632 | 43000 | A | 12709 | 1 | 777 | |
| 12633 | 43001 | A | 12710 | 1 | 439 | KTQVAPSTDGIQPPSSNSRTDE REFFIASYNRKKEDEGENVWIA KSSAGAKGEGILISSEASELLDFI DNQAQVHVQKYLEHPLLEPG HRKFDIRSWVLVDHQYNIYLY REGVLR TASEPYHVDNFQDKT CHLTNHCIQKKKKK |
| 12634 | 43002 | A | 12711 | 1 | 394 | SGTRPVFLVPHTIGIPHPAIVTP QVKQEHPTHDSDLMHVKPQHE QRKEQEPKRPKPLNAFMLY MKEMRANVVAECTLKESAAIN QILGRRWHALSREEQAKYYEL ARKERQLHMLYPGWSARDN |
| 12635 | 43003 | A | 12712 | 1 | 789 | |
| 12636 | 43004 | A | 12713 | 1 | 870 | |
| 12637 | 43005 | A | 12714 | 1 | 729 | |
| 12638 | 43006 | A | 12715 | 1 | 828 | |
| 12639 | 43007 | A | 12716 | 1 | 213 | |
| 12640 | 43008 | A | 12717 | 1 | 664 | |
| 12641 | 43009 | A | 12718 | 1 | 695 | |
| 12642 | 43010 | A | 12719 | 96 | 269 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12643 | 43011 | A | 12720 | 3 | 241 | |
| 12644 | 43012 | A | 12721 | 213 | 660 | EGPARHRLLSPPVRASKMTKKR RNNGRAQKRAARHVRGSPSLK/ CFPSGPLPPNCAR\CVPK\DKAIK KF\VI\RNIVEAAA\AR\DISEASV FDAYLALPKL\YVKLH\YCVSCAI HKQK*SGNRSS*SPAKTRTPPPR FR\PGG*LPHGPPTKSP |
| 12645 | 43013 | A | 12722 | 1 | 303 | |
| 12646 | 43014 | A | 12723 | 610 | 928 | FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFFLWRSFAVVAQAV VQWHNLSSLPFGFKQFSCLSLP SSWDYRCPPPRPANFCIFTRDG VSPCCPGWSRTSDLR |
| 12647 | 43015 | A | 12724 | 1 | 2775 | |
| 12648 | 43016 | A | 12725 | 1 | 6039 | |
| 12649 | 43017 | A | 12726 | 2 | 3661 | |
| 12650 | 43018 | A | 12727 | 1 | 1173 | |
| 12651 | 43019 | A | 12728 | 1 | 1632 | MPNPKNSKGGGRKNKRANSSGD EQENGAGALAAAGAAGAAAG GALAAAAGCGAAAAGAPGAG GAAGAGGAGTGAANAAAAAG AAAAGDAKNEAPCATPLICSFG RPVDLE\KDDYQKVVCNNEHC PCSTWMHLQCFYEWESSILVQF NCIGRARTWNEKQCRQNMWT KKG\YDL\AFRFCSCRCGQGNL KKD TDWYQVKRMQDEK KKS GSEKNTGRPPGEAAEEAKKCRP PNKPQKGPSHDLP RRHSM DRQ NSQEKA VGAAAYGARSPGGSP GQSPPTGYSILSPA HFSGPRSSR YLGEFLKNAIHLEPHKKAMAG GHVFRNAHFDYSPAGLAVHRG GHFDTPVQFLRRLDSELLTHIP RHKLNTFHVRMEDDAQVGQG EDLRKFILAALSASHRN VVNCA LCHRALPVFEQFPLVDGTLFLSP SRHDEIEYDVPCHLQGRMLHL YAVCVDCLGVHKIICKCKSR WDGSHWLGTMYTYDILAASP CCQARLNCKHCGKPVIDVRIG MQYFSEYSNVQQCPHCGNLDY HFVKPFSSFKVLEAY |
| 12652 | 43020 | A | 12729 | 1 | 1485 | |
| 12653 | 43021 | A | 12730 | 1 | 1074 | |
| 12654 | 43022 | A | 12731 | 2 | 3394 | |
| 12655 | 43023 | A | 12732 | 1 | 2190 | |
| 12656 | 43024 | A | 12733 | 1 | 1251 | |
| 12657 | 43025 | A | 12734 | 1 | 1710 | |
| 12658 | 43026 | A | 12735 | 3 | 679 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12659 | 43027 | A | 12736 | 209 | 337 | |
| 12660 | 43028 | A | 12737 | 365 | 538 | |
| 12661 | 43029 | A | 12738 | 2 | 196 | |
| 12662 | 43030 | A | 12739 | 1 | 2639 | |
| 12663 | 43031 | A | 12740 | 3 | 173 | |
| 12664 | 43032 | A | 12741 | 1 | 1479 | |
| 12665 | 43033 | A | 12742 | 1 | 921 | |
| 12666 | 43034 | A | 12743 | 1 | 798 | |
| 12667 | 43035 | A | 12744 | 2 | 773 | |
| 12668 | 43036 | B | 12745 | 75 | 321 | |
| 12669 | 43037 | A | 12746 | 321 | 738 | |
| 12670 | 43038 | A | 12747 | 1 | 3190 | |
| 12671 | 43039 | A | 12748 | 287 | 1636 | ACGAMERAPDGPLNASGALA GDAAAAGGARGFSAAWTA VL AALMALLIVATVLGNALVMLA FVADSSLRTQNNFFLLNLAISDF LVGAFCIPLYVPYVLTGRWTFG RGLCKLWLVDYLLCTSSAFNI VLISYDRFLSVTRAVSYRAQQG DTRRAVRKMLLVWVLAFLLYG PAILSWEYLSGGSSIPEGH CYAE FFYNWYFLITASTLEFFT PFLSV TFFNLSIYLN IQRRLRLD GAR EAAGPEPPPEAQSPPPPGCWG CWQKGHGEAMPLHRYGVGEA AVGAEAGEATLGGGGGGGSVA SPTSSSGSSSRGTERPRSLKRG S KPSASSASLEKRMKMVSQSFTQ RFRLARDRKEAKSLAVIVSIFG LCWAPYTLLMIIRAACHGHCVP DYWYETSFWLLWANS AVNPV LYPLCHHSFRRAFTKLLCPQKL KIQPHSSLEHCWK |
| 12672 | 43040 | A | 12749 | 1 | 2142 | |
| 12673 | 43041 | A | 12750 | 3 | 711 | VWWNSDLMVINRSTTELPLTV SYDKVSLGRLRFWIHQDAVY SLQQGFSEKDADEVKGIFVDT NLYFLALTFFVAAFHLLFDFLA FKNDISFWKKKKSMIGMSTKA VLWRCFSTVVIFLFLDEQTSLL VLVPAGVW/AAAIELWES*RK/ VI*RTWTFWRGLMPEFQFGTYS ESERKTEEYDTQAMKYLSYLL YPLCVGGAVYSLN IYKSWY SWLINSFVNGVYA FGFLFMLPQ |
| 12674 | 43042 | A | 12751 | 1 | 2025 | |
| 12675 | 43043 | A | 12752 | 494 | 747 | ATVKWITLCRNRNIKLPTFIKKE GTGKAPKSRKSVLGLGP*VHT SPGDPAEGEGLPAGERPDGNLS QSPNSLRFYIKKKKAYK |
| 12676 | 43044 | A | 12753 | 9 | 731 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12677 | 43045 | A | 12754 | 143 | 641 | RSWVLLGVGARGSTPRTYQVP SPSLAPSALC*VS*VPLESLSCSH ADNWKQELTKFISPDQLPVEFG GTMTDPDGNPKCLTKINYGGE VPKSYYLCKQVRLQYEHTRSV GRGSSLQVENEILFPGCGLRVL RFYNTYSLVHSKRISYTVEVLL PDQTFMEKMEKF |
| 12678 | 43046 | A | 12755 | 1 | 1506 | |
| 12679 | 43047 | A | 12756 | 2 | 526 | CQPVRAA*RHGNTPLATV*PAS T/WWKWSEKQKEEQEMQNWR ESAS/VSGYPQDILSCAMSQNPR KRKRPRNVSAPPVHQAQMNI SVEQMETS KTHQATPLTWGQM KRLAHVAEENLRSQNKPLTTSN LMVAMMVVISLAVSLPVAGAD QNYIYWAYIPFPH |
| 12680 | 43048 | A | 12757 | 1 | 1443 | |
| 12681 | 43049 | A | 12758 | 3 | 766 | |
| 12682 | 43050 | A | 12759 | 29 | 253 | |
| 12683 | 43051 | A | 12760 | 34 | 252 | |
| 12684 | 43052 | A | 12761 | 1362 | 1611 | SSVLHPWDARLVQHT\KSIHHH HINRTNDKNHMIISIDAEKAFD KIQQDFMLKTLNKLIGDGYLK IVRATYDKPTASILLNG |
| 12685 | 43053 | B | 12762 | 1 | 1755 | |
| 12686 | 43054 | A | 12763 | 1 | 2109 | |
| 12687 | 43055 | B | 12764 | 1 | 1497 | |
| 12688 | 43056 | B | 12765 | 1 | 1527 | |
| 12689 | 43057 | B | 12766 | 1 | 1746 | |
| 12690 | 43058 | B | 12767 | 1 | 2853 | |
| 12691 | 43059 | B | 12768 | 1 | 1479 | |
| 12692 | 43060 | B | 12769 | 1 | 1932 | |
| 12693 | 43061 | A | 12770 | 1269 | 1581 | NTGKPNPAAHQKGYPPRSSGPH PWDARLVQHT\KSINIIHHINRT KDKNHMIISIDAEKAFDKIQLPF MLKTL SKLGVSYNMFTRLTPI AQVDTRGNQLPSYLI |
| 12694 | 43062 | B | 12771 | 1 | 4404 | |
| 12695 | 43063 | B | 12772 | 56 | 2080 | |
| 12696 | 43064 | B | 12773 | 1 | 5445 | |
| 12697 | 43065 | B | 12774 | 295 | 2831 | |
| 12698 | 43066 | A | 12775 | 89 | 459 | |
| 12699 | 43067 | A | 12776 | 2 | 980 | |
| 12700 | 43068 | A | 12777 | 1 | 378 | |
| 12701 | 43069 | A | 12778 | 1 | 363 | PGVALPGRRCRQAPADLLP*MR AYWPDVIYSFANRSRFWKHEW EKHGTC AAQVDALNSQNKYFG TSLELYRELDLNSVLLKLGKPS INYYQVADFKDALR VYGVIP KIQCLPPSQDEDRQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 12702 | 43070 | A | 12779 | 1 | 577 | QRFKND CRDPRDTGPIHGLWPD KSEG/CNRSW/PFNLEEIKDLCP EMRAYWPDVIHSFPNRSRFWK HEWEKHGTCAAQVDALNSQK KYFGRSLELYRELDL/NQVADF KDALARVYGVIPKIQCLPPSQD EEVQTIGQIELCLTKQDQQLQN CTEPGEQPSPKQEVWLANGAA ESRGLRVCEDGPVFYPPPKKTK |
| 12703 | 43071 | A | 12780 | 1 | 624 | MRPAALRGALLGCLCLALLCL GGADKRLRASVSRPFSLEHPEP GHCLDLHLRAYPAR\WSS*PWP QDFWVR*PTWES/VSDLLPEMR AYWPDVIHSFPNRSRFWKHEW EKHGTCAAQVDALNSQKKYFG RSLELYRELDLNRGERVPTQFP RELVVNRSLAPPPTPGFLSGHVI SVHTSSPLPSAMSGSFLRPLPEA ESGSMLLGQPADP |
| 12704 | 43072 | A | 12781 | 1 | 612 | |
| 12705 | 43073 | A | 12782 | 113 | 1149 | RGAPRGPRQGCGHSRSPAR GPRDTGLGRPRAPGPGGRCCS GGSAAARGLGDSVSPGSLPRAA GGKWEPERQLAAFSPQVGTMR PAALRGALLGCLCLALLCLGG ADKRLRDNHEWKKLIMVQHW PETVCEKIQND CRDPPDYWTIH GLWPDKSEGCNRSWPFNLEEI KDLLPEMRA YWPDVIHSFPNRS RFWKHE/WPKRHGTCAAQVD ALNSQK\KYFGRSLELY\RKLDL NSVLALKLGKPSINYYQVADFK DALARVYGVIPKIQCLPTSQGE\ EVQTIGQ\IDLCLIKARTRQLQN\ CTEPGEQPSPKQEVWLANGA\ AESRGLRVCEDGPVFYPPPKKT |
| 12706 | 43074 | A | 12783 | 2 | 515 | |
| 12707 | 43075 | B | 12784 | 62 | 359 | |
| 12708 | 43076 | B | 12785 | 219 | 523 | |
| 12709 | 43077 | A | 12786 | 1010 | 1550 | DTENIPSSRRRERSKVPYIVRQC VEEIERRGMEEVGIYHVSGRIV AADIQALKA AFNVSECRPAQD GMEVWAVVSAMRSQSAPRPRH VTSFSVSFLHLSGSSRRPLHFRA LS\NNKDVSVMMSMDVNAIA GSLKLYFRELPEPLFTDEFYPNF AEGIGEHW RPWPHGRLLHVH CCPQRL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12710 | 43078 | A | 12787 | 2 | 951 | GSNLYCTLEGDSFGYFVNKAK TRVYRD/THADPNWNEEFIEL EGSQTLRILCYEKCYNKTKIPKE DGESTDRLMGKGQVQLDPQAL QDRDWQRTVIAMNGIEVKLSV KFNSREFSLKRMPSRKQTGVFG VKIAVVTKRERSKVPIYIVRQC VEEIEPPKALEGGWASTACPAG VATDIQALKAAFDGNNKDVS MMSEMDVNIAIGTLNLYFREL PEPLFTDEFYPNFAEG/IRVAEK EAVNNMSLHNLATVFGPTLLR PSEKESKLPANPSQPITMTDSW SLEVMSQVQVLLYFLQLEAIPA PDSKRQSILFSTEV |
| 12711 | 43079 | A | 12788 | 3 | 644 | |
| 12712 | 43080 | A | 12789 | 168 | 378 | |
| 12713 | 43081 | A | 12790 | 1 | 486 | |
| 12714 | 43082 | A | 12792 | 83 | 536 | |
| 12715 | 43083 | A | 12793 | 1 | 662 | |
| 12716 | 43084 | A | 12794 | 3 | 357 | |
| 12717 | 43085 | A | 12795 | 2 | 421 | |
| 12718 | 43086 | A | 12796 | 2 | 908 | |
| 12719 | 43087 | A | 12797 | 1 | 846 | |
| 12720 | 43088 | C | 12798 | 87 | 413 | |
| 12721 | 43089 | A | 12799 | 1 | 508 | MCQGD TYAWGGHMC RGGHLR RGHSHERDTPRGPERPPPPAR DRESKDERRRPPPKDPPAVRTC\ PDSPSTATPPPPPPPPPPPPPPPP PAAPSAFAALRLRGPRK WTA RGQLPLPATAPPEARVRALPRGG YSSPGRATSARGPAPWPLPSRT GKPPRPCSANTQEHC |
| 12722 | 43090 | A | 12800 | 1 | 393 | |
| 12723 | 43091 | A | 12801 | 1 | 582 | |
| 12724 | 43092 | A | 12802 | 1 | 1422 | |
| 12725 | 43093 | A | 12803 | 1 | 1080 | |
| 12726 | 43094 | A | 12804 | 2 | 261 | SCPFGGNC FYKHA YPDGRREEP QRQK VGTSSRYRAQR RNHFWE LIEERENS NPFND EEEV VTFEL GE\MLLMLLAAGG DDEL TNS |
| 12727 | 43095 | B | 12805 | 60 | 802 | |
| 12728 | 43096 | A | 12806 | 2 | 238 | |
| 12729 | 43097 | A | 12807 | 1 | 1017 | |
| 12730 | 43098 | B | 12808 | 1 | 939 | |
| 12731 | 43099 | A | 12809 | 1 | 708 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12732 | 43100 | A | 12810 | 1 | 2653 | MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDIYRNLHP ESTEYTFFSAPHHTYSKIDHILG SKAPLSKYRRSEIKINCLSDHSA IKLELRIKKLTQNRSTTWKLNN LLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTLKA VCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLLARLIKKKR EKNQIHAIKNDKGD MSTNHT EI QTTIREYYKHL YANKLENLKEI DKFLETYSLPRLNQEEVESLNR PITGSEIEA INSLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNIPCSWVGRINIVKMAIL PKNWKKTTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEIMPHIYNHLIFDKPDK NKKWKGKDSL FNKWCWENWLA ICRKLKLD PFLTPYTKINSRWIK DLNVRPKTIKTLEENPGNTIQDI GMGEDFMSKTPEAMATKAKID KWDLIKLSFCTAKETTIRLNR PPTEWEKIFAIYSSDKGLISRIYN ELQQIYEKKTNNPIKKWAKDM NRHLSKEDIYAAKRHMKKCAS |
| 12733 | 43101 | B | 12811 | 1 | 2748 | |
| 12734 | 43102 | A | 12812 | 1 | 1962 | |
| 12735 | 43103 | B | 12813 | 1 | 1833 | |
| 12736 | 43104 | A | 12814 | 176 | 421 | QQPASPTRSVLLFPKTAHISGSP APPNVGLLNPSTGAAQKKTMT SAGLGRLSL*K*LNLPECVACA GETWVTSMMSGNQC N |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12737 | 43105 | A | 12815 | 1 | 1615 | LISNFSKVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKR MKYLGIQPTRDMKDLFKENYK PLLNEIKEDTNKWKNIPCSWVG RINIVKMAILPKNWKKTTLKF WNQKRARIAKSILSQKNKAGGI MLPDFKLYYKATITKTAWYWY QNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGKDSL FNK WCWENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTIKTLE ENPGNTIQDIGMGEDFMSKTPE AMATKAKIDKWDLIKLKSFCT AKETTIRLNRPTEWEKIFAIYS SDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYAA KRHMKKCASSLAIREIQIKTTM RYHLTPVRMAIIKSGNNRCW RGCGEIGTLLHCWWDCCLVQP LWKS VWRFLRDLELEIPDPAIP LLGIYPKDYKSCCYEDTCTHMF IVALFTIAKTWNQPKCPTMIDW IKKMWHIYTMEYYADIKKDEF MSFVRTRMKLETIILSKISQIEK KTKHRMFSLIGGN |
| 12738 | 43106 | A | 12816 | 1 | 996 | |
| 12739 | 43107 | A | 12817 | 1 | 756 | |
| 12740 | 43108 | A | 12818 | 1 | 1428 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12741 | 43109 | A | 12819 | 1 | 2377 | MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NIVQHINRTNDKNHMIISIDAEK AFDKIQQRFMLKTLNKLIGDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGILTRDVKDLFKEN YKPLLNDIKEDTNKWKNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMFTFFTELEKTTLKFIWN QKGARIAKSILIYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKWGND LFNKWCWENWLAICRKLKLD FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNTIQDIAMGKDFMS KTPKAMATKAKIDKWDLINLK SFCTAKETTIRVNRQPIEWEIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSSLAIREMHI KTTMRHHLTSVRMAIHKLG DWCWRGCGEIGRLLHCWDC KLVQPLWKS VWRFLRDLELET PFDPATPLLGIYPKDYKSCCYK DICT/RVCVPAALFTIANTWNPT |
| 12742 | 43110 | A | 12820 | 1 | 4840 | |
| 12743 | 43111 | A | 12821 | 578 | 630 | EYKNR*GLSLNPWGKTVHISW DVWSVGSSKAKRNWESWES*C RGIQKKASLRSGTNHSASSGI* ESRV*GLGTTGYRGITASLSL RSCTRLH |
| 12744 | 43112 | A | 12822 | 8 | 214 | EEWPKRKSEIRERPRP*SWPSDK QTLVVQRGQKMEQANHPDPTD HMSQLMWTACPKGLGIALICL VRH |
| 12745 | 43113 | A | 12823 | 33 | 240 | GGGRNTWLQAVPGFPGW*RTL RTAVWDRRLTLRKPHHCPGGS QFPGPQRQVIGLLHFLSSLNHQ GWV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12746 | 43114 | A | 12824 | 1 | 411 | MSTITQRKEENPSVFLEWLWEA /CKKIYSPVTRLTRGSIDPKR*V YYAISHRYQQKAPKPSGP*TK SGGIKPGNLGVLY*GPRGTGQ KKGARSEKGC SL SHGPQTNKP WWFREDRKWSRPITWYGFLSV WFARTP |
| 12747 | 43115 | A | 12825 | 1 | 611 | |
| 12748 | 43116 | A | 12826 | 120 | 493 | KYRAQRRMIARWLPQDLERGE AMLPNSSGWYKSLKGI/VLISEA FSCCKRAASLTADWL*VKQHS SPKKVQSPFSAVRRSKPWQFW RVTA AKQSIWDCRVRIDFVISC KLRNPLRVCGSRILK |
| 12749 | 43117 | A | 12827 | 1 | 2195 | VGEEGPAGVEGLNFFPAQSRRLP GPQQCSPGAEQGASARARRPRP RPRPAAMVPGVPGAVLTCLW LAASSG\SWRPAPARL\CAAAG RVAVCRERPARS\CASRCLSLQI TRISAFFQHFNNGSLVWCQNH KQCSKCLEPCKESGDLRKHQC QSFCEPLFPKKS YECLTSCEFLK YILLVKQGDCAPEKASGFAAA CVESCEVDNECSGVKKCCSNG CGHTCQVPKTLYKGVPLKPRK ELRFTELQSGQLEVKWSSKFNI SIEPVIYVVQRRWNYGIHPSED DATHWQTVAQTDERVQLTDI RPSRWYQFRVA AVNVHGTRGF TAPSKHFRSSKDPSAPPAPANLR LANSTVNSDG/AV*TVTIVWDL PEEPDIPVHHYKVFWSWMVSS KSLVPTKKRRKTTDGFQNSVI LEKLQPCDYVVELQAITYWG QTRLKSAK VSLHFTSTHATNNK EQLVK\TRKGGIQTQLPFQRRRP TRPLEVGAPFYQDGLQVKVY WKKTEDPTVNRVHVRWFPEAC AHNRTTGSEASSGMTHENYIIL QDLFSCKYKVTVPQIRPKSHS KAEAVFFTPPCSALKGKSHKPI GCLGEAGHVLSKVLA KPENLS ASFIVQDVNITGHFSWKMAKA NLYQPMTGQVTWAEVTTESR QNSLPNSIISQSILPSDHYVLT PNLRPSTLYRLEVQVLTGEGEG |
| 12750 | 43118 | A | 12828 | 1 | 1410 | |
| 12751 | 43119 | A | 12829 | 2 | 299 | |
| 12752 | 43120 | B | 12830 | 81 | 510 | |
| 12753 | 43121 | A | 12831 | 3 | 436 | |
| 12754 | 43122 | A | 12832 | 1 | 769 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12755 | 43123 | A | 12833 | 15 | 413 | ERM CAGPWRKGAETGPYFCND TVRHRKASLLCPF*RMNGDQN SDVYAQEKQDFVQHFSQIVRVL TEDEMGHP EIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFREL VEPRKQDADSLQRAWTVGWC VELLQA |
| 12756 | 43124 | A | 12834 | 1 | 795 | MNGDQKSDVYAQEKQDFFQHF SQIVGVLTEDMGHSEIGDAIA RLKDVLEYN AIGGKYHRGLTV L VAFQELDAINYAILLEACIYYL LKLYCQAQPYLNLIELFLQISC QPEIGQTLDLITAP/QDNVDFGR FT/EKQHANA*KILLEI/GEFFQI QDGYLDLFGDPTVTRKVGTDIQ DNKCSWL VVQCLQRSTLEQYQ ILKENYGQKKAKKV VQVKALY EELDLP AVFLQYEEDGYSHIMG LTEQYAAPLLPAMFLGLVYKIY |
| 12757 | 43125 | B | 12835 | 1 | 328 | |
| 12758 | 43126 | A | 12836 | 2 | 868 | |
| 12759 | 43127 | B | 12837 | 118 | 1138 | |
| 12760 | 43128 | A | 12838 | 100 | 374 | KHISPALKALELPFERNLII/PLQ LLKVRI LKEGEML/DI*HWFL** GMGT VQKGMPHKCYHGKTGR VYNVTQH AVGIVVNKQVK*VV |
| 12761 | 43129 | A | 12839 | 1 | 1035 | |
| 12762 | 43130 | A | 12840 | 13 | 600 | INPPPPFRPELPSSNSPKMTDH KGERGEATRYMFSRPFKKTMG VVPLGHNN*RFYKKGDIVDNIK GMGYCVQNGMPHKCYPWPKL EGVLQLLPQHA/VAIVVNQPVL GQSFFPRE*IVRIEHIKHF*EPEIS FLK/RVLKENDSEKERSPNEKG TWGSNLKRHLAPPQKKHTL*R TNGKEPELLEPIPYEFHGHN |
| 12763 | 43131 | A | 12841 | 1 | 317 | QRPSEAKEIKLYAQIPPIEKMDA SLSMLANCEKLSLSTNCIEKIAN LNLAEAVGDTLEELWISYNFIE KLKGIHIMKKLKILYMSNNLVK DWGTPVIKGDEEEDN |
| 12764 | 43132 | A | 12842 | 155 | 588 | |
| 12765 | 43133 | A | 12843 | 1 | 954 | |
| 12766 | 43134 | A | 12844 | 1 | 486 | |
| 12767 | 43135 | A | 12845 | 1 | 367 | |
| 12768 | 43136 | A | 12846 | 1 | 190 | LISRAKEDDMTLNIAEGVHPSY NIVLNTLHT/CGISVKSTWRPSK GAAP*ARMPGGTAGPCLAS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12769 | 43137 | A | 12847 | 1 | 2376 | MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLEI ASQVFVNRDVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLHQA KLTFHPTVNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA\WQQLPC*YKIVPSILRIS SSDGKYKAFSTCGSHLAVVC |
| 12770 | 43138 | A | 12848 | 1 | 636 | MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLEI ASQVFVNRDVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLHQA KLTFHPTVNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA\WQQLPC*YKKQIS |
| 12771 | 43139 | B | 12849 | 180 | 811 | |
| 12772 | 43140 | A | 12850 | 1008 | 1265 | FLGVPTLGGWRPIQHELK/PRE VTPVLLRDLIRFRPPLWIGSDN GPAFLAALVQKTAKGIQNNITG GVYTLCDIDSHILFRSGY |
| 12773 | 43141 | B | 12851 | 1 | 996 | |
| 12774 | 43142 | A | 12852 | 1251 | 1424 | DSPRGEAES*A*LPEKLLEMSG NRLVDNKDPGKKQTQRRIPHSP SQIPVPLPEIWCT |
| 12775 | 43143 | A | 12853 | 1 | 1121 | |
| 12776 | 43144 | A | 12854 | 189 | 621 | |
| 12777 | 43145 | A | 12855 | 2207 | 2308 | |
| 12778 | 43146 | A | 12856 | 1 | 762 | |
| 12779 | 43147 | A | 12857 | 1 | 678 | |
| 12780 | 43148 | A | 12858 | 3 | 496 | |
| 12781 | 43149 | A | 12859 | 107 | 258 | NALGKRTSFTNRNFLASGR LFD SVTYARRLQQYPAPL*KTAI*SF SLLNH |
| 12782 | 43150 | A | 12860 | 2 | 410 | SPDPWVSTYKSTCHIAQEIAEKI HLRNQYERKGE*APRSNLMSE DANGGAPNPWLFEEPEETIGW GFDEIRQQQHNIIR*QDAGLDA LSSIISRQKQMGIEIGNELHEQN EIIDDLANLMENTDEKL RNETR RVN |
| 12783 | 43151 | A | 12861 | 3 | 1402 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12784 | 43152 | A | 12862 | 1 | 711 | MAPDPWFSTYDSTCQIAQEIAE KIQQRNQYERKGEKAPKLTVTI RALLQNLKEKIALLDLLRAV STHQITQLEGDRRQNLDDLVT RERLLASFKNEGAEPDLIRSSL MSEEAARGAPNPWLFEEPEETR GLGFDEIRQQPQKI\QEQDARL DALSSISSQKQMGQEIGNELD EQNEIIDDLANLVENTDEKLRN ETRRVNMVDRKSASCGMIMVI LLLLVAIVVVAVWPTN |
| 12785 | 43153 | A | 12863 | 1 | 936 | |
| 12786 | 43154 | A | 12864 | 1 | 1023 | |
| 12787 | 43155 | A | 12865 | 1606 | 2238 | |
| 12788 | 43156 | A | 12866 | 3 | 347 | |
| 12789 | 43157 | A | 12867 | 1 | 1665 | |
| 12790 | 43158 | A | 12868 | 1 | 589 | |
| 12791 | 43159 | A | 12869 | 19 | 1677 | |
| 12792 | 43160 | A | 12870 | 1 | 906 | |
| 12793 | 43161 | A | 12871 | 1 | 228 | |
| 12794 | 43162 | A | 12872 | 1 | 320 | |
| 12795 | 43163 | A | 12873 | 1 | 398 | TSKAPGAQGEQGFEECFLAVAL AGRPLPSLWALFQATTPVLQG LKEAFFRPEVPLRRDLPLLLFR\ TQSDPAMPLPTMIGLLAEARR AGCLSYQTSLSVDGETWHVMG ISSLLP\SLEG\WKQ\HVTEAFQF HF |
| 12796 | 43164 | A | 12874 | 3 | 322 | SAGGSGRRTLHSRTMAQFVRN LVEKTPALVNAAVTYSKPRLAT FWYYAKVELVPPTPAEIPRAIQS LKKIVNSAQTSFKQLTVKVTT G*MKTDVHNRKCLPLGFF |
| 12797 | 43165 | A | 12875 | 91 | 425 | WTFHPTTMAPFVRDLGEKTPA LGKAAVTYLPRLAAFYYH\ QVELVPPTPA\EIPRAIQSLKKIV NSAQTSFKQLTVKEALLNDL VATEVSTWFYVREITGKRGIIG* NV |
| 12798 | 43166 | A | 12876 | 179 | 664 | HSSPAVPGRTDFSHSQNPWPQF CPVTLVGEDPRALVNAAVT/YT RKPRIGLHFWYYA\KVELVP\PT PAEIPRAIQSLKKIVNSAQGT LANSSHVKEAV/L*NGLVATEV\ LMWFLCSERLLGKRGHSLGYG CFEDQSFNIIWFILFILELFVW DHVVDPC |
| 12799 | 43167 | A | 12877 | 25 | 164 | |
| 12800 | 43168 | A | 12878 | 2110 | 2260 | |
| 12801 | 43169 | C | 12879 | 32 | 1429 | |
| 12802 | 43170 | A | 12880 | 172 | 322 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12803 | 43171 | A | 12881 | 1060 | 12039 | |
| 12804 | 43172 | A | 12882 | 1 | 810 | |
| 12805 | 43173 | A | 12883 | 3 | 146 | |
| 12806 | 43174 | A | 12884 | 1 | 1211 | GPQDGNQQPAPPEKVGWVRKF CGKGIFREIWKNRYVVLKGDQ LYISEKEVKDEKNIQEVFDLSD YEKCEELRKSKSRSKKNHSHKFT LAHSKQPGNTAPNLIFLAVSPEE KESWINALNSAITRAKNRILDE VTVEEDSYLAHPTRDRAKIQHS RRPPTRGHLMMAVASTSTSDGM LTLDLIQEEDPSPEEPTSCAESFR VDLDKSVAQLAGSRRRADSDRI QPSADRASSLSRPWEKTDKGAT YTPQAPKKLTPTEKGRCASLEEI LSQRYAASAHTLQLRAEEPPTP ALPNPGQLSRIQ\DLVARKLEET QELLAEVQGLGDGKRKAKDPP S/RSPDSES\EQLLL\ETER\LLG EASSNWSQAKRVLQQVREL RD LYRQ\MDLQTPD\SHL\AQTTPH S\Q\YRKSLM |
| 12807 | 43175 | A | 12885 | 617 | 1041 | TTLINPGGPAPLLSLPTSSITGFT TFYHPNLKPLRTCPS*VQAWPC RHPI*SRDYQRDAEPTTCISKLL GENIRRDEFWKVQIKARSGETE QNPRSTAFAGELPLANREELN LLNKGILPLCDQRQEIESECAF TIFCAGDANCFPPSPHLPLTAL QQRPCGLSGSASKEAWGNSLV CGPRGDTLPMAIAKPHRSASKH STLHQYPTPPRSLCHQHRDEQP TNHLQTLNTIPAWIHTKWVPG DHINKPWRSCSSSQSAYLFYHW LHYFLPPKLKTSKDLSILSAGLA MSAPHLIFRVSAITSNSSCKPSS TSKACEELFKEHQCLGSTDPIH IQGGAPFSAVSPQRLVLRGSQD GSHMVRPRLPFPDSAGLANFHL FSKLFLD |
| 12808 | 43176 | A | 12886 | 1 | 606 | |
| 12809 | 43177 | A | 12887 | 174 | 350 | VSWRFVQVFI*VAGGSRICAAA GLSPGTPPPCATSLIGACSLIFIP RLLSLFCGDEAL |
| 12810 | 43178 | A | 12888 | 3 | 265 | |
| 12811 | 43179 | A | 12889 | 1 | 1209 | |
| 12812 | 43180 | A | 12890 | 53 | 369 | VAHQEKGIAEPGLRPTGDSRQT HRRLDVERSTSVQEHMGGCHF SPFPEREKLSLIRGIHQAPAL WQATDQWIDIEF/GLGQPEESL GR*ITRLQGKTLIPFGSPIC |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12813 | 43181 | A | 12891 | 1 | 345 | |
| 12814 | 43182 | A | 12892 | 2 | 451 | |
| 12815 | 43183 | A | 12893 | 2 | 286 | |
| 12816 | 43184 | A | 12894 | 217 | 1071 | GENPRSENTRLATILEVACCHF GSSPPPS\GSSGRKDPPLTFGDH EGTSKAEPSPALGLTPEHKGNV GHAARIQQPGPLSLWSRKAGK GVQDCYIDLKQIKIDLDKFSDN PDGYIDVLQGLGQSFDLTWRNI MLLLNQTLTPNERSATITAARE FGDLWYLSQVNDRIAAEKREK FLTGGQAVPSVGSWDTSEH GDWCCRHLITCMLEGLRKTRK KPMNYSMMSTITQGKEENPTA FLERLREALRKHTSLSLDSIEGQ LILKDTFITQSAADIRK\NFKSPP |
| 12817 | 43185 | A | 12895 | 1 | 756 | |
| 12818 | 43186 | A | 12896 | 473 | 1015 | |
| 12819 | 43187 | C | 12897 | 152 | 322 | |
| 12820 | 43188 | A | 12898 | 146 | 1079 | PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHNRAA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPSLPLCSGVS PRAGLGSAPKIPFLGIREAKN PRSENTRLATILEAGHRHLGTS VSKDHPVTFWRPRRDLQSDLK QIKIDLGKFSDNPDGYIDVLQEL GQSFDLTWRDIMLLLNQTLTPN ERSATITAAREFGDLWYISQVV AAVAGLVSEAVKIIQGSYCVDI HDVNGILTAKGDLWLSDNHLL KYQALLLEGVLRRLRTCATLNP ATFLPDNEEKIEHNCQQVIAQT |
| 12821 | 43189 | A | 12899 | 189 | 1798 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12822 | 43190 | A | 12900 | 194 | 1729 | NPAAQTPFFVVKKGKRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSPCNTPTLA VQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEAEWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVLPQGFRDSLH LFGQALAQDLSQFSYLDLVLQ YMDDLVLVTHSETWCHQATQA LLNFLATCGYKVSQNAQLCS QQVKNLGLKLSKGTRALSEERI QPILAYPHPKTLKQLRGFLGITS FCRIWIPRIKAVKLQIILQMEPQ MQSMTKIYHGPLDRPTSPSSNV NDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYLTVWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKP\IN*SMISTI TQGKEENPTAFLERLREALRKH |
| 12823 | 43191 | A | 12901 | 1 | 642 | |
| 12824 | 43192 | C | 12902 | 54 | 254 | |
| 12825 | 43193 | A | 12903 | 32 | 221 | NGVGHNRMGTNGSGGGEWGP PAPASA*GCSLASAFASAPRW WFEMGCRGIYDAQQVALSRSF |
| 12826 | 43194 | A | 12904 | 203 | 538 | |
| 12827 | 43195 | B | 12905 | 131 | 536 | |
| 12828 | 43196 | A | 12906 | 1 | 1251 | |
| 12829 | 43197 | A | 12907 | 38 | 475 | ESERRGEFCLCKIISEQGRAVCV EDEQTSHFALTGNNGIYRKSQQ QWQQELSDLARDPPAQCSAGP VGDDMFHWQATIMGPNDSPYQ GGVFFLTIHFPTDYPFKPPK VAF VTTRIYHPNINSNG\SI CDILRSQ WSPAFNQFPKSS |
| 12830 | 43198 | A | 12908 | 282 | 849 | QSCPAAGIIKSFGRTFEHTPREV RKPDDKHTLLALKRINKDLSDL ARDPPAQCS\AGPV\GDDMFHW QATIMG\PNDSPYQGGVFFLTIH FPTDYPFKPP*GLHFTTRFY\HP WINSKWAAFCLRYS*DSQW\SP ALTFSKVLLS\CSLL\CDPNP\DI DPLVPGDWHGSY*NRTGDKYN RISREWTQKYAM |
| 12831 | 43199 | A | 12909 | 1 | 397 | |
| 12832 | 43200 | A | 12910 | 245 | 535 | |
| 12833 | 43201 | B | 12911 | 68 | 333 | |
| 12834 | 43202 | A | 12912 | 265 | 562 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12835 | 43203 | A | 12913 | 1 | 872 | MVNTECQLDWIEGCKVLILGVS KEASQGLGGRSRGRNVRQSTD ADIRPTSEKDARSLMTRQEDN ISVDQRGFLSGVQKKGSCANGL KGSVCGGFYWMAVIRMGVG KAMGLNLKLGKFEIKKGYLKG CRDSLRLSPTGFGKFTATSHEV AATVPIKVVLELTQTHKILRG VFAHLTSCQLHSLPPGSSMDS AKARRQLQVAGQGHSLVKQK GFHVEAPDHPVQLSDISCKSY RWGHKLIKINFLIPPLWYYDL EEVKREQSEEKQQA KIMADIIG DALNAQKAFKGNPKGHKPLPF SAGQMENW*CPECPSI |
| 12836 | 43204 | A | 12914 | 7 | 231 | |
| 12837 | 43205 | A | 12915 | 1 | 223 | MEILTTCDKGLIFTGNTRKSETS TSECTCPLDINCSLHSPSPSDE ETQHHTDSLHVRPRKGYLLCIY HIPDIVAVMVNIQCQLDWIEGC KVLFLGVSVKVLPEINTGISGL GKADPPSIWKS*QHVT KDLYLQ VILENQKLVPANALVRWILTVP FPTLLRALQMRKHSTTLTVCMS DRGKDIYCASTIYQI |
| 12838 | 43206 | A | 12916 | 1083 | 1273 | NKMSFKLKEDCFGRSKCNL*T* CWKSINEA*K/DLELQLQFGPQE KLFALEQQVKKLNLVPDA |
| 12839 | 43207 | C | 12917 | 1 | 1506 | |
| 12840 | 43208 | A | 12918 | 3 | 1219 | |
| 12841 | 43209 | A | 12919 | 1 | 735 | |
| 12842 | 43210 | A | 12920 | 2 | 94 | |
| 12843 | 43211 | A | 12921 | 362 | 460 | WLILSVNLIGLKDAKYCSCVCL *GCCQRRLTF |
| 12844 | 43212 | A | 12922 | 1235 | 1474 | |
| 12845 | 43213 | A | 12923 | 1 | 250 | |
| 12846 | 43214 | A | 12924 | 1 | 261 | |
| 12847 | 43215 | A | 12925 | 2 | 85 | |
| 12848 | 43216 | A | 12926 | 1 | 291 | |
| 12849 | 43217 | A | 12927 | 1 | 321 | |
| 12850 | 43218 | A | 12928 | 1 | 370 | |
| 12851 | 43219 | A | 12929 | 1 | 684 | |
| 12852 | 43220 | C | 12930 | 1 | 210 | |
| 12853 | 43221 | A | 12931 | 2 | 91 | |
| 12854 | 43222 | A | 12932 | 1 | 243 | |
| 12855 | 43223 | A | 12933 | 2 | 353 | WMKLETHLSKLS*GQKTKHRM SSLIGSTDQQRLVVKNVQGRVC PGSTGHGAWEAWTAMRKVDS PLQTGSLRPGWCRQVGSHARS GSAEAAGNPGLHPGICPRVEDG IQVAENFPEV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12856 | 43224 | C | 12934 | 1 | 289 | |
| 12857 | 43225 | A | 12935 | 1 | 1194 | |
| 12858 | 43226 | A | 12936 | 140 | 237 | |
| 12859 | 43227 | A | 12937 | 1 | 292 | |
| 12860 | 43228 | A | 12938 | 2 | 178 | |
| 12861 | 43229 | B | 12939 | 1 | 1245 | |
| 12862 | 43230 | A | 12940 | 2 | 241 | |
| 12863 | 43231 | A | 12941 | 1 | 675 | |
| 12864 | 43232 | A | 12942 | 1515 | 1920 | TPTNLQEKNKQPHQKVGE GYEQTLLKRRHLCSQKTHGKNAHH HWPSEKCKSKPQ/WIPSISHQLE WQSLKSQETTGTWMKLETHLS KLLQGQKTKHHMFSLIGGNRT RRTHGHRKGNITLWGLSDSV NCASSSG |
| 12865 | 43233 | A | 12943 | 608 | 891 | |
| 12866 | 43234 | A | 12944 | 1 | 3956 | MGSCPGGFTAIFYQRYKEELVP FLLKLFQSIEKQGTLPNSFYEAS IILIPKPRDITTKENFRPISLMN IDAKILNKILTNRQQHIKLIHH DQVGFIHGMQGWFNIRKSINVI QHINRTNDKKHMIISDAEKAF DKIQPFMLKTLNKLGTWMKL ETILSKRSQGQKTKHRMFSLIV NIPTIKILIKQNMETLCPIF KLEGDTMDNPIANRRVRTAVP TSVVCLHVGTEPEARLPHGPMI TAQSPFG |
| 12867 | 43235 | A | 12945 | 1 | 855 | |
| 12868 | 43236 | A | 12946 | 1 | 255 | |
| 12869 | 43237 | A | 12947 | 273 | 3484 | |
| 12870 | 43238 | A | 12948 | 3 | 377 | |
| 12871 | 43239 | A | 12949 | 85 | 333 | |
| 12872 | 43240 | A | 12952 | 22 | 308 | |
| 12873 | 43241 | B | 12953 | 30 | 383 | |
| 12874 | 43242 | A | 12954 | 3 | 448 | |
| 12875 | 43243 | A | 12955 | 1 | 453 | |
| 12876 | 43244 | A | 12956 | 3 | 491 | |
| 12877 | 43245 | A | 12957 | 2 | 749 | |
| 12878 | 43246 | A | 12958 | 155 | 637 | |
| 12879 | 43247 | A | 12959 | 1 | 510 | |
| 12880 | 43248 | A | 12960 | 2 | 559 | RPHASAHASGRQRSQDVTTMV WALLLLTLLTQGTGWSAQSA LQTQPPSASGSPGQSITISCTGLIND VASYNFVSWYQQHPGKAPKL MIYEVTKRPSG\VPDRFSGSKSG \NTASLDHLWGSRLDEADYYC LLICRRLHPGGGIRRWDPRTV LGSAGRPTPTVTSGSRPSSEGAP SQQGHTSVSDQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12881 | 43249 | A | 12961 | 1 | 1958 | MSVQRKDRVRTQQGGSVASSM LTQEPVGSVALGQSARDRDPD CSDSVSVYLMDTWQSVHGF SAATLGDPPELPMHPEGSEASY ELTQPPSVSVSPGQTARITCSGD ALPKQYAYWYQQKPGQAPVL VIYKDSERPSGIPERFSGSSSGTT VTLTISGVQAEDEADYYCQSAD SSGTYPTVTQADRETPTHQYSR HPSYAKGFVFLWGSWAQSALT QPASVSGSPGQSITISCTGTSSD VGSYNLVSQYQKPGKAPKL MIYE/VDSKRPSGVSNRFGSKS GNTASLTISGVPLRDEGADYY CCSYAGSVASYELTQLPSVSVS PGQTARITCSGDVLGENYADW YQKPGQAPELVIYEDSERYPG IPERFSGTSGNTTTLTISRVLTE DEADYYCLSGDEDNPSVTQAD GEDTGIRSHYEGTLALYLYPEP VKATCSVTSYVLTQPPSVSVAP GQTARITCGGNNIGSKSVHWY QQKPGQAPVLVYDDSDRPSGI PERFSGSNSGNTATLTISRVEAG DEADYYCQSLSTLGPCTLGDTV LRPMIYSVSIQASGVDPDGFSGSK SGNTASMTISGFQAEDEADYYC NSHRRGSVVSELTDPAVSVA LGQTVRITCQGDLSRSYYASW YQHPGKAPKLIYDGH |
| 12882 | 43250 | A | 12962 | 2 | 367 | |
| 12883 | 43251 | A | 12963 | 2 | 376 | QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW |
| 12884 | 43252 | A | 12964 | 2 | 1178 | |
| 12885 | 43253 | A | 12965 | 1 | 732 | |
| 12886 | 43254 | B | 12966 | 99 | 716 | |
| 12887 | 43255 | A | 12967 | 1 | 1011 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 12888 | 43256 | A | 12968 | 3 | 1263 | GRTIQTKGKEV\ENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERSAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTQPORYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRILFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSGPGGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQEIQRTQPOR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK |
| 12889 | 43257 | A | 12969 | 1 | 1392 | |
| 12890 | 43258 | A | 12970 | 1 | 1224 | |
| 12891 | 43259 | A | 12971 | 1 | 970 | |
| 12892 | 43260 | A | 12972 | 1 | 954 | MDGDLHKGVAVFWPPDAAGG HTCCRSMVCRSLGGAQWKFH SFRCRIRFELILHMIQERNISINIS QKDVHTETPSETHHHQRPKVD KSMKMRRNQCKKAENSKNQK ASSPPKEHNSWRAREQNWTEN EFDKLTEVGFRRWVITNSSELK EHILTQCKEAKNLEKTLEELLT RITSLEKNINDLMKLKNTA*EL REAYTSINSQISQAEERISEIEDQ LNEMKHEHRIREKRMKRNKQS FQEIWDYVKRPNLRLISVPESD GENGNK*ENILQDIIQENFPNL ARQANIQIQEIQRTQPORYSSRA TPRHIIVRFTKV |
| 12893 | 43261 | B | 12973 | 1 | 1346 | |
| 12894 | 43262 | A | 12974 | 1 | 318 | GSRGELLLSLCYNPSANSIIVNII KARNLKAMDIGGTSDPYVKVW LMYKDKRVEKKKTVTMKNRL NPNFNES\FAFDIPTEK\LRETTII ITVMDKDKLSRNDVIGK |
| 12895 | 43263 | A | 12975 | 17 | 389 | SWGPHCTHKLKKSFSLMPMET DAMDREMR/RGSKKDV/R*VLG GCAATWTPRAGGRQQSPGTTV DKREDTPDCAMCDQSTSHIPISA SSPSLLPGSSFTTQTFFPGIAHYR ASFLIVAYYPSNKNKSK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12896 | 43264 | A | 12976 | 84 | 282 | GEGQVGWPQGEVQQDEEVIEE VGA*DAAGSYQEEEGPQSLRR EVVGVELVVGADPSGEGPKED |
| 12897 | 43265 | A | 12977 | 1 | 1179 | |
| 12898 | 43266 | A | 12978 | 3 | 634 | |
| 12899 | 43267 | A | 12979 | 234 | 619 | CYVVQEVLPSSLCHCLVICSRP GRTAEWPPG*GF*SPPHRGWW GC*GHD/HRRGTSIFPTH/V*SPP ASYPGSLCRPGGQEEREREGEW QREGRRPGTR*CGAEAEARGW RAAAKATAVAGARNRRPGISG |
| 12900 | 43268 | A | 12980 | 1 | 1182 | |
| 12901 | 43269 | A | 12981 | 3 | 763 | |
| 12902 | 43270 | A | 12982 | 32 | 949 | |
| 12903 | 43271 | A | 12983 | 1 | 1299 | |
| 12904 | 43272 | A | 12984 | 1 | 1176 | |
| 12905 | 43273 | A | 12985 | 1 | 421 | |
| 12906 | 43274 | A | 12986 | 81 | 404 | VKFGPEIWCRRSDQGRGGVGT SLGRSIPCPALCSVRKIYLRPL VLRPTSPRNISPILNRDPTVQLT WQPLPEPELELWPKAL*LTPSQIY SA*RLKTDAAARLPKPPR |
| 12907 | 43275 | A | 12987 | 1 | 378 | |
| 12908 | 43276 | C | 12988 | 1 | 751 | |
| 12909 | 43277 | A | 12989 | 302 | 629 | ICLSYPAPPCKRFPHYTRVLYH* SLFNENTSQSCFTSR/WKLESFT TRAIERHQIPLL*ATLTLIRWLD KKLAFQLLSLTASFSPSYQSLPP TPPLKLPIISSHTRQMV |
| 12910 | 43278 | A | 12990 | 14 | 380 | |
| 12911 | 43279 | A | 12991 | 189 | 608 | QSDLSASQHGLFPLATEVRSSG AASCPDSDSICPAPTAPGRATP PQANCWASEGTLRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLFSNLQGP RSRPVAFLSKQLDLTVLGWPSC L\VQQLPP |
| 12912 | 43280 | A | 12992 | 1 | 513 | |
| 12913 | 43281 | A | 12993 | 2 | 462 | WSMGLPRRSGCVSLQPLSQEDL GRSQESLGPEFQGLWEWLPEQ LPRSFIALGSLSYFPRTLMNLS WPLCLRKGWYL/SLYLPFQVGL PSTVPWPLILPSKVPEEEGQLQS TLPCGIKLLPVFTSHHAF LGVFC NQWVSDVFLALFLMKLLGAQ |
| 12914 | 43282 | A | 12994 | 59 | 213 | |
| 12915 | 43283 | A | 12995 | 1 | 1159 | |
| 12916 | 43284 | C | 12996 | 1 | 864 | |
| 12917 | 43285 | A | 12997 | 1 | 1155 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12918 | 43286 | A | 12998 | 879 | 1163 | SRRLPLFMGLVRVLCKMSGGRP LCFPGGHWIVFLWGGTVLWLW T*SPHWHRKAN*DLFLQKLPRL *VSHQCDPLPVCHLWNCFLFL PLWGPPAG |
| 12919 | 43287 | A | 12999 | 1 | 179 | |
| 12920 | 43288 | C | 13000 | 1 | 410 | |
| 12921 | 43289 | A | 13001 | 42 | 365 | FGLRLSLAPPFCMFPLTT*HS*P SVLPASFPAALGIPQARAVTPFV SP*LLASLSFWAPPCSLCLDASV *HGSHLWHAQSSCRLRWSFGL AASQMQPEEP SHGPRRK |
| 12922 | 43290 | B | 13002 | 1 | 741 | |
| 12923 | 43291 | A | 13003 | 8 | 265 | |
| 12924 | 43292 | B | 13004 | 1 | 646 | |
| 12925 | 43293 | A | 13005 | 1 | 1158 | MKLVTIFLLVTISLCSYSGYWPE NEQMSVGGGDDNGEVLYSALR GASEVIGQCQSSATKPRRSGKE SVREPWARVPGALGVGVREID QTLGIDTILCHHHERLLQSHYGI HKSSLMSVGN SQVAALYQLNV YVVADTVGLI KSNSILDSVQPN YCSNKHIELRTQVGGARNLRA NSPMTSSYNQESSMENV SALS LLTVESPTSMFDYCDDSL ERVK SALDIFSMI IYTVTFFLGLAGNG LVIWVVG FHM SCTVNTCLPSDP HLHGPLTCDPVANLVLEQLHTS KGNSGALEDLAFGNLFLCSLLD LQGN S W W K V S P S L Y N Q Y D L Q NETQGSHQLWKEIIPW*PSAFV V/SSGYWPENEQMSVGGGDDN GEV/RVFRPEGGFRGDRAVSF SH*AEKIWEGISQRAL/VPEFQG LWEWV/CREIDQTLGIDTILCHH HERLLQSHYGIHKSSLMSVGN S QVAALYQLNVYVVADTVGLI KSN S I L D S V Q P N Y C S N K H I E L R T QVGGARNLRANS P M T S S Y N Q E SSSMENV S A L S L L T V E S P T S M F DYCDDSL ERV K S A L D I F S M I I Y T VTFFLGLAGNGLVIWVVG F H M SCTVNTCLPSDPHLHGPLTCDP VANLVLEQLHTSKGNSGALED LAFGNLFLCSLLDLQGN S W W K V S P S L Y N Q Y D L Q N E T Q G S H Q L WKEIIPWHQTLVTTAHFFFGFF |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12926 | 43294 | A | 13006 | 3 | 371 | AGARFNVRSR*RNDRVRPHRD VYSLQGR LSDHSPTFGGCQTQ GRLPWSFTLSGKFRFSGEGATT SPAHKNFQTPEPQWP GIPPEPPP TGACYTCRKSGHWAKECPQAR IPPKPHPICV GPH |
| 12927 | 43295 | A | 13007 | 77 | 332 | RWKKNCLSPPRMS*QR*WKP* MQQAACSVGETQPPCTQVK*T ALLLTQSLFGGLFTRTHMKFGA VTRIGGPPLGDQSPVLLLFAP |
| 12928 | 43296 | A | 13008 | 1048 | 1349 | RVVEQDDAERLFRFRFAA/GDL PYGAFGEIF*ETQCQEMQQLAE DHASVTMISLEAWRLYRK MVC RIWASMLRLSVCHLCAPKR VV SLISRNGYHLP GSIH |
| 12929 | 43297 | A | 13009 | 213 | 499 | PEQRTSHRQQRRQPP PQSRS*P FCPSLPRSALSFLCDGYAAP* AYRE*IPVTEDHFAE*/ISWCPC *YREALGQLLAKMRR*SARKRF QLSP |
| 12930 | 43298 | A | 13010 | 2 | 431 | |
| 12931 | 43299 | A | 13011 | 2 | 367 | |
| 12932 | 43300 | B | 13012 | 1107 | 2083 | |
| 12933 | 43301 | B | 13013 | 1 | 627 | |
| 12934 | 43302 | A | 13014 | 712 | 2671 | AHVGRGST*ALPRAMGSDAF*C PLQ*MTPASFGSKAALS RVFIKE ALMMEDPCVVRKPLSAHMTA WWCRIWKAYLESV |
| 12935 | 43303 | A | 13015 | 50 | 1362 | WEQIPHGLVLSLQQLPRRSGSIS LQPLSQEDLGRSQSESLGPEFQ GLWQWLSDFQT*HQW FVSGFQ AFSDRLKAALSASLLRFGDSD WLPSSSACKCLMLGLHFVIVGN ICATLKEYSSMLHLDVTM KK NGEKRTLQKRKKGMPPHPAY EDLNIAAITLPANVVLHQPSGFR TSGQLDPVWWSLDTDAHEIWC QDPGLGSGDFPWEITPLSSYSLL HEKDPPTTSGPQTDQPKKHLTN FKSKTKETGFIHGPKTPAPVTD WEGSLPLVFNHCRDTS LIHPCF KGVRRRDACLGPSPLAASPAF LEKGQDLINLAFKVYNNRKKL QFLASTVRQTPATSPA HKNFQT TEPQQPGVPPEPPPTGACYMCR KIWPLGQANARSPGFLLSRVPS VWDPTGNRTVQLTWQPLPEPL ELWPKALCLTDSFPDLLGLAA |
| 12936 | 43304 | A | 13016 | 1 | 507 | |
| 12937 | 43305 | A | 13017 | 5 | 271 | |
| 12938 | 43306 | A | 13018 | 1 | 618 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12939 | 43307 | A | 13019 | 1 | 429 | |
| 12940 | 43308 | A | 13020 | 1 | 3567 | |
| 12941 | 43309 | A | 13021 | 1 | 353 | |
| 12942 | 43310 | A | 13022 | 1 | 338 | |
| 12943 | 43311 | A | 13023 | 1 | 1175 | |
| 12944 | 43312 | A | 13024 | 3 | 326 | |
| 12945 | 43313 | A | 13025 | 150 | 494 | PSPSLGYLVGTRGTALRL*DAR AAMRPFDPSTLLPTCWDYWTY AGSLTPPLTESVTWIIQKEPVE VAPSQLSAFRTLLFSALGEEEEK MMVNNYRPLQPLMNRKVWAS FQATNEG |
| 12946 | 43314 | A | 13026 | 2 | 975 | DSREHHPLQTGVSGNRPKMLG RNTWKTSAFSFLVEQMWAFLW SRSMRPGRWCSQRSCAWQTSN NTLHPLWTVPSVPGGTRQSPI NIQWRDSVYDPQLKPLRVSYE AASCLYIWNLTGYLFQVEFDDA TEASGISGGPLENHRYLKQFHF HWGAVNEGGEHTVDGHAYP AELHLVHWNSVKYQNYKEAV VGENGLAVIGVFLKLGAAHHQT LQRLVDILPEIKHK\DARAAMR PFDPSTLLPTCWDYWTYAGSLT TPPLTESVTWIIQKEPVEVAPSQ LSAFRTLLFSALGEEEEKMMVN NYRPLQPLMNRKVWASFQATN |
| 12947 | 43315 | A | 13027 | 1 | 1233 | |
| 12948 | 43316 | A | 13028 | 761 | 1000 | IPFISFSCIALARTSNTMLNKG ERGHPSLVVPVFIGNASSFCPVSM ILAVGLS*IALIILRYVPSIPNLLR VFSMKGC |
| 12949 | 43317 | B | 13029 | 697 | 1527 | |
| 12950 | 43318 | A | 13030 | 1 | 1695 | |
| 12951 | 43319 | A | 13031 | 434 | 925 | VAKIFSHFVCCFLFTLMVVSFAV QKLFSLIRSHLSILSFVAIDFGVL DMKSLPMPMS*MVMPRFSSRV FIVLGLTFKSLIHLELIFV*GVRK GSSFSFLHMASQFSQHLLNRE SFPHCLFFSGFSKIR*L*ICGIISE GSVMFH*SISLFWYQYHAVLVT VAL |
| 12952 | 43320 | A | 13032 | 1124 | 1234 | KITPKKQIRQSPNLTQNTGQQ*S LQLWEHFQISTHF |
| 12953 | 43321 | A | 13033 | 929 | 1261 | |
| 12954 | 43322 | A | 13034 | 1118 | 1354 | IPFISSCLIALARTSNTMLNRSGE RGHPCLVPVFKGNASSFFPFSMI LAVGLS*IALIILRYIPSIPSLLRV FSVKGC |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12955 | 43323 | A | 13035 | 2 | 348 | HQHLLFPDFLMIAILTGMRWYL IVVLCISLRASDDEHF/YHVS GCINVFF*EISVHILRPLFDGVV* FFLVNLFKFFVDSGYEPFVRWV DCKNVLPFCRLPVHSDGSFFCC AEAL |
| 12956 | 43324 | A | 13036 | 578 | 712 | LISNFSKVSQYKINVPKSQAFLY TKNRQTAKS*VNSHSQLLQRE |
| 12957 | 43325 | A | 13037 | 1 | 1833 | |
| 12958 | 43326 | B | 13038 | 1 | 1587 | |
| 12959 | 43327 | B | 13039 | 1 | 1851 | |
| 12960 | 43328 | A | 13040 | 1349 | 1444 | |
| 12961 | 43329 | A | 13041 | 953 | 1277 | MVLPRFSSRVFMVLGLTFKPLI HLELIFV*GVNFV*GSSFSFPHM ASQFSQHLLNRESFPHFLFLSG LSKIR*L*MCGIIEGSLVLFHWS ESLFWYQYHAVLVTVL |
| 12962 | 43330 | B | 13042 | 804 | 4236 | |
| 12963 | 43331 | A | 13043 | 1 | 744 | |
| 12964 | 43332 | A | 13044 | 137 | 797 | |
| 12965 | 43333 | A | 13045 | 210 | 418 | |
| 12966 | 43334 | A | 13046 | 1 | 927 | |
| 12967 | 43335 | A | 13047 | 1 | 1415 | MGFLGTGTWILVLVLP IQAFPK PGGSQDKSLHNRELSAERPLNE QIAEAEEDKIKKTPPENKPGQ SNYSFVDNLNLLRAITEKEKIEK ERQSIRSSPLDNKLNVEDVDST KNRKLIDDYDSTKSGLDHFQ DDPDGLHQLDGTPLTAEDIVHK IAARIYEENDRAVFDKIVSKLLN LGLITESQAHTLEDEVAEVLQK LISKEANNYEEDPNKPTSWTEN QAGKIKEKVTMAAIQDGLAK GENDETVSNTLTLTNGLERRTK TYSEDNFRDFQYFPNFYALLKSI DSEKEAKEKETLITIMKTLDIV KMMVKYGTISP EEGVSYLEGL DEMIALQTKNKLEKNATDNIS KLPAPSEKSHEETDSTKEEAA KMEKEYGSLKDSTKDDNSNPG GKTDEPKGKNRSPWKPIRKNI EWLKKHDKKGNKEDYDPFQR* EVSFNNKADAIYVEKGILDKEE AEAIRIYSSL |
| 12968 | 43336 | A | 13048 | 1 | 879 | |
| 12969 | 43337 | A | 13049 | 3 | 640 | |
| 12970 | 43338 | A | 13050 | 134 | 382 | DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPWMN/WPPH*IKHIQS |
| 12971 | 43339 | A | 13051 | 87 | 500 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12972 | 43340 | A | 13052 | 1 | 1356 | |
| 12973 | 43341 | A | 13053 | 1 | 447 | |
| 12974 | 43342 | A | 13054 | 3 | 107 | |
| 12975 | 43343 | A | 13055 | 3 | 2377 | |
| 12976 | 43344 | A | 13056 | 1 | 2193 | |
| 12977 | 43345 | A | 13057 | 1 | 2724 | |
| 12978 | 43346 | A | 13058 | 253 | 490 | QSSIPAIMSSFLGTGAETMPVPL GAGMRRTSTEPQRVCFTGIIF KTSSLREAPRKKS MISDSL MGR E/WMPVTKLGRLVKDMKIKSLE EIYLFSLPIKSEIIDFFLGASLKD EVLKIMPVQKQTRCGSVLVRLI PAPRGTGIVSAPVPKLLMMA GIDDCYTSARGCTATLGNF/AK ATFDAISK TYSYLPDLWKETV FTKSPYQEFTDHLVKTHTRVSV QRTQAPAVATT |
| 12979 | 43347 | A | 13059 | 1 | 819 | |
| 12980 | 43348 | A | 13060 | 1 | 623 | MARRKNGKWESEIIDFCLGGSL KDEV LKIMPVQKQTRAGQCTR FKA FVAIGDYNHIGLGIKCSK E/LATAIRRAILAKLSIVPVCRG YWG NKISKPHIVPCRG TGIVSA PVS KLLMMASINDCYTSARG CTAILGNFDKATFDAISK TYSYL TPNLWKETVFTKSPYQEFTDHL VKTYTRVSMQSTQAPALAKLP RVAVQPRAEV |
| 12981 | 43349 | A | 13061 | 1 | 949 | KWRITPVPTGRP/GGPGGPGMG KPRCF/RGEVFGIVIRAGSPGPG TGPGRG\GEAAGAKAED*EWM PV\TKLGRLVKDMKIKSLEEIYL FSLAIKKSEIMS FLLGGLSRDE VFE*LCPVQEQ\TRAGQ/RATRF KAFVALTTLGTTNG\HVGLGC* VPPREVATGNSWGP FILGQALH SSPVRRGLLGGTKNSAKPPTLV PWQR*PRAACGLCAGYAFIPLQ PRGQLASVSA\VPV\KLLMMA GTDG\CNNSQRRGCTATVGNL AKATTFDAISK TYSYLPDLWK ETVFTKSPYQEFTDHLVKTHTR VSVQRTQAPAGATT |
| 12982 | 43350 | A | 13062 | 92 | 265 | SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIADCGQLE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 12983 | 43351 | A | 13063 | 2 | 797 | NRVLLAMVNPTVFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIG\LFADKVPKTAENFR/A L*SIEEKGFGL*GVPCFHRLFPR VLCVRGGDFHTAINGTGGKSI YGEK\FEDENFILKHTGPGILSH GKMLDPNTNGSQFFICTAKTÆ WLDGKHVVFGKVKEGMNIVE AMEA\FGSRDCKTSKKITIA\DF GQLRIKFDFVFLSLTTKIISFCAL LSGEHPLHPIWLGVILESMWLS LAVPFWVPCFPCSLPCLAGLQS |
| 12984 | 43352 | A | 13064 | 1 | 720 | |
| 12985 | 43353 | B | 13065 | 98 | 2074 | |
| 12986 | 43354 | A | 13066 | 596 | 841 | |
| 12987 | 43355 | A | 13067 | 66 | 326 | |
| 12988 | 43356 | A | 13068 | 1 | 441 | |
| 12989 | 43357 | A | 13069 | 2 | 325 | WCPSQAAAAGARATRDMPGGS MTCLCRALWWLFSWLKVHR*R QGQQGRPAAPSAGPAKPTPTRN SSWLLLAAPVPTRTSPSTPPCKL REPAPALASPERGSHSAAVG |
| 12990 | 43358 | A | 13070 | 38 | 1066 | |
| 12991 | 43359 | B | 13071 | 1 | 324 | |
| 12992 | 43360 | A | 13072 | 2 | 680 | |
| 12993 | 43361 | A | 13073 | 2 | 165 | |
| 12994 | 43362 | A | 13074 | 1 | 1110 | MASLLKSARPQTHWKEETPETS KRLKEQTPDIPSLRAVTLIAKVH SFIPEVCETKNPLEGIHSGHILAP NVGPSPSRRQARVQVFENVSVR ATKSDLPQSSLWSRRKTTVSAA ASKKTSKEISKGPQKPPGY/PVT SPSSCRGRGIWPNP/EYMSTSPS LI*/SIKVDLGKISDDPDYIDV LQGLGQTLDSLWRDVMLLLDQ TLAFNEKNAALAAAEFGDTW YLSEVNDRMATAERDKFPTED GEPIKDCQQIIVQTYAAQDDIL EVPLANPDLNLYTDGSSFVENG IRRAGYAIVSDVTILERPNIIFRA IQQVVKACEVCQRKNPLVHPP NYLYKTLNLTHSLNQSNSPLA NDCWLCSSLSVSAEPYN |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 12995 | 43363 | A | 13075 | 450 | 1776 | RGGRACLRP*AA/SPGPSTP*WP PPRGVQAAAILSGPPRPAPPKG AASQRLCGGFVEARQAWVGRR GGRRGVPVGETQPPPSVIQPPSRG AG/PRDQQPAMPEPPTPSVGSC AARASQISAAPCSTAPSPIDHPR AEECRRTVWDWQAAPPAAQV RDPLGEASWAPESGGDVENLY VLLRDCKYTSQHPVSSSGSVNA PIDTLYLATLLRDCKYTNRHSV SSSRFVNTPISTVSSEFANAPID TLHLATLKEETPNTSEHQKEQT PDMPPLRRTVTVTARVRGFILDV SETKNPPIPDTFWRPRWDLRQS PSNQTLAFNEKNAALAAAEF GDTWYLSQVNDRMTAEERDKF PTEFIPSSGFLVLLTSRMKPQTF AASVTALKDGVSRVCSFRCVQS FFLPSADWCYKPLARYRALIG AFLQSAHWCYKPLARHSVLI GAFTNL |
| 12996 | 43364 | B | 13076 | 1 | 1999 | |
| 12997 | 43365 | A | 13077 | 3 | 469 | |
| 12998 | 43366 | A | 13078 | 224 | 410 | |
| 12999 | 43367 | A | 13079 | 478 | 675 | |
| 13000 | 43368 | C | 13080 | 55 | 237 | |
| 13001 | 43369 | A | 13081 | 109 | 239 | |
| 13002 | 43370 | A | 13082 | 2 | 88 | |
| 13003 | 43371 | A | 13083 | 2 | 178 | |
| 13004 | 43372 | C | 13084 | 278 | 460 | |
| 13005 | 43373 | C | 13085 | 50 | 217 | |
| 13006 | 43374 | A | 13086 | 3 | 251 | |
| 13007 | 43375 | A | 13087 | 1 | 759 | |
| 13008 | 43376 | A | 13088 | 2 | 604 | |
| 13009 | 43377 | A | 13089 | 1 | 558 | |
| 13010 | 43378 | A | 13090 | 3 | 1055 | |
| 13011 | 43379 | A | 13091 | 1 | 466 | MDKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAIFYQRLISNFSKVSQYRIN VQES/QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRNIVKMAILPK |
| 13012 | 43380 | A | 13092 | 2 | 848 | |
| 13013 | 43381 | A | 13093 | 458 | 625 | |
| 13014 | 43382 | A | 13094 | 482 | 745 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13015 | 43383 | A | 13095 | 1 | 742 | MNIDAKILNKILANRIQQHIKKL IHHDQVGFIQPMQGWFNIRKSI NVIWHINRTKDKNHMIIISIDAE KVFDKIQQPFMLKTLNKLIGDG TYLKILRAIYDKPTANIILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEKEIKGIQLGKE EVKPSLFADDVIVYLENPIISVQ NLLKLISNFSKIKYLGILTRNV KYLFKENYKSLLEIKEDTNK WKNIPCSWIGRINIVKMAILPK |
| 13016 | 43384 | A | 13096 | 1 | 1458 | |
| 13017 | 43385 | A | 13097 | 2 | 1624 | |
| 13018 | 43386 | A | 13098 | 1 | 1095 | |
| 13019 | 43387 | A | 13099 | 1 | 2913 | |
| 13020 | 43388 | A | 13100 | 2 | 1887 | |
| 13021 | 43389 | A | 13101 | 1 | 972 | |
| 13022 | 43390 | A | 13102 | 1 | 873 | |
| 13023 | 43391 | A | 13103 | 1 | 1365 | |
| 13024 | 43392 | A | 13104 | 1 | 867 | |
| 13025 | 43393 | A | 13105 | 1 | 591 | |
| 13026 | 43394 | A | 13106 | 1 | 990 | |
| 13027 | 43395 | A | 13107 | 1 | 2109 | |
| 13028 | 43396 | A | 13108 | 1 | 843 | |
| 13029 | 43397 | A | 13109 | 1 | 1203 | |
| 13030 | 43398 | B | 13110 | 1 | 1221 | |
| 13031 | 43399 | A | 13111 | 1 | 1092 | |
| 13032 | 43400 | A | 13112 | 1 | 931 | |
| 13033 | 43401 | A | 13113 | 1 | 1293 | |
| 13034 | 43402 | A | 13114 | 1 | 544 | |
| 13035 | 43403 | A | 13115 | 3 | 718 | |
| 13036 | 43404 | A | 13116 | 693 | 1397 | ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWNI PCSWIGRINIVKMAILPKVIYRF SAPIKLPMTFFTELEKKNWLAI CRKLKLDFFIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATKAKRA SAQQKKLPSE |
| 13037 | 43405 | A | 13117 | 1 | 2814 | |
| 13038 | 43406 | A | 13118 | 1 | 1302 | |
| 13039 | 43407 | A | 13119 | 1 | 1542 | |
| 13040 | 43408 | A | 13120 | 3 | 1327 | |
| 13041 | 43409 | A | 13121 | 1 | 1023 | |
| 13042 | 43410 | A | 13122 | 1 | 1448 | |
| 13043 | 43411 | A | 13123 | 1 | 1038 | |
| 13044 | 43412 | A | 13124 | 3 | 1711 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13045 | 43413 | B | 13125 | 1 | 1756 | |
| 13046 | 43414 | A | 13126 | 1 | 923 | |
| 13047 | 43415 | B | 13127 | 1 | 1515 | |
| 13048 | 43416 | B | 13128 | 1 | 1560 | |
| 13049 | 43417 | A | 13129 | 1 | 4032 | |
| 13050 | 43418 | A | 13130 | 1 | 2684 | MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLS DHS AIKLELRIKNLTQSRSTPWKLN NLLLNDYWVHNEMKAEIKMFF ETNKNKDTTYQNLWDAFKAV CRGKFIALNAYKRKQERSKIDT LTSQLELEKQEQT HSKASRRQ EITKIRAELEKETQKTLQKINES RSWFFERJINKIDRPLARLIKKR EKNQIDTIKNDKG DITDPTEIQ TTIREYYKHLYANKLENLEEM DTFLD TYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPDG FTAIFYQRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEV LARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQLMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWNI PCSWVGRINIVKMAILPKVIYR FNAIPIKLPMFTFFTELEKTTLKFI WNQKRARIAKSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIIPHIYN HLIFDKPEKNKQWGKDSL FNK WCWENWLAICRRLKLD PFLTP |
| 13051 | 43419 | A | 13131 | 1 | 1149 | |
| 13052 | 43420 | A | 13132 | 127 | 329 | |
| 13053 | 43421 | A | 13133 | 1 | 1132 | |
| 13054 | 43422 | A | 13134 | 1 | 1020 | |
| 13055 | 43423 | A | 13135 | 803 | 2009 | |
| 13056 | 43424 | A | 13136 | 1 | 1944 | |
| 13057 | 43425 | A | 13137 | 1 | 1282 | |
| 13058 | 43426 | A | 13138 | 1 | 2423 | |
| 13059 | 43427 | A | 13139 | 1 | 2694 | |
| 13060 | 43428 | A | 13140 | 1 | 1195 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13061 | 43429 | A | 13141 | 6082 | 6984 | KLAQDRDALSPPLLFNIVLEVL ARAIRQEKEIKGIQLGKEEVKLS LFADDMIVYLENPIV\SAPKSPL RLISNVSKV*GYKINVQKS\QA FLYTNNTDKQESQIMSELPFTT ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEVKEDTNKWKNIPCS WVGRINIMKMAILPKVNYRFI NSMPSIPIKL\PMFTFFTELEKNYF KVHMEPKKSPHCQVNPKTKEQ SWRHQRYLTSNYILQGYSNQK STISMVLVPKQHGTGKTEIIDQ WNRTEPSEITPHIYNYLIFDKPL LEKNKQWGKGFPI |
| 13062 | 43430 | A | 13142 | 193 | 335 | MVEEKLTLPKDEK*KSKQRSIY RKTQLQELKNKNEKRNRKNKW QVKTH |
| 13063 | 43431 | A | 13143 | 131 | 427 | |
| 13064 | 43432 | A | 13144 | 1 | 360 | |
| 13065 | 43433 | A | 13145 | 2 | 376 | |
| 13066 | 43434 | A | 13146 | 1 | 360 | |
| 13067 | 43435 | A | 13147 | 2 | 376 | |
| 13068 | 43436 | A | 13148 | 3 | 469 | |
| 13069 | 43437 | A | 13149 | 224 | 410 | |
| 13070 | 43438 | A | 13150 | 478 | 675 | |
| 13071 | 43439 | A | 13151 | 32 | 161 | |
| 13072 | 43440 | A | 13152 | 1 | 1671 | |
| 13073 | 43441 | A | 13153 | 1 | 1656 | |
| 13074 | 43442 | A | 13154 | 62 | 1295 | |
| 13075 | 43443 | B | 13155 | 149 | 320 | |
| 13076 | 43444 | A | 13156 | 12 | 89 | |
| 13077 | 43445 | A | 13157 | 28 | 417 | |
| 13078 | 43446 | A | 13158 | 2 | 440 | |
| 13079 | 43447 | A | 13159 | 190 | 553 | EIVREGASF\SIRHLRWSRHRKC RFSVKTLTGEDPSTLEV\EPS\DT IE\NVKAK\IQDKEGI\PPDQQRL/ VSFAGKQL\EDGRDLSGYNIQ KGSLLLHPCV*DFRGGAKKKEE ESLYTTSPRKD |
| 13080 | 43448 | A | 13160 | 3 | 415 | PVK/VGA*GGQVINGVLAQV*L TVGPGVGRTHPVVIFPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13081 | 43449 | A | 13161 | 5 | 405 | HCCGIPHSIASEQDTYFMAKEV WQWAHAHGIHWSYHVPHHLE AAGLIEQWNGLLMSQLQHQLG DNTLQGWGKVLQKVYALNQ RSIYGTVSPIARIHGSRNQGV EVALLTVTPNDPL/GKY*LPVPV TLHSDR |
| 13082 | 43450 | A | 13162 | 138 | 387 | |
| 13083 | 43451 | C | 13163 | 184 | 297 | |
| 13084 | 43452 | A | 13164 | 1 | 430 | |
| 13085 | 43453 | A | 13165 | 1 | 867 | |
| 13086 | 43454 | A | 13166 | 35 | 601 | CLSRRASPVYLASMSGRGKTG G\KARA\KAMSRSSRAGRPSQ VGR\VHRLLRKGHYAERVVGR QPCCYLGG*CMEYLT*ESWS MAG\NAARNM\KKTRIIP\RHLQ\ LA\IRNDEELNKLAWAALTIAQ GSR/VLPNIQARCCGPR*TSATV G\PKAPSGGEERATQASARSTK RARAAAGRPSVPMPPQRP |
| 13087 | 43455 | C | 13167 | 11 | 313 | |
| 13088 | 43456 | B | 13168 | 1 | 552 | |
| 13089 | 43457 | A | 13169 | 1 | 621 | |
| 13090 | 43458 | A | 13170 | 55 | 296 | |
| 13091 | 43459 | A | 13171 | 959 | 1182 | WVYLF*PSCKGVIYP*AAGFESI FWWVTINKNIDWINIYYNQ QFMNYTRDAVKGIAEQLGTNC QMAWENRIALDMILAERGGVC IMIKTECCAFIPNNTAPNGSITK ALQGLTALSNELASSGVNDPF TGWLEKWFGKWKGITASILTS TAVMGVLILVGCCVIPICGLV QRHRGPPLVVIETKPLGLERLA GLPVGHALKLGSGIQATPQNGE NADRREAFPAAS |
| 13092 | 43460 | A | 13172 | 1 | 540 | |
| 13093 | 43461 | A | 13173 | 2 | 142 | |
| 13094 | 43462 | A | 13174 | 42 | 384 | |
| 13095 | 43463 | A | 13175 | 102 | 329 | |
| 13096 | 43464 | A | 13176 | 1 | 1257 | |
| 13097 | 43465 | A | 13177 | 1 | 378 | |
| 13098 | 43466 | A | 13178 | 1 | 1143 | |
| 13099 | 43467 | A | 13179 | 1 | 481 | SDSELNRPRVTMKFNPVTSR SKNRKRHFNAPSHVRRKIMSSP LSKELRQKYNVRSMPIRKTDEV QVVRGHHYKGQQIGQGSRCTR KKYVIYIER\VQREK\ANGTNC TWGISPKARWLFTRLKLDKDR KKILERKAKSRQVGKEKGKYK EELIEKMQE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13100 | 43468 | A | 13180 | 39 | 556 | AAAGYFAEDCEASCVCVKHPP SVKKARCFLSELIKPSGGSVTL SESTAIISHGTTGLVTWDATLYL AEWAIENPAAFTNRTVLELGSG AGLTG/VAICKMYRPRAFIFSDC HSRVLEQLRGNVLLNGLSLEAD ITANLDSRVTVQAQLDWDVAT VHQLSAFQPDVVIAADVLY |
| 13101 | 43469 | A | 13181 | 46 | 231 | |
| 13102 | 43470 | A | 13182 | 1 | 1503 | |
| 13103 | 43471 | A | 13183 | 3 | 340 | FFFANTFYCVFNVLVNAPLRFL SLPSTQSLEAKLRDSSDSELRRD ILQKVRIPESLGLMTLPPELRK T*EKNRRCACTL*KITPVQRTKP LSQHCRWVWAPPTAPALSFSKT |
| 13104 | 43472 | A | 13184 | 2 | 594 | |
| 13105 | 43473 | A | 13185 | 1 | 1470 | |
| 13106 | 43474 | B | 13186 | 79 | 1355 | |
| 13107 | 43475 | A | 13187 | 248 | 540 | |
| 13108 | 43476 | A | 13188 | 386 | 1388 | |
| 13109 | 43477 | A | 13189 | 386 | 1334 | |
| 13110 | 43478 | A | 13190 | 3873 | 4070 | |
| 13111 | 43479 | A | 13191 | 146 | 510 | PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHNRAA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAWPKIPFLGIREAKN PRSENTRLTT |
| 13112 | 43480 | A | 13192 | 21 | 95 | KCSSNGAPDAVHE*DLPWTPGP AC |
| 13113 | 43481 | B | 13193 | 1 | 477 | |
| 13114 | 43482 | A | 13194 | 228 | 935 | PLSSSMAAELEFAQIIIVVVVTV MVVVIVCLLNHYKVSTRSFNR PNQSRREDGLPQIMHAPRSRD RFTAPSFQDRFSRFQPTYPYV QHEIDLPTISLSDG\EEPLYQV PCTLQLRDPEQQMELNRESVRA PPNRTIFDS\DLIDIAMYSGGPCP PSSNSGISASTCSSNGRMEGPPP TYSEVMGHHPGASFLHHQRSN AHRGSRLQFQQNNAESTIVPIK GKDRKPGNLV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13115 | 43483 | A | 13195 | 526 | 1629 | FYSFDSARGEPARPWRVRGLEG RVELGQQLGLLTLGPAFPGGGLG GTQRVGLPGPAGPGAGEEGQA GPAEAGQVPVGGGLADEAVEHG VGDAVEAGEQEGEVVGVENAL GEVAAGLPDAAHQQQHVVGQ EAGQEDDHGAEHQPLDLVLAA LLGAVAPAHGAQDALVGRQQ QADGEEEA/LPGSGSS*WHAAM PGWWSAQSTRGAGSRPR*PPRA SGSRCWSAAPWPR*PR*RRRPP SGSGTGGSGRDGPQPGSGPR/T MQQRKPTLM*MFSYRR\IRTPG RTGRRETSCRAAARTAAARRAA SRCRRGRPPSGCTGTRPARSGP* SAGSVEVEGQAVGREAHHQHG NIDHRGQRLVDGMVDGTAHRG VVCSDVPH |
| 13116 | 43484 | B | 13196 | 2699 | 7361 | |
| 13117 | 43485 | A | 13197 | 67 | 1523 | |
| 13118 | 43486 | A | 13198 | 1 | 287 | |
| 13119 | 43487 | A | 13199 | 2 | 563 | |
| 13120 | 43488 | A | 13200 | 96 | 401 | |
| 13121 | 43489 | B | 13201 | 1 | 480 | |
| 13122 | 43490 | A | 13202 | 1 | 924 | |
| 13123 | 43491 | B | 13203 | 13 | 1512 | |
| 13124 | 43492 | A | 13204 | 1 | 402 | |
| 13125 | 43493 | A | 13205 | 609 | 803 | RDPRHNPSSAFQAGGIALMLI TRGEDLTGGVIHQYPGPGMNL WMQGTAGNQRRAAENAAQQQ |
| 13126 | 43494 | A | 13206 | 3 | 526 | VTETALTPLYLVAKHGYFLPD LAKRTETMNWLFWLQGAAPFL GGGFGHFYHYAPVKIEYAINRF TMEAKRLLDVLDKQLAQHKFV AGDEYTIADMAIWPWFGNVVL GGVYDAAEFLDAGSYKHVQR WAKEVGERPAVKRGRIVNPTN GPLNEQLHERHDPDFQTNTN\ NNRQG |
| 13127 | 43495 | A | 13207 | 1 | 250 | |
| 13128 | 43496 | A | 13208 | 1 | 489 | |
| 13129 | 43497 | A | 13209 | 209 | 601 | |
| 13130 | 43498 | A | 13210 | 1 | 96 | |
| 13131 | 43499 | A | 13211 | 1 | 1110 | |
| 13132 | 43500 | A | 13212 | 1 | 595 | |
| 13133 | 43501 | A | 13213 | 1 | 240 | |
| 13134 | 43502 | A | 13214 | 1 | 675 | |
| 13135 | 43503 | A | 13215 | 1766 | 1957 | |
| 13136 | 43504 | A | 13216 | 1 | 426 | |
| 13137 | 43505 | B | 13217 | 94 | 3238 | |
| 13138 | 43506 | A | 13218 | 1 | 2370 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13139 | 43507 | A | 13219 | 1 | 2796 | |
| 13140 | 43508 | B | 13220 | 43 | 566 | |
| 13141 | 43509 | A | 13221 | 1 | 903 | |
| 13142 | 43510 | A | 13222 | 3 | 110 | |
| 13143 | 43511 | A | 13223 | 2 | 755 | |
| 13144 | 43512 | A | 13224 | 1 | 1338 | |
| 13145 | 43513 | A | 13225 | 1 | 807 | |
| 13146 | 43514 | A | 13226 | 1 | 918 | MARADTVSVPMFMGLAAKPC WRDTEPNTGYRGPHVRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDAC\LSNAILVHNKKGGP LADGIVITPSHNPPEDGGIKYNP PNGGPA\VPTSLKWWKTGPTH WPMA*KA*SVSPRRSDGIRSKN DVIDTSDDDM**QCLSRRSN\G HPGAKVANLVPKTTFIDGVDQT SFFLTNGQSNRKA EHYFLNGK LAAVRMDEFKYHVLIQQPYAY TQSGYQGGFTGTVMQTAGSSV FNLYTDPQESDSIGVRHIPMGV PLQTEMHAYMEILKKYPPRAQI |
| 13147 | 43515 | A | 13227 | 1475 | 2904 | FWRAAAPIDCWRS GAVKKQH VEVTQLDWTTPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGFTGT VMQTAGSSVFNLYTDPQESDSIG VRHIPMGVPLQTEMHAPGLPLA SSMKRWIRATGFIFGKEQFED VVPVLGSKVNGVQFNAELVAD SLGISQIRCRAIFLTVVFFPVLH KQAFDLISLLLQQPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFTT LVQGSLPELHQA WQAVDERPH ANRFLPPDEIEQSLNGVHYQHH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRILTRS QLRLQ LAWPQQQGRYPLTYHLFLGVI |
| 13148 | 43516 | A | 13228 | 215 | 525 | LAWARRCRLLAKATSLIRAPS SEMRAS TPCRGQRPSGYSWY GRSPRAVLEGLRVGAHL SRAN CPWPSR/SQVVELIPDGFPVFLD FTKIPGRDTQNEHIVLLH |
| 13149 | 43517 | A | 13229 | 1 | 942 | |
| 13150 | 43518 | B | 13230 | 1 | 1201 | |
| 13151 | 43519 | A | 13231 | 685 | 921 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13152 | 43520 | A | 13232 | 2 | 251 | |
| 13153 | 43521 | A | 13233 | 2 | 100 | |
| 13154 | 43522 | A | 13234 | 5 | 1093 | |
| 13155 | 43523 | A | 13235 | 2 | 482 | |
| 13156 | 43524 | A | 13236 | 1 | 2496 | |
| 13157 | 43525 | A | 13237 | 572 | 912 | RCRPDKAFTPHPAIGARCLMRR LRVLSCLQPLPNVGWIRRLRRJR QFSAPDEGAKCRVAILQ/DFDA QYGRFLEVTSQAQQRFQTD*K HAAALPFFFPSSAYSALAAISVVF GFR |
| 13158 | 43526 | C | 13238 | 5 | 127 | |
| 13159 | 43527 | A | 13239 | 1 | 444 | |
| 13160 | 43528 | A | 13240 | 17 | 261 | |
| 13161 | 43529 | A | 13241 | 173 | 397 | |
| 13162 | 43530 | A | 13242 | 169 | 421 | LKPKNLDEKLLPASSSSCRIWA TSPVHHLWQVLKKILFGWNPT KSPRCLS/TRQAMFSLSKKASLP WTIAARSADQRCRTRIAEL |
| 13163 | 43531 | A | 13243 | 17 | 744 | RPHQEQRIAGCGVNALSSLRSA TAVGMIRRASVASG/DRAPIAG CGVNALSGLHRHFIEVTCTHFL LVRYEGIAIFRGGKFRLHFLN VVLHTLALGIGVCQVKHVEPH AVDTCQGDELELVAHIRQLLLE AGNSFVVEVYLPVERRRAVISQ QFARIFRVDLSCKATRQFQIRRG RSHQTGQHMGIIRRVDAAHAD DRRTSGRVPPLIQVCPAHSSEA VVVVVDVDVDVDVDVDVIGAV |
| 13164 | 43532 | A | 13244 | 954 | 1104 | |
| 13165 | 43533 | B | 13245 | 54 | 1169 | |
| 13166 | 43534 | A | 13246 | 35 | 3066 | VGHSTRPAASPGPAAGIGRSPA RLVQQPQRS LAKPLNRPAAQR GLLPQRRHPKRTKRKRKAQN PQKRLPHRQPVRRRHRHRRLL QKMRRPDKRQQRRAAPRRHPR RRQRLLA VRRRQLRAKVRNRP RQRAPRQQLNGQRILHPPWRLR MQVRRKRG*YSSAVRPTVRLK RWRQRQRQ*NQPMTMQRNVC RKTRTALIYP/YKGCFLNNINAV SKTDFADKRGMRVYVRVNAPAG ATSGKYYPVVVMRSAGSFHI |
| 13167 | 43535 | A | 13247 | 1 | 2919 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13168 | 43536 | A | 13248 | 1 | 3211 | MEFTSLTPDDLRLVLELYRTPFS DGYVFHSMQFHIFDLLKSGQN VVL SAPTSMGKSAIVDSL LGMG TLKRLVLVPTVALADETRRRL QERFGDRYQIIHSSQVCHSDQ AVYVLTQERVNERDDIVIDLF VIDEFYKLAFRQLKSGDIDHQD ERVIELNIALSKLLKVS RQFYLT GPFVNSIRGLEKLGYPHTFVST DFNTVALDVKTSASKRMTTKP SSKRWGKSRTCVDADHIKNGIG LHFGALPRALQQYT |
| 13169 | 43537 | A | 13249 | 486 | 3882 | LRLRGEALPVASGCLANATDTP AGTTLWADTERHAVQ**TCEA DTLGSCGYAAKPCLSPVAVWQ MLLTRLLEQHYGLTLNDTPFSD EPVLTAPIDAAALRGIEFGKFQL GNMVVGDIIECGSDVTDYAVG DSVCGYGPLSETVIINAVNNYK LRKMPQGSSWKNVAVCYDPAQF AMSGVRDANGARRGFWWGGL GAIRVQLAFKWLNAAGRLPGG GLGGPIPYSAHRCDIARRHGAD FCLNPIGTDVGKEIKTLTG |
| 13170 | 43538 | B | 13250 | 1 | 1116 | |
| 13171 | 43539 | A | 13251 | 729 | 985 | SAPPQLAPSLPD RATDPDTCWP PG*RPARYLPSRQIDCFNTRFRL QRLTASQCAEAVDVAFRLTV QQTPHFRCAQLRQRAFRID |
| 13172 | 43540 | A | 13252 | 395 | 605 | |
| 13173 | 43541 | A | 13253 | 1 | 1140 | MIYVFVTVKHRNDHFTKNTLA SYRGRTLLGTLFKGVYHLYKD ETYLYQSGKGHTIQEVRIKGL NNPDLDAAVGEDLAQQLRDEL ELVKGASNEFDKELFLAGEITP VFFGTALGNFGVDHMLDGLVE WAPAPMPRQTDTRTVEASEDK FTGFVFKIQANMDPKHRDRVA FMRVVSGKYEKG MKLRQVRT AKDVVISDALTFMAGDRSH/AY PGDILGLHNHGTIQIGDTFTQG EMMKFTGIPNFAPELFRIRLK DPLKQKQLKGLVQLSEEGAV QVFRPISNNDLIVGAVGVLQFD VVVARLKSEYNVEAVYESVNV ATARWVECADAKKFEFKRKN ESQLALDGGDNLAYIATSMVN LRLAQERYPDVQFHQTREH |
| 13174 | 43542 | A | 13254 | 1 | 1495 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 13175 | 43543 | A | 13255 | 372 | 1365 | IRYFENRGLFAHCATRTGQFPP HCILASYKCGEQPDSSSNHPRN LFVWRSNLLGSSG\KGHEYM K YLLGTESGIQGEELGASDGIK EEVEWQTAAIEGKLDLLVTLDF RMSSTCLFSDIVLPTATWYEKD DMNTSDMHPFIHPLSAAVDPA WESRSDWEIYKGIKAFAFSQVCV GHLGKETDVVLQPLLHDSPAEL SQPCEVLDWRKGECDLIPGKTA PNIVAVERDYPATYERFTSLGP LMDKLGNGMDLTDYANMALSI PSANTDIWNLEQDTVGTRLTNS RHGLADNGGAWVS YFGGNFN GDNGTINYDQDVNGIMVGVDT KIDGNDG |
| 13176 | 43544 | A | 13256 | 3 | 1444 | |
| 13177 | 43545 | A | 13257 | 61 | 1058 | LPYLIALLARAWFNGLLTSRTR LYIKNGNIVDLPKLQEMVADVS HHFPLRLPAPTPKALYSPCEIRH LAINVNLEYDPTAAFRNQVVHF DFRKLDVFSFGENQNCLVGNV DLL\YRNSWNEVRTLHFNGEQS MIEALKTILGKMHQDAAPPDSV EVFCYSQHRLRLIRTRVQQLVS ECIELRLSSTRQETGRFKALRVS GQTWGLFFERLNVSVQKLENAI EFYGAISHNKLHGLSVQVETNH VKLPAVVDGFASEGIIQFFFEET QDENGFNIIYILDESNRVEVYHH CEGSKEELVRDVSRFYSSSHDR FTYGSSFINFNLQDPYLRARVSI |
| 13178 | 43546 | A | 13258 | 1 | 1133 | |
| 13179 | 43547 | A | 13259 | 2 | 240 | ISSARHFGALACTLELGKALT GQNDLRQFAVTASAIAALL/SR HSPSFEMHMASDTLNFMPFEK GTLLAQDGEERFTVTH |
| 13180 | 43548 | A | 13260 | 1 | 358 | LPFLPSGLRGLAAENKIRPHSA GSFLGPPCGLRGKLV/ISAAALM STTIPISRVQGLLQFLNSKSPISR AERSWSTFGASAAFLTTLASLL FLFPPLAISSLANSAKVFPTPC AGSP |
| 13181 | 43549 | A | 13261 | 1 | 1635 | |
| 13182 | 43550 | A | 13262 | 1 | 1363 | |
| 13183 | 43551 | A | 13263 | 5 | 249 | |
| 13184 | 43552 | A | 13264 | 15 | 280 | |
| 13185 | 43553 | A | 13265 | 6 | 363 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13186 | 43554 | A | 13266 | 78 | 346 | TRYAMLTRHDNHLKSFYLARG RYRADFHAPETNTGERCYRYK PLPYWLE*RRGRNRYPALQ*TM FLPADGPARCLSRQAAILKESV LPK |
| 13187 | 43555 | A | 13267 | 568 | 831 | ELQRHVLVVFAGFWIVKNSRN LFLVCRAEHKRSVVKGLLRQQ GQGFWFHFQDGFAVEVGNNAN VIGSE*IVFGIVFPHRERCLVDK |
| 13188 | 43556 | A | 13268 | 3 | 419 | |
| 13189 | 43557 | A | 13269 | 1 | 561 | |
| 13190 | 43558 | A | 13270 | 1 | 741 | |
| 13191 | 43559 | A | 13271 | 2 | 1040 | |
| 13192 | 43560 | B | 13272 | 1 | 1974 | |
| 13193 | 43561 | A | 13273 | 2111 | 2340 | EVFIRDKLMERRNRRTGRTEKA /RDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPVKVLQSQCI |
| 13194 | 43562 | A | 13274 | 470 | 813 | KTTSFPAKLFNACRISLLASAEV NPNISAYLATWISQIPSCSCRVP SDFLIWSTNRYRIRF*SRERLVG EAVA/AAAADGVTFSVPVTPHT FRHSYAMHMLYAGIPLKVLQS LMGH |
| 13195 | 43563 | C | 13275 | 440 | 1180 | |
| 13196 | 43564 | A | 13276 | 1 | 1290 | |
| 13197 | 43565 | A | 13277 | 1 | 1036 | MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMENTSRRFEQRGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMLKNVVRETDEVG KDPRPLPYLGHDEPYTFDINLS VNLKSMVVG GTDMGQEPLKQ MGAWGPLSLKAMFGFFIRGYG FFTPFGRTLFLPLGFGSTPPFTFPL LTKTIGVFILDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA GAAAAADGVTFSVSVTPHTFR HSYAMHMLYAGIPLKDLQSLM GHKSISSTEGYTKDFSLDVGAR HRVQFAMPESDAVAMLKQLF |
| 13198 | 43566 | A | 13278 | 366 | 672 | RNGTHPRYIEAVPWGALPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSRALRELQQAV HAGLPQQAIFDGGSEIGKIPH IVLYKPVQCSLWAFVH |
| 13199 | 43567 | A | 13279 | 2602 | 2976 | |
| 13200 | 43568 | A | 13280 | 982 | 1347 | |
| 13201 | 43569 | A | 13281 | 1 | 780 | |
| 13202 | 43570 | A | 13282 | 568 | 891 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 13203 | 43571 | A | 13283 | 1 | 718 | MKEKPSSPRQYSYSFLSSMILLG GGESWNLLRADQRLIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEAVAAAA ADGVTFSPVTPHTFRHSYAM HMLYAGIPLKVLQSLMGHKSIS STEVYTKVVFALDVAAPHPESTP VHLPSRENKIPPPIMRIPCGLPTS PIEQKQGKISATGTQWRRLKQE TRLSSVSARLMSYVGVMC |
| 13204 | 43572 | A | 13284 | 1 | 496 | AMFGFFIRGYGFFTFPGRTLFP LFGSTPPFTFPLLTKTIGVFILDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEAGAAAAADGVT FSVSVTPHTFRHSYAMHMLYA GIPLKDLQSLMGHKSISSTEGYT KDFSLDVGARHRVQFAMPES DAVAMLKQLF |
| 13205 | 43573 | A | 13285 | 2 | 545 | |
| 13206 | 43574 | B | 13286 | 1 | 735 | |
| 13207 | 43575 | A | 13287 | 1 | 1599 | |
| 13208 | 43576 | A | 13288 | 583 | 1005 | |
| 13209 | 43577 | B | 13289 | 31 | 1239 | |
| 13210 | 43578 | A | 13290 | 1 | 1023 | |
| 13211 | 43579 | A | 13291 | 1 | 933 | |
| 13212 | 43580 | A | 13292 | 1 | 1278 | |
| 13213 | 43581 | A | 13293 | 1 | 705 | |
| 13214 | 43582 | A | 13294 | 2 | 893 | |
| 13215 | 43583 | A | 13295 | 88 | 429 | |
| 13216 | 43584 | B | 13296 | 1 | 1419 | |
| 13217 | 43585 | A | 13297 | 1 | 2784 | |
| 13218 | 43586 | A | 13298 | 163 | 416 | RNGTHPRYIEAVPWGALPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSRALRELQQAV HAGLPQQA KILFDGGSEIGKI |
| 13219 | 43587 | A | 13299 | 740 | 1431 | CCQTLPVFHPPHPSHLGPRPCPP TH/HLPSEHRSFLAACHDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRHRLHR PQQPSPPLGIPHPSSL\TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVVFALDVAARHRVQFAMP ESDAVAMLKQLS |
| 13220 | 43588 | B | 13300 | 1 | 858 | |
| 13221 | 43589 | B | 13301 | 1 | 1098 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13222 | 43590 | A | 13302 | 1 | 1047 | MNRQLSDSYTEDTKEPSDVTTSE ERTRSPGSAKTTMIDTLKKLQ DVLKTEDSKNPTKSAADLLEQ YVKATGPPIIILQKATKTMEMI MIVEEKASDELQDPPELQQRVI HSVRGKPGLVKQRTQEIETRLR LAGLTVSSPLKRSHSLAKLGSL TFSTEDLSSRPPGPPPGPGLHP GPPPRRPPKLPAPPAGCSVHC CHYPLHFVVSPLGFGYCSLMRI QIVFVTAHVHDSALLPLDASL APEALQNFQRYTGIQHVHRIGM AERMWCDNRNRHTVSSSGGN RLPNPAPLPNPGVLSAPPNLIQR PKADDTSAATIEKKATATISAK PQITNPKAEIT*NPRVWQGSWI GEAVAAAAADGVTFSPVTPH TFRHSYAMHMLYAGIPLKVLQ SLRSQ*SVRGKPGLVKQRTQEI ETRLRLAGLTVSSPLKRSHSLA KLGSLTFSTEDLSSRPPGPPGP PPGLHPGPPRRPPKLPAPP GCSVHCCHYPLHFVVSPLGFGY CSLMRIQIVFVTAHVHDSALL PLDASLAPEALQNFQRYTGIQH VHRIGMAERMWCDNRNRHT VSSSGGNRLPNPAPLPNPGVLS APPNLIQRPKADDTSAATIEKK ATATISAKPQITNPKAEITRFCPL |
| 13223 | 43591 | B | 13303 | 1 | 1185 | |
| 13224 | 43592 | A | 13304 | 529 | 774 | |
| 13225 | 43593 | B | 13305 | 1 | 1089 | |
| 13226 | 43594 | A | 13306 | 712 | 1024 | GVESNLVVVVALCHRLIYLVW GTRTVRTWIGEAVAAAAADGV TFSVAVTPHTFRHSYAMHMLY AGIPLKVLQSRVVALDVAARH RVQFAMPESDAVAMLKQLS |
| 13227 | 43595 | A | 13307 | 556 | 1040 | |
| 13228 | 43596 | A | 13308 | 1 | 984 | |
| 13229 | 43597 | A | 13309 | 95 | 428 | |
| 13230 | 43598 | C | 13310 | 1 | 426 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13231 | 43599 | A | 13311 | 116 | 1746 | SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSPV VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVTYTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPVGIFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLKKNVDLKGFEVDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KARLTWGIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEVDVRILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVTYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS |
| 13232 | 43600 | A | 13312 | 1 | 1593 | |
| 13233 | 43601 | A | 13313 | 1 | 2536 | |
| 13234 | 43602 | A | 13314 | 887 | 1205 | RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEVTYTKVFALDVAAR RHRVQFAMPESDAVAMLKQLS |
| 13235 | 43603 | A | 13315 | 79 | 351 | |
| 13236 | 43604 | A | 13316 | 1 | 2320 | |
| 13237 | 43605 | A | 13317 | 187 | 798 | |
| 13238 | 43606 | A | 13318 | 2089 | 2610 | |
| 13239 | 43607 | A | 13319 | 1 | 1407 | |
| 13240 | 43608 | B | 13320 | 154 | 3682 | |
| 13241 | 43609 | A | 13321 | 1 | 1206 | |
| 13242 | 43610 | A | 13322 | 1 | 255 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13243 | 43611 | A | 13323 | 3058 | 3160 | GSAA*LPPPLPAAFSGSCWLSQ RHP ELHV*NEIYHLLH*KSFTSC *HNLSS*PRYPYLSSERV LW*CL SFISKI*SVTMP*SDLISLW*KLE PLTCRSTSHFRQKLAQ/RLP/AY QQGHQDLFILRSDLPSQVFIRDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEAVAAAAADGVT FSVPVTPHTFRHSYAMHMLYA GIPLKVLQSLMGHKSSISSTEVT KVFDALDVAARHRVQFAMPESD AVAMLKHYPEINALALYLKCG TEWIC |
| 13244 | 43612 | A | 13324 | 1 | 1812 | |
| 13245 | 43613 | B | 13325 | 1 | 1776 | |
| 13246 | 43614 | A | 13326 | 583 | 751 | |
| 13247 | 43615 | B | 13327 | 826 | 2097 | |
| 13248 | 43616 | A | 13328 | 1810 | 4163 | |
| 13249 | 43617 | A | 13329 | 686 | 2939 | |
| 13250 | 43618 | A | 13330 | 1085 | 1690 | SYFIMVKVGTSYVPINVSFSPKV GPGASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGR/IYK ARIWEVTDRTVR/TWICRGG PAAAADGVTF\SDPGPP\HTFRH SYAMHMLYAR*YR*KFLQSLM GHKSHPINGKATPKVFGPGMG LARA/HRGAGWQWPKSDAVG MPKQLSLRINALGLYMETGKPE GIMLFFGC |
| 13251 | 43619 | A | 13331 | 3 | 327 | |
| 13252 | 43620 | A | 13332 | 3 | 337 | |
| 13253 | 43621 | C | 13333 | 167 | 413 | |
| 13254 | 43622 | A | 13334 | 1 | 1256 | |
| 13255 | 43623 | A | 13335 | 1 | 1078 | |
| 13256 | 43624 | A | 13336 | 3 | 976 | |
| 13257 | 43625 | A | 13337 | 1 | 1004 | |
| 13258 | 43626 | A | 13338 | 2 | 291 | WRKIYEANGKKRKQRLQS*SL MKQTLNQQRSKETKKASA/SM RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWNIPCSWVG RINIVKMAIPPK |
| 13259 | 43627 | A | 13339 | 1 | 2022 | |
| 13260 | 43628 | A | 13340 | 1 | 2262 | |
| 13261 | 43629 | A | 13341 | 5 | 283 | |
| 13262 | 43630 | A | 13342 | 1 | 1245 | |
| 13263 | 43631 | A | 13343 | 1 | 1203 | |
| 13264 | 43632 | A | 13344 | 1 | 687 | |
| 13265 | 43633 | B | 13345 | 1 | 1371 | |
| 13266 | 43634 | A | 13346 | 1 | 2241 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13267 | 43635 | A | 13347 | 1 | 832 | LKKCIKTPEIPSKHVRNWPVKV LEQRRQGLEYTLQVASITLIPKA DEDTPKKKTDDKNSWTGTDK VFNKILEIKFSSILKRLYWPVLE VLARAMRQEKEIKGIQLGKEEV KLSRFADDMIVYLENPVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQ\TESQIRIKYLGIQ LTRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKRYPFQCLCHQSAISTTKG VFTSILPLLMIEQLVSGRSCPSV AWSSMECTTV |
| 13268 | 43636 | A | 13348 | 1 | 1314 | |
| 13269 | 43637 | A | 13349 | 1 | 843 | |
| 13270 | 43638 | B | 13350 | 1 | 1011 | |
| 13271 | 43639 | A | 13351 | 1 | 173 | |
| 13272 | 43640 | A | 13352 | 1 | 323 | |
| 13273 | 43641 | A | 13353 | 3 | 2020 | |
| 13274 | 43642 | A | 13354 | 1 | 1473 | |
| 13275 | 43643 | B | 13355 | 1 | 636 | |
| 13276 | 43644 | B | 13356 | 1 | 456 | |
| 13277 | 43645 | A | 13357 | 1 | 619 | |
| 13278 | 43646 | A | 13358 | 1 | 1293 | |
| 13279 | 43647 | B | 13359 | 79 | 1041 | |
| 13280 | 43648 | A | 13360 | 3 | 718 | |
| 13281 | 43649 | A | 13361 | 1 | 612 | |
| 13282 | 43650 | A | 13362 | 1 | 992 | |
| 13283 | 43651 | A | 13363 | 1 | 1236 | |
| 13284 | 43652 | A | 13364 | 1 | 1071 | |
| 13285 | 43653 | A | 13365 | 359 | 1250 | KLPMGVAVVKLLHLPKVIIVFW LASWMMSRWLHYPDWVTIAQ QVLMNVVSVMQADCRMNLLEI FLRWLMRKIFHVRLLPAVSTPP NCLNQLLLFFLTPVNYLPGQVM HFKKPLQIKRNYLSSRHFTMS RKKLKGK VSGYKIHVQKS\QAF SANSQTESQIMSELPFTMASK RIKYLGIQLTRDVKDLFKEYK SLLNEIKEDTNKWNNPCSWV GRINIMKMAILPKVIYRFNAIPI KLPMTFFTELEKTTFKFIWNQK RAHIAKSNLSQKNKAGGITLPD FKLYYKATVTKTT |
| 13286 | 43654 | A | 13366 | 1196 | 2132 | |
| 13287 | 43655 | A | 13367 | 1 | 2271 | |
| 13288 | 43656 | A | 13368 | 2 | 1105 | |
| 13289 | 43657 | A | 13369 | 1 | 2117 | |
| 13290 | 43658 | A | 13370 | 1 | 1447 | |
| 13291 | 43659 | A | 13371 | 1 | 1669 | |
| 13292 | 43660 | A | 13372 | 1 | 2823 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13293 | 43661 | A | 13373 | 1089 | 2539 | |
| 13294 | 43662 | A | 13374 | 1 | 1787 | |
| 13295 | 43663 | A | 13375 | 1205 | 1207 | |
| 13296 | 43664 | B | 13376 | 1 | 2745 | |
| 13297 | 43665 | A | 13377 | 1 | 2063 | |
| 13298 | 43666 | A | 13378 | 1 | 4380 | |
| 13299 | 43667 | A | 13379 | 1 | 3347 | MGDFNIPLSTLDRSTRQKVNKD TQELNSALHQADLIDSYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSHSA IKLELRIKNLTQNCSTTWKLNN LLNDYWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKA VCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEKETQKTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDA IKNDK |
| 13300 | 43668 | A | 13380 | 1 | 2367 | |
| 13301 | 43669 | A | 13381 | 1 | 1116 | |
| 13302 | 43670 | A | 13382 | 1 | 1095 | |
| 13303 | 43671 | A | 13383 | 670 | 1500 | QTESSTSKSLSTM IKWASSLG WQGWFNIRKSINVIQHIKGIQR QKPHDYLNRCRKS L*QNSTTLH AKNSQ*TAQNLLKLISFNKVS GYKINVQKSQAFLYTSNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIVKMAILP KVIYRFNAIPIKLPM TFFTELEK TTLKFIWNQKRAHIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYWYQNM CYRSMEQNRALS YYVAYLQPSDL |
| 13304 | 43672 | A | 13384 | 441 | 3131 | |
| 13305 | 43673 | B | 13385 | 1 | 5688 | |
| 13306 | 43674 | B | 13386 | 916 | 2165 | |
| 13307 | 43675 | A | 13387 | 1 | 1529 | MDPPAGAARRLLCPALL*LPAG *PLRPRLAGAAPAGTALLHER AMPL*LRPGLHDVHGVPDL |
| 13308 | 43676 | A | 13388 | 1 | 714 | |
| 13309 | 43677 | A | 13389 | 3 | 457 | |
| 13310 | 43678 | A | 13390 | 2 | 492 | |
| 13311 | 43679 | A | 13391 | 3 | 1201 | |
| 13312 | 43680 | A | 13392 | 1 | 309 | |
| 13313 | 43681 | A | 13393 | 2 | 1073 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13314 | 43682 | A | 13394 | 3119 | 6984 | CIVKHAAMRSAMTSLAARITVL NPTRATTPNT/RVADDQGFLRQ WSKVAKERKLQRLYIGEPSAEA VAAQMPDLILISATGGDSALAL YDQLSTIAPTLIINYDDKSWHPR LSFNKADEITTVFCGSKKSLAN GIPMANILFPTSVIATQQTQHFR FVDDFNAQFLRFASLDPAA SPA ITISGKATLEIPGTEL VFYAALE KKLNIKPGQTTFDGRFTLLPTC CLGNCDKGPNNMIDEDTHAHL TPEAIPPELLER |
| 13315 | 43683 | A | 13395 | 3 | 587 | |
| 13316 | 43684 | A | 13396 | 1 | 315 | |
| 13317 | 43685 | A | 13397 | 430 | 636 | |
| 13318 | 43686 | A | 13398 | 1 | 84 | |
| 13319 | 43687 | A | 13399 | 1 | 1647 | |
| 13320 | 43688 | A | 13400 | 1 | 2652 | |
| 13321 | 43689 | B | 13401 | 1 | 1494 | |
| 13322 | 43690 | A | 13402 | 1 | 750 | |
| 13323 | 43691 | A | 13403 | 1 | 513 | |
| 13324 | 43692 | A | 13404 | 1 | 2254 | |
| 13325 | 43693 | A | 13405 | 1 | 746 | |
| 13326 | 43694 | A | 13406 | 3 | 428 | LGDDFVRAANIILHCEGKVVVS GIGKSGHIGKKIAATLASTGTPA FFVHPAEALHGD LGMIESRDV MLFISYSGGAKELDLIIPRLEDK SIAL\GKPTSPLGLAAKAVLDIS VEREACPMHLAPTSSTVNTLM MGDALAMAV |
| 13327 | 43695 | A | 13407 | 1 | 1431 | |
| 13328 | 43696 | A | 13408 | 943 | 2481 | |
| 13329 | 43697 | B | 13409 | 1 | 783 | |
| 13330 | 43698 | A | 13410 | 3 | 729 | |
| 13331 | 43699 | A | 13411 | 1 | 843 | |
| 13332 | 43700 | A | 13412 | 3 | 128 | |
| 13333 | 43701 | A | 13413 | 1 | 136 | |
| 13334 | 43702 | A | 13414 | 1 | 492 | |
| 13335 | 43703 | A | 13415 | 3 | 619 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13336 | 43704 | A | 13416 | 1 | 1600 | GQACHASSSPLKGSRGSPNFEI LYGPIFEDSLAPD*PKVIAGQNT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLDFALYFFHNYQA LLAKGSGPYFYLPKTQSWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDEILHALR DHIVGLNCGRWDIYFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTCCHKRGAFAMGGM AAFIPSKDEEHNQVLNKVKA DKSLEANNGHDGTWIAHPGLA DTAMAVFNDILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKGSQNLWKFA VYSGLRHGELAALAWEDVDLE KGIVNVRRLTILDMFGPPKTN AGIRTVTLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAGIRRRNP YHTRHTFACWLLTAGANPAFIA SQMGHETAQMVEIYGMWID DMSDEQIAMLNARVM |
| 13337 | 43705 | A | 13417 | 2 | 278 | |
| 13338 | 43706 | A | 13418 | 3 | 662 | GHLWIRIDLSQSAVSHSVKELE NHTGVRLLDRTTREVVLTDA GQQLALRLERLLDELNSTLRDTG RMGQQLSGKVRVAASQTISAH LIPQCIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIV IDPGPVGDLQCEAILSEPFLL CHRD SALAVEDYVPALPLPE GSPLVVKRITPVVERQLMLV RRKNRSLSTAAEALWDVVRD QGNALMAA |
| 13339 | 43707 | A | 13419 | 1 | 646 | GQQLSGKIVRVAASQTISAH LIPQCIAESHRRYPDIQFVLH DRPQQWVMESIRQGDVDFGIV IDPGPVGDLQCEAILSEPFLL CHRD LAGGDYVPWQALQGA KLVLDYASGSRPLIDAALARN GIQANIVQEIGHPATLFPMA AAGIGISILPALALPLPEGS PLVVKRITPVVERQLMLVRR KNRSLSTAAEALWDVVRDQ GNALMA\GRE |
| 13340 | 43708 | A | 13420 | 1 | 1068 | |
| 13341 | 43709 | A | 13421 | 1 | 381 | |
| 13342 | 43710 | A | 13422 | 3 | 938 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13343 | 43711 | A | 13423 | 595 | 1630 | CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGHYDHDYEFELGTR FRAVIIKLCNGDSLRFMTSVY ALVKCFHEGDPLHKTGCQHLIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVEMLLREAGKAGFC RFRNHHQTGFSPAGANQRGPL AATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGNSYDHDYEFELGTHQ RLGAVARIVGDDLLNELRRDV VDARAGDVDQHAAEKGDFR |
| 13344 | 43712 | A | 13424 | 1 | 1395 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13345 | 43713 | A | 13425 | 1307 | 1992 | DKLNPVAHQKAYLAQSSQCHP QNARLVQHTQIRILPISEPPSNRI FACWGKPAWTACCN/FSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQLKHKEVESPNRPI TSSEIQVLIKSLPIKKSPPDGFT AEFYERYKEELVPFLLKLFQTIE QERLLPNSFYEASIILTSKPSRD ATKKDNFRPTSLMNIYAKILNK IGQTESSSTSKSLFSTIKSVSSPE CKAGSTYANQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQETTPWSPFSDPVLAFDY KVFMAFVYNVVRVSQRMVVA GCISAFNDKLLNDLICFPVAPVS SKQIFPSDVKVAEPDHSCVSSY RIGSMAPNLTLEMPRHNYFPA GNSVDHDNEFEL |
| 13346 | 43714 | A | 13426 | 560 | 844 | |
| 13347 | 43715 | B | 13427 | 200 | 1519 | |
| 13348 | 43716 | A | 13428 | 950 | 1230 | CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRK TLAPNTQTASPRALADSLMQLA RQVSRLESGQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13349 | 43717 | A | 13429 | 695 | 1060 | FRQRSVAFPPPTVPNACVSVRSR ERDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTTAPNTQTASPRALA DSLMQLARQVSRLESGQ*AQR N*CRKHRLSIPRK |
| 13350 | 43718 | A | 13430 | 1 | 1558 | MRDIFWVPDICKVMLYL VFFRS MGTPLRVAVAMGLVITSWKIAQ KPRDFADFGTTINQDFRLLGQT SVDRLQLSQGQAVKGNQLLP VSLKTDTKAKNLYLTKAYYGG GTNFFRKESQKLQQSACKRDA ELANGALGIIELNNDYTLKKVM KPLITSNTGFADFGTTIKQDFRL LGQTSVDRLQLSQGQAVKGN QLLPVSLVKRKTTTAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN |
| 13351 | 43719 | A | 13431 | 391 | 1676 | FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTTAPNTQTASPRALA DSLMQLARQVSRLESGQ*AQR N |
| 13352 | 43720 | B | 13432 | 1 | 1638 | |
| 13353 | 43721 | A | 13433 | 1 | 2430 | |
| 13354 | 43722 | B | 13434 | 1 | 1282 | |
| 13355 | 43723 | B | 13435 | 1 | 1225 | |
| 13356 | 43724 | A | 13436 | 350 | 709 | |
| 13357 | 43725 | A | 13437 | 1 | 2236 | |
| 13358 | 43726 | A | 13438 | 548 | 1698 | RSWLRSSLSGSIPIATEISCTSCE ASTSS/VRDFPGVKDLTFQWHD RLIFAIARLLGRSACGVTFHKEQ LGTVKVLRGTISQFARQRAAG QLFTHHFFGRTH TALGAGNRH LRQQFSRLNVLVQPQDKGIFHH ARNECRALTRRETPAFFRIRAVF NSQLSQTQLHIFTARPAGLAS KCRKPPQACYLWDFADFGTTIK QDFRLLGQTSVDRLQLSQGQ AVKGNQLLPVSLVKRKTTTAP NTQTASPRALADSLMQLARQV SRLESGQNIESAKGLHVWDSW PLHNADGTVDEYNGYHVVFAL AGSPKDADDTSIYMFYQKVG NSIDSWKNAGR VFKDSDKFDA NDPILKDQTQEWSGSATFTSDG KIRLFYTDYSGEHYG |
| 13359 | 43727 | B | 13439 | 448 | 1116 | |
| 13360 | 43728 | A | 13440 | 97 | 1636 | |
| 13361 | 43729 | A | 13441 | 1 | 1296 | |
| 13362 | 43730 | B | 13442 | 1 | 2160 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13363 | 43731 | A | 13443 | 485 | 865 | FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLARQVSRLESGQS*NSS KTKNTKCLNSINQRLKILSLQK DLMCGTAGRCKTLTEQ |
| 13364 | 43732 | A | 13444 | 816 | 1194 | SLILFLRRRRRAVEKRGKVWKDS CPNGTTTLTSGAIFLFIRDFADF GTPITQDFRLLGQTSVDRLLHLS QGQAVKGNQLLPVSLVKRKTTL LAPNTQTASPRALADSLMLA RQVSRLESGQ*AQRN |
| 13365 | 43733 | B | 13445 | 1 | 2710 | |
| 13366 | 43734 | A | 13446 | 2027 | 2934 | NPRILPISEPPSNRIFACWGKPA WTACCN/FSQGQAVKGNQLLP VSLVKRKTTLAPNTQTASPRAL ADSLMLARQVSRLESGQDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLVKR KTTLAPNTQTASPRALADSLMQ LARQVSRLESGQSRVHSHSLGP LPTTTTGSINQKKGGVSGGPG SKEQAEISCLKERKDLGLGILGS TVGILKVKHQGASTKQGHSD LIKILLSDTSLSTPAAPMVDSLIA RVGVMARGNAITLPCGRDVK FTLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLLTGQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSA YERGQ RYASRLQYMNLLPIFLRWLMR KIFHDEHGV PQDQEEEPISETII EEEIPSINSDLGNELYFVKLPKF LSIEPKDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMLARQVSRLESGQP HSTDSATHRKMTLSLADRCST QKIRILPMAGRDPECQRTEMIK SSDLMAEIIQEHEKEDQLPELEQL EHIGLFSHAEIKAIKKASDLQY RIQERALFKDDFINYVLHEIPLF EQIQRRTIGYSLKHGIRAVKA TIVRALYGRIPAGVVVTRSPV |
| 13367 | 43735 | A | 13447 | 1 | 5240 | |
| 13368 | 43736 | A | 13448 | 4733 | 4753 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13369 | 43737 | A | 13449 | 299 | 761 | LNTTAITLCLLLREARKTLMTH QSTCFIKRDFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN**PVPKEKRRRGDRQE HQQPCRNTEGTALRVWAARDQ |
| 13370 | 43738 | A | 13450 | 3925 | 4190 | FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMQLARQVSRLESGQ*AQR N |
| 13371 | 43739 | A | 13451 | 2 | 1040 | |
| 13372 | 43740 | A | 13452 | 58 | 350 | HLASWVVALVLHWGCVWVTA ESSTSKTRSPFRARSWIGEAVA AAAADGVTFSPVTPHTFRHSY AMHMLYAGIPLKVLQSLMGH KSISSSTGVPSSNS |
| 13373 | 43741 | A | 13453 | 1 | 1290 | |
| 13374 | 43742 | A | 13454 | 289 | 1338 | |
| 13375 | 43743 | A | 13455 | 1 | 732 | |
| 13376 | 43744 | A | 13456 | 982 | 1347 | |
| 13377 | 43745 | A | 13457 | 116 | 1746 | SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEVTYKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIERYQLPQSYQLY YFELAIPVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIVPTPAELFDYTSALQ FFDMLRDLKKNVDLKGFEADV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVVRETDEVG KARLTWIGTINVVCAADVLIV PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEADVRIILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEVTYKVFALDVAAR HRVQFAMPESDAVAMLKQLS |
| 13378 | 43746 | A | 13458 | 1 | 780 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13379 | 43747 | A | 13459 | 116 | 396 | SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAARHR |
| 13380 | 43748 | A | 13460 | 3 | 514 | |
| 13381 | 43749 | A | 13461 | 2 | 545 | |
| 13382 | 43750 | A | 13462 | 1 | 1110 | |
| 13383 | 43751 | A | 13463 | 1 | 870 | |
| 13384 | 43752 | A | 13464 | 1 | 1422 | |
| 13385 | 43753 | A | 13465 | 1 | 1599 | |
| 13386 | 43754 | A | 13466 | 614 | 1236 | TARVAAARRRCQCWGSACGS ALTLPRTSSLTLTETPIVQQTRM VVRCPASLPSQWRSCPSSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVDRTVVRTWIGEAVAAAAAD GVTFSVPVTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS |
| 13387 | 43755 | A | 13467 | 1 | 1023 | |
| 13388 | 43756 | A | 13468 | 1 | 699 | |
| 13389 | 43757 | B | 13469 | 1 | 1281 | |
| 13390 | 43758 | B | 13470 | 77 | 751 | |
| 13391 | 43759 | A | 13471 | 1 | 705 | |
| 13392 | 43760 | A | 13472 | 2 | 893 | |
| 13393 | 43761 | A | 13473 | 206 | 837 | CAGAGGIARRRAEKEKALSAV NLDPTSRRLSSTSLPGAPPNPRV AAAGLSRRRPTPESAGRKS/GR WPRASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVVRTWIGEAVAA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS |
| 13394 | 43762 | A | 13474 | 1 | 1416 | |
| 13395 | 43763 | A | 13475 | 1 | 765 | |
| 13396 | 43764 | B | 13476 | 1 | 519 | |
| 13397 | 43765 | A | 13477 | 1 | 2784 | |
| 13398 | 43766 | A | 13478 | 1 | 624 | |
| 13399 | 43767 | A | 13479 | 2089 | 2454 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 13400 | 43768 | A | 13480 | 740 | 1431 | CCQTLPVFHPPHPSHLGPRPCPP TH/HLPSEHRSLFLEAACHDS LEPLNLSSGSKTKSPSLPPKAKK PKGLEISA/RPAGALRHRHRLHR PQQSPPLGIPHPSL\TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS |
| 13401 | 43769 | A | 13481 | 2 | 2309 | |
| 13402 | 43770 | A | 13482 | 1 | 603 | |
| 13403 | 43771 | A | 13483 | 1 | 762 | MVPHSTGKSWNGCDPTSATLD QLVTVFFMKLFSIGDARIPCLGP RSHSYRRSDYYSGTTIHSCCRA DYWSGTTAHL YCRSDYHPVPS FILVTSTTNHQPLKPSISEASWN PLFASL/HHLQLITES/W/YMSLA TTVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAVAA AADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS |
| 13404 | 43772 | A | 13484 | 1 | 762 | |
| 13405 | 43773 | A | 13485 | 1 | 615 | |
| 13406 | 43774 | A | 13486 | 887 | 1203 | RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVA RHRVQFAMPESDAVAMLKQLS |
| 13407 | 43775 | A | 13487 | 1 | 855 | |
| 13408 | 43776 | A | 13488 | 1 | 927 | |
| 13409 | 43777 | A | 13489 | 1 | 921 | |
| 13410 | 43778 | A | 13490 | 1 | 3216 | |
| 13411 | 43779 | A | 13491 | 1 | 1974 | |
| 13412 | 43780 | A | 13492 | 1 | 1221 | |
| 13413 | 43781 | B | 13493 | 1 | 2337 | |
| 13414 | 43782 | A | 13494 | 1 | 1273 | |
| 13415 | 43783 | A | 13495 | 1 | 1251 | |
| 13416 | 43784 | A | 13496 | 1999 | 3237 | |
| 13417 | 43785 | A | 13497 | 1 | 1773 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13418 | 43786 | A | 13498 | 1 | 633 | AQALIATYGRDRDPGRPLWLG SVKSNIGHTQAAAGVAGVIKM VMAMRHGQLPRTLHVESPSPE VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEAVAAAA ADGVTFSVPVTPHTFRFSYAMH MLYAGIPL*VLQSLMGHKSIS TEVYTKVFALDVAARHRVQFA MPESDAGGPGTCACSQQGCR LGSSVSPGRQHPQPHVRV |
| 13419 | 43787 | A | 13499 | 101 | 1943 | |
| 13420 | 43788 | A | 13500 | 686 | 3925 | |
| 13421 | 43789 | A | 13501 | 1 | 2084 | |
| 13422 | 43790 | A | 13502 | 734 | 834 | |
| 13423 | 43791 | A | 13503 | 1 | 1075 | |
| 13424 | 43792 | A | 13504 | 1 | 357 | |
| 13425 | 43793 | A | 13505 | 795 | 1273 | SHPFFSTDWSTDTGFRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMRWLHYPDWVT IIAQQVLMNVVSVMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLLFFLTPVNYLPG QVMHFKKPLQIKRNYLSSRHLT FMSRKKLG |
| 13426 | 43794 | A | 13506 | 344 | 449 | SHPFFSTDWSTDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASCMMSRCPHYDPWVTI IAQQVLTPRKDVMQADCRMNL LEIFLRWLMRKIFHGFGM |
| 13427 | 43795 | A | 13507 | 1197 | 1511 | WHYREPLLLRAQLTNPPSGQLV SITKYLQPEY*AYVLE*QAH HYQLKSVDQWPVQKQFSSGSD LYQLHPFHVQHFLEPCFPRHPE FAPPSTGTESHYYCCIW |
| 13428 | 43796 | B | 13508 | 1 | 1494 | |
| 13429 | 43797 | A | 13509 | 1 | 554 | MTARKARKITRRWRIGEAADL VGVSSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVFGTRLRRAEDVFPPVIGVAA HKGNDPQGTASMYHGWPDL HIHAEDTLLPFYLGEKDDVTYA IKPTCWPGLDIIPSCALHRIETE LMGKFDEAQP NLGIGT/N*CRM CC*CADCSHAC |
| 13430 | 43798 | A | 13510 | 1771 | 2068 | DTYSVSWIGEAVAAAAADGVT FSPVTPHTFRHSYAMHMLYA GIPLKVLQSQYPIFKLSYKNPVT QTAWFWFPNRIFGPVPINVSFS PKVGPGLPGII |
| 13431 | 43799 | A | 13511 | 65 | 277 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13432 | 43800 | A | 13512 | 327 | 748 | VHQFHGSLHEGFCAGCGCPAP GTVCDAGGFCRFRNHHQTGFSP AGANQRGPLAATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AKSIWCHRNCRW/RVAVVKLL HLPKVIIVFWLAS |
| 13433 | 43801 | A | 13513 | 512 | 580 | |
| 13434 | 43802 | A | 13514 | 2096 | 2272 | EWRNVCVGTGTENVTPSAAAA QPPPQSRPFSWILRPF*RP*RKIS TSFIRPLFTFLPA |
| 13435 | 43803 | A | 13515 | 402 | 2784 | RKNPFILH*LFR*TLRQTKPDNS AGKCVKI**HTQNQRSGRSQSD F*RRRNISERSAAYR*RQLYIR RQPYAERPSHVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIIELNNDYTLK KVMKPLITSNTVTDEIERANVF KMNGKWYLF TDSRGSKMTIDG INSNDIYMLGYVSNSLTGPYKP LNKTGLVLQMGLDPNDVTFTY SHFAVPQAKGNNVVITSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQGQLTWLQVA KRAGLGGCQSGRTVLRERLPN YKNFKGTIQELGQNQYAVSGEI FVVDRTVEITELPVRTWTQVY KEQVLEPMLNGTDKTPALISDY KEYHTDTTVKFVVKMTEEKLA QAEAAGLHKVFKLQTTLCNS MVLFDHMGCLKKYETVQDILK EFFDLRLSYGLRKEWLVGML GAESTKLNNQARFILEKIQQKIT IENRSKKDLIQMLVQRGYESDP VKAWKEAQEKCDNLKTCHTSH GSVMAETAVINHKKRKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVFYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRLS |
| 13436 | 43804 | A | 13516 | 2 | 199 | WRKKS LDIPPLIIPNGIVKNILRH FSQLLNVPITRPFWSILRPF*RP* RKISTSFIRPLFTFLPA |
| 13437 | 43805 | A | 13517 | 1 | 1887 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13438 | 43806 | A | 13518 | 125 | 828 | ECRKHTKLKLQPTIWHVLKI/Y NSEKLLVYRKLLQVLTGLYKRS NLGVRLYACCGLLCPAYPQH FAHGYPVDKIPGYPRAGTLTGL HPMQCDNLKTCHTSHGSVMAE TAVINHKKRKNSPRIVQSNDLT EAAAYSLSRDQKRMLYLFDQIR KSDGTLQEHDGICEIHVAKYAE IFGLTSAEAILRYFIKHSADMEA ITNGMMNLNRQRHQHLVALRII FAHGENGGEEVVHIGHV |
| 13439 | 43807 | A | 13519 | 504 | 755 | EPCFPAHPEFAPLSTGAESHY CCIW*AKYVHQARTL*DQRS*A DHEAYRKTAVRRCSTTQQAW EQLVHQQHILPSSCRYPG |
| 13440 | 43808 | B | 13520 | 1 | 1980 | |
| 13441 | 43809 | A | 13521 | 923 | 1063 | |
| 13442 | 43810 | B | 13522 | 1 | 1932 | |
| 13443 | 43811 | A | 13523 | 383 | 1383 | RKVFFIALKRMPAMKKAMNLF LGLSNVRTVHPEGFTVYISTHIS FPSLSGYKTRLRSFGLVKQKKS PILLEVLAREIRQE/KEIKGIQFG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKN PCSWVGRINIVKMAILPKLSRM HGRPHQPPNAASTLPFPKRSH YGQKSERLSRSGDNRKSHPECR HWQSCAKKSRCCLAFTRTVRHT PRSAAYLLTRTIELLESSALWHV QTQRIYAPLYETLDPGNRTHCE |
| 13444 | 43812 | B | 13524 | 107 | 1000 | |
| 13445 | 43813 | A | 13525 | 1778 | 1897 | |
| 13446 | 43814 | A | 13526 | 273 | 421 | SHPPFFSTDWSTDGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFSSAS |
| 13447 | 43815 | A | 13527 | 273 | 697 | SHPPFFSTDWSTDGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMRWLHYPDWVT IIAQQVLMNVVSVMQADCRMN LLEIFLRWLMRIIFHVRLLPAVS TPTNCLNQLLFFLTPVNYLPG QSGTTVPLVSSV |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13448 | 43816 | A | 13528 | 273 | 688 | SHPFFSTDWSTDTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVGSVMPADCRMN LLEIFLRWLMRKIFTTGLRSFGL VKQKKSPIRMPCVYTNPVSIV SRMGQASSL |
| 13449 | 43817 | B | 13529 | 1 | 1053 | |
| 13450 | 43818 | B | 13530 | 1 | 1869 | |
| 13451 | 43819 | A | 13531 | 120 | 430 | EDLSDTGVRKSIWCHRNCRW/ RVAVVKLLHLPKVIIVFWLASW MSRWLHYPDWVTIIAQQVL MNVVSVMQADCRMNLLEIFLR WLMRKIFHSSLEDPRNWHL |
| 13452 | 43820 | B | 13532 | 148 | 334 | |
| 13453 | 43821 | A | 13533 | 2 | 147 | TSMDKGLQGALKKKI*DL*KK* LKNIPVDKWITPREVFSGIVCK QNI |
| 13454 | 43822 | A | 13534 | 151 | 325 | KAICHNTFSKPSMDKGL/LRRS KKEGFKTYKKNIYKNIPVDKWI TPREVFSGIVCKQNI |
| 13455 | 43823 | A | 13535 | 283 | 406 | HRTKISIVPEGIFKSFSPLAGIM TEQYFL*TLHRLRLIM |
| 13456 | 43824 | B | 13536 | 1 | 1902 | |
| 13457 | 43825 | A | 13537 | 508 | 1041 | LWREASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPW/C YQT\WHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIDWIIERYQLPQSYQRMPDF RRRFLQVCVNEINSRTPMRLSYI EKKKGRQTTHIVFSFRDITSMTT |
| 13458 | 43826 | A | 13538 | 1 | 1422 | |
| 13459 | 43827 | B | 13539 | 1 | 1002 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13460 | 43828 | A | 13540 | 1 | 160 | MVLIVAATVVVVVVVGLCWM AKSECRSAMRLSSLQVRIFTYLI GREAAFADNLKWMACANKES ALLDRFIFLILLCKEPWECHCL PLFKVAMPSKCDIPVICAHINIG FTLRQLRGFGPCNIGSFEAKDS KNPQVRVISQKHKALRCIWFIT CSICNPEFTEGALQGNKQRKRQ CLQWFRAKALESNEPGFEFIQD KLLTQSLCFFPYTFLWLTGPHPS GSSYTDPCSSKADVTPSSTAVQ EHSSALELKTIVSPITRQQHGF FTQISTLADVQENVMEYLHVLS RPKVIDQEHDVWTEAYIDSTV CRVKRRQLLLQQVPLTRKQQF LPAPYVDLDSARTRTNKQQQN PIIYTGSKQGSHVILFHYGESWN LLRADQRLIFAKSWPRASRYQQ GHQDLFILRSDLPSQVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYTK VFALDVAARHRVQFAMPESDA VAMLKQL*QPQWWWWSW*D CAGWRKVNAAPCVCLPFRFA SSHTSLDERLRLQTI |
| 13461 | 43829 | A | 13541 | 48 | 668 | |
| 13462 | 43830 | A | 13542 | 1 | 1278 | |
| 13463 | 43831 | A | 13543 | 100 | 157 | |
| 13464 | 43832 | A | 13544 | 1 | 1122 | |
| 13465 | 43833 | B | 13545 | 1 | 1131 | |
| 13466 | 43834 | A | 13546 | 273 | 812 | SHPFFSTDWSTDTGVRKSIWC HRNCRWESPS*SC/WHLPKVIIV FWLASWMMSRWLNYPDWVTII AQQVLMNVVSVMQADC\KRIC WKYFCAG*CGKIFTYQ**TWN NTETSMSQKPCMKRI/YSREE LAV*KMDHHSDLISLW*KLEPL TCRSTSHFRQKLAQGFPVSTGT PGFIYSAK |
| 13467 | 43835 | B | 13547 | 1 | 987 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13468 | 43836 | A | 13548 | 246 | 2065 | LVGWLDGWLDGWLIVALPFM MIPWHSSIQPFTIHPFNWNFG*M PELCPQIGMDSWLAGWM/CWL DGWLDGW*MAKLRKPVL*PD KEGNEIWVDMYTVKPSGWTVR TFDKPRKRFIAFFIAGILFRAIKN HFLPRETLQCLPYILTGFRRGQS EYFSIFSNDLADTVMFLIVAL PFMMIPWHSSIQPFTIHPFNWNF G |
| 13469 | 43837 | A | 13549 | 2 | 118 | |
| 13470 | 43838 | A | 13550 | 397 | 729 | THGIRIGDFFCFTKRKLKRPVL* PDKEGNEIWVDMYTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRRG QSEYFSIFSNDLADTVMFL |
| 13471 | 43839 | A | 13551 | 147 | 417 | SSSWGRSSPQLVCGIFQTAGPQS LCKWNQ*VLAQTNKKTAGTSA DLYVPV*QL*RKAVVLPTNAP WRFWRTRQEWFSRGRSGYQS QET |
| 13472 | 43840 | A | 13552 | 1 | 2418 | |
| 13473 | 43841 | B | 13553 | 1 | 1848 | |
| 13474 | 43842 | A | 13554 | 188 | 490 | EWRNVCVGTGTEKVTPSAAAA ATASPIQVLTVLSVTSQIRAFSV LPVRRLLRRSMLSRLNTCVNRF CNPIKKGMRYGILICPL*SLLDGL CARLINQKDS |
| 13475 | 43843 | A | 13555 | 83 | 440 | SLLFKCSGVIVLRRPLGYRQVM NVTRRCLLRTHWMISSLLFY*L VNRHRRSVVEEYLVSYTLPMGV AVVKLLHLPKNFVSLITPRGRL EKERAFLFQHMRISITGLKIFV MHTSCPMVVC |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13476 | 43844 | A | 13556 | 1337 | 2583 | QQR*MCQNLMT*HQNQRSGR SQNDF*RRRNISERSAVYR*R QLYIRRPYAERPS\HVEDKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFFRKESQKLQQ SAKKRDAELANGALGIIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEVTYK VFALDVAARHRIRKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLIPFFIGLQNR TQFRLSETKEITNPYAMRV TNP CVSIVCVNEINSRTPMRLSYIEK KKGRQTTHIVFSFRDITSMTTG |
| 13477 | 43845 | B | 13557 | 1 | 696 | |
| 13478 | 43846 | A | 13558 | 326 | 1577 | SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRF*ADHEA YRKTA VRRCSQTTQQAWEQSA HQQHIRH |
| 13479 | 43847 | B | 13559 | 1 | 3822 | |
| 13480 | 43848 | A | 13560 | 848 | 1476 | VNVTSFGSRPICSTSPVLFSGL* GPVKEFDT*PSM*ISFELIPSIVIF EPRESVNKYHLPFILKTFARSISS VTVFEVISGFITFFNV*SLFNMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFEYKVFMAFVFN VV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV |
| 13481 | 43849 | A | 13561 | 1 | 2196 | |
| 13482 | 43850 | A | 13562 | 326 | 3746 | SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRS*ADHEA YRKTA VRRCSQTTQQAWEQSA HQQHIRH*SCRYPS*ARCQ*LTG QIVHRGEKKEQQLI |
| 13483 | 43851 | A | 13563 | 3802 | 4075 | IRCFTYSPAGYFPRFRAVILLC NGDSLRFMTSVYALQEAAAE VRHTLVTLRQLVTL YDPVDFQ RDDA*AIRAYDTDTGIRINAWH TDW |
| 13484 | 43852 | A | 13564 | 1708 | 3198 | |
| 13485 | 43853 | A | 13565 | 1 | 1401 | |
| 13486 | 43854 | A | 13566 | 1214 | 1357 | NKINMFIAALFTIAKTWNQPK\ CPTMIDWIKKRGSSRVASSSPT RTR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13487 | 43855 | A | 13567 | 3363 | 3852 | SHPFFSTDWSSDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMSRWLHYPDWVT IIAQQVLMNVVSVMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLFFLTPVNYLPG QGFAGFRNPPSNRIFACWGKPA WTACCNSLRARR |
| 13488 | 43856 | B | 13568 | 350 | 742 | |
| 13489 | 43857 | A | 13569 | 248 | 599 | HRDSYKRMA YGLVISVVSLSR KLRKPVL*PDKEGNEIWVDMY TVKPSGWTVRTFDKPRKRFI FIAGILFRAIKNHFLPRETLQCLP YILTGFRRGQSEYFSIFSNDLA DTVMFL |
| 13490 | 43858 | B | 13570 | 1 | 2148 | |
| 13491 | 43859 | A | 13571 | 3064 | 5069 | RSDPDENCC*TGH*STLFNWC WRNALSIEWPVCNEIFYRLIKPR WEIRWGKRAPVIPKHTLNTQPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSFLTGTGQTP AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGELDDEQMAA LSRLGNDYRPTSAYERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSHPRQ APCMKSNNALIVILGTVTLDAV GIGLVMPDLALKGLRVLLVEG NDPQGTASMYHGWPDLHIHA EDTLLPFYLGEKDDVITYAIKPT CWPGLDIIPSCALHRIETELMG KFDEGKLPTDPHMLRLAIETV AHDYDVIVIDSAPNLGIGTINVV CAAHALIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEADV RILLTKYSNSNGSQSPWIEEQIS DAWGSMVLKNVHAIVTGDAV GMDDIPQEARQYRHNQAYAYS IQGDGAEDDDERIVRFHTRVTV DSDTLASDAARLTCRHGLGNQ RNGGVLIEDKFECFFSLTAVFA TRAYYAVYHLTGARHSDIVVA HGYAGCNVRFVALLGTNTTLE TYLSNQGSNGFSCLHFGEDVGG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 13492 | 43860 | A | 13572 | 1408 | 5578 | CSHLLIIQLANQNTIITFGKCSSF TTATPIGNFYDTRYSSTERRCLL TSQ*KRRDEIIQCVLSKQL\RAR SLPDPTRKVFSTLSPRSTFRVNF TSRPHTGKVWAFREPFLPPHL RKPDTDTGYLYKRMA YGSVIS/ ICFTKPKLRKPVL*PDKEGNEIW VDMYTVKPSGWTVRTFDKPRK RFIAFFIAGILFRAIKNHFLPRET LQCLPYILTGFRRGQSEYFSIFS NMDLADTVMFL |
| 13493 | 43861 | A | 13573 | 2678 | 2884 | SAPLQRNTARRFLLFLKACSNR FCYR\WRHMTAIPSYNRSKLREI KGGLYHMGIFRRFLASKETPTF CY |
| 13494 | 43862 | B | 13574 | 1 | 7903 | |
| 13495 | 43863 | A | 13575 | 1 | 880 | |
| 13496 | 43864 | A | 13576 | 1 | 996 | |
| 13497 | 43865 | A | 13577 | 763 | 778 | NRCEPPV*GTRFSQQLLLALKA TLLEELYALT VHSWRPKW |
| 13498 | 43866 | A | 13578 | 2 | 254 | |
| 13499 | 43867 | A | 13579 | 1 | 2358 | |
| 13500 | 43868 | A | 13580 | 206 | 382 | |
| 13501 | 43869 | C | 13581 | 1 | 1137 | |
| 13502 | 43870 | A | 13582 | 79 | 906 | |
| 13503 | 43871 | A | 13583 | 2 | 383 | SPPEVVRLGYHPPRHGHQ\HLF ASCRKGDVGRVRP*TRDPGSD LLPAQVPAGAARRGGTMPACV GTRSWYSTFWPMEPAARPTPS MVSAASMGH*VTPSAGLYAITS RSRLPAGGGITMTTSCSGF |
| 13504 | 43872 | A | 13584 | 1 | 1092 | |
| 13505 | 43873 | A | 13585 | 173 | 262 | |
| 13506 | 43874 | A | 13586 | 898 | 1391 | QLGILRVNLLGIDLRVTGHQAA PPLHLLDLLQMH/SSPPCRPQ*A TSSPPSLRCRAPH R*SLAAP*A PPRP SLSAGSPHRKGP GPAPT GSWSSGNQAGLPCCLGWASVF LCPSHLPPPHLPQSSASLAFHRV KHLIHLHNSVIDKMKYQLKFLC LLGEYLSV |
| 13507 | 43875 | A | 13587 | 1 | 960 | |
| 13508 | 43876 | A | 13588 | 1318 | 1369 | RDFHPK*HTIGIQYIWQQLEINQ CDTSLSMVLP\R*RD FHPKSHLL PGAAQIQ |
| 13509 | 43877 | A | 13589 | 212 | 385 | |
| 13510 | 43878 | A | 13590 | 377 | 505 | |
| 13511 | 43879 | A | 13591 | 69 | 193 | CSLRSLAQMLPFYPRRSLCLSCS L**PHCCLWLAALRSESK |
| 13512 | 43880 | A | 13592 | 1 | 230 | |
| 13513 | 43881 | A | 13593 | 2 | 341 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13514 | 43882 | A | 13594 | 1 | 2421 | |
| 13515 | 43883 | A | 13595 | 1 | 623 | |
| 13516 | 43884 | A | 13596 | 1 | 906 | |
| 13517 | 43885 | A | 13597 | 1 | 568 | |
| 13518 | 43886 | A | 13598 | 107 | 199 | |
| 13519 | 43887 | A | 13599 | 42 | 328 | GGASGVCSF*CSE/LSSFWWVR GLAGSGVKLQTFATQEPSWLH PVDPVPGQLQVELPASPAPCART PQPLGGRWDSAPWSRGRSSG AHGIDVALLP |
| 13520 | 43888 | A | 13600 | 5 | 124 | IWILWFFVSLT*RSRGPSQ*VLQ LIKAPHVDLLVVTFCG |
| 13521 | 43889 | A | 13601 | 827 | 973 | IHQSAICI*LKFYTSLTHPVISLV VETLVWW*YLMK*KKLWSWI RGRG |
| 13522 | 43890 | A | 13602 | 2 | 503 | |
| 13523 | 43891 | A | 13603 | 56 | 792 | |
| 13524 | 43892 | A | 13604 | 1 | 411 | |
| 13525 | 43893 | A | 13605 | 1 | 1554 | |
| 13526 | 43894 | A | 13606 | 1 | 363 | |
| 13527 | 43895 | A | 13607 | 1 | 966 | |
| 13528 | 43896 | A | 13608 | 932 | 1189 | |
| 13529 | 43897 | A | 13609 | 146 | 323 | |
| 13530 | 43898 | A | 13610 | 1 | 1827 | |
| 13531 | 43899 | A | 13611 | 2 | 412 | |
| 13532 | 43900 | A | 13612 | 1 | 2238 | |
| 13533 | 43901 | A | 13613 | 2 | 411 | GATDCVCYYTVGFNDTKTSAL HMVVGDSLAMDVSSVHHNSTL LRYSVTLLGYGFYGDIIKDSK KRRLGLARYDFLCIKTFFSHH* YEGTVTFLPAQHTVGSPDRKP CRAGCFVCRQSKQQLLEEQKT ALYGLEL |
| 13534 | 43902 | A | 13614 | 3 | 2185 | |
| 13535 | 43903 | A | 13615 | 206 | 1568 | |
| 13536 | 43904 | A | 13616 | 165 | 417 | TWDYIRPNE*YM*MAKKKMP MD\VWCNGKNWRPAG\EFVDD GTETHFSIGNHDCYIKA VSSGK RKEGIIHTLIVDNREIPEIAS |
| 13537 | 43905 | A | 13617 | 463 | 837 | |
| 13538 | 43906 | A | 13618 | 1 | 765 | |
| 13539 | 43907 | A | 13619 | 3 | 510 | AGVHKIEFEHGTTSGRVVYV DGKEEIRKEWMFKLVGKETFY VGA AKTKATINIDAISGFAYEY TLEINGKSLKKYMEDRSKTTNT WVLHMDGENFRIVLEKDAMD VWCH\GKKIRRPAGEFVDDGTE TPLQYPGPMTCYIKA VSSG\KR KEGIIHTLIVDNREIPEIAS |
| 13540 | 43908 | A | 13620 | 342 | 585 | |
| 13541 | 43909 | A | 13621 | 1 | 1119 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13542 | 43910 | B | 13622 | 48 | 1104 | |
| 13543 | 43911 | A | 13623 | 656 | 916 | GWRKYLQGAADMGIAEGGGS VWSSWASSSLISVPVR*LCESTQ RSAPGWPLTGGSCSESVALWL CVNDFEFQMRLMPSRDSEPAC |
| 13544 | 43912 | A | 13624 | 179 | 682 | |
| 13545 | 43913 | A | 13625 | 1 | 7511 | |
| 13546 | 43914 | A | 13626 | 56 | 8669 | |
| 13547 | 43915 | A | 13627 | 42 | 8716 | |
| 13548 | 43916 | A | 13628 | 1 | 2457 | |
| 13549 | 43917 | A | 13629 | 3 | 571 | |
| 13550 | 43918 | A | 13630 | 1 | 867 | |
| 13551 | 43919 | A | 13631 | 1 | 2238 | |
| 13552 | 43920 | A | 13632 | 171 | 396 | |
| 13553 | 43921 | A | 13633 | 1 | 3940 | |
| 13554 | 43922 | A | 13634 | 554 | 619 | |
| 13555 | 43923 | A | 13635 | 1 | 1359 | |
| 13556 | 43924 | C | 13636 | 208 | 359 | |
| 13557 | 43925 | A | 13637 | 2 | 513 | PSHDHSLGTRASGKVIHGEH AAVHGKVALAVSLNLRNFLRL QPHSNGKGDLSLPNIGIKRAW VARLQSLDTSFL/RWTKEDLELI NKWAFQGERMIHGNPSGVDNA VSTWGGALRYHQKISSLKRSP ALQILLTSTRG\PRNIRALVGGG RNRLALEVPDMGGPILLSW |
| 13558 | 43926 | A | 13638 | 3 | 1331 | RVDDFVGELLRLRRGGAADVE AAAAAGFPGAMLSQVLLVSAP GKVILHGEHAVVHGKVALAVS LNLRTFLRLQPHSNGKVDNLNLP NIGIMRAWVARLHSLDTSFLG ECKEEKPEQGDVTTPTSEQVEK LKEVAGLPDDCAVTERLAVLA FLYL\LSICRKQRALPSL\DIVV WSELPPGAG\LGSSAAYSVCLA AALLTVCEEIPNPLKDGDCVN RWTKED\LELINK\WAFQGER MIHGNP\SGVDNAVQHLGEGA LRLPSRGRFSFL*RGSPVFQI/LG LTNTKVPSAITRALVAGVRNRL LKFPEIVAPLLTSIDAI\LECERV LGEMGEAPAPEQYLVLEELIDM NQHHLNALGVGHASLDQLCQV TRARGLHSLTGAGGGGCGITL LKPGLAQPEVEATKQALTSCGF DCLETSIGAPGVSIHSATSLDSR |
| 13559 | 43927 | A | 13639 | 1 | 950 | |
| 13560 | 43928 | A | 13640 | 1 | 1653 | |
| 13561 | 43929 | A | 13641 | 1 | 2601 | |
| 13562 | 43930 | A | 13642 | 2 | 513 | |
| 13563 | 43931 | A | 13643 | 47 | 367 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 13564 | 43932 | A | 13644 | 1 | 633 | |
| 13565 | 43933 | B | 13645 | 1 | 1110 | |
| 13566 | 43934 | A | 13646 | 172 | 1095 | |
| 13567 | 43935 | A | 13647 | 1 | 855 | |
| 13568 | 43936 | A | 13648 | 3 | 440 | |
| 13569 | 43937 | A | 13649 | 2 | 230 | |
| 13570 | 43938 | A | 13650 | 2 | 606 | AEFDLCCSPCRRRLGREEAGE EPTSPVTQYLQPRSPEECKMFA CAKLA\CTP\SLIRAGSRVAYRPI SASVLSRPEASRTGEGSTVFNG A\QNGVSQLIPKGSFKTSAISKK TLDTAAKFIG\AGAGNS*GVG WFLVAGIG\TVFWASLIHWVM ARKPFRWKQQLFSY\AILGICL VLKAMGSPFVLMVAFLILFAHV TEITA |
| 13571 | 43939 | A | 13651 | 200 | 2320 | |
| 13572 | 43940 | A | 13652 | 224 | 640 | |
| 13573 | 43941 | A | 13653 | 1 | 357 | |
| 13574 | 43942 | A | 13654 | 43 | 183 | |
| 13575 | 43943 | A | 13655 | 3 | 478 | SSAGREPDPDDLPRRLCFTHRLP AARRWVQLCVHASPEPGGQGV CPGRSERMVIRVFIASSGFVAI KKKQQDVVRFLANKIEFEEVD ITMSEEQRQWMYKNVPPDKKP TQGNPLPPQIF\NGDRYCGDYD RLFESKESNTVFSFLGLKPRLAS KAEP |
| 13576 | 43944 | A | 13656 | 2 | 428 | CRDGKDVVSLVRATVWALSKR KLQPTRA/ALTPTPSAVNLIKQF LKDKPELVDVKVGVTRGCGNG LSYTV EYTKTKGNSDEVIQDEA RVFIEKKAQLTPLGTEM DYVED KLSSE/FMFNNPT*TCGCGAPGK LVETLGLTEEIM |
| 13577 | 43945 | A | 13657 | 1 | 1377 | |
| 13578 | 43946 | A | 13658 | 1 | 1215 | |
| 13579 | 43947 | A | 13659 | 1 | 452 | REA EAADLRSEAPGRRDGEDV GFLSSGQLSGLCSKRKLQPTRA ALTPTPSAVNLIKQLLKE*P*AC RLKVGVRTRGCGNLSYTYEY TKTGDSDEEVIQDGV RVFIEK\K AQLTLL*TEM DYVEDKLSKGV GVH\SPNIKGTGCGGESFNI |
| 13580 | 43948 | A | 13660 | 3 | 763 | |
| 13581 | 43949 | A | 13661 | 1 | 306 | |
| 13582 | 43950 | A | 13662 | 738 | 1022 | GQHHPETKAWQRHNKKREF*T NILDEH*CKNPH*NTGKPNPAT HQKAYPP*SSGLHPWDARLVQ HTKINKCNPAYKQNQRQKPHD YLNRCRKGL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13583 | 43951 | A | 13663 | 2 | 516 | QKIDLPEYQGEPDEISIQKCQEA VRQVQGPVLVEDTCLCFNALG GLPGPYIK\WFLEKLKP\EGLHQ FLAGVEGKS\AYALCTFALSTG DPSQPVRLFRGRTSGRI\VAPRA CQDFGWD\PCFQPDGYEQTYAE MPKAEKNA\SHRFRA\LLELQ EYFGKFGQLDFCKLEAGPFR |
| 13584 | 43952 | A | 13664 | 7 | 227 | |
| 13585 | 43953 | A | 13665 | 1 | 415 | |
| 13586 | 43954 | A | 13666 | 234 | 510 | |
| 13587 | 43955 | A | 13667 | 2 | 402 | |
| 13588 | 43956 | B | 13668 | 530 | 1544 | |
| 13589 | 43957 | A | 13669 | 1 | 603 | |
| 13590 | 43958 | B | 13670 | 1 | 1527 | |
| 13591 | 43959 | A | 13671 | 1 | 1179 | |
| 13592 | 43960 | A | 13672 | 2 | 413 | |
| 13593 | 43961 | A | 13673 | 100 | 374 | KHISPALKALELPFERNLII/PLQ LLKVRILKEGEML/DI*HWFL** GMGTVQKGMPHKCYHGKTGR VYNVTQHAVGIVVNKQVK*VV |
| 13594 | 43962 | A | 13674 | 1 | 1035 | |
| 13595 | 43963 | A | 13675 | 2 | 564 | GPFGRNRHLPVIRQNDGPQRGK RRGTPKYVF*/RPFRK\HGGGPL GPPYM\RIYRKGDIVDIKGMG\ TVQNGMPHKCYHGKTGRVYN VTQHAV\GIVVNK\QVKGKILA K\RIINVRIEHI\KHSKSPR*ASLK/ RVLKENDQEKERSPKKKGTWG SNLKRHPAPPQKKHTL*RTNGK EPEL\LEPIPYEFHGHN |
| 13596 | 43964 | B | 13676 | 68 | 391 | |
| 13597 | 43965 | A | 13677 | 1 | 404 | PTRTWTRGRIPRLSAPPSRGAR GTMADPRVRQIKIKTG\VKRL V\KEKVL\YEKEPKQ\QEEKIEKM RAEDGENYDIKKQAEIL\QESR MMIPDCQRRLEAA\YLDLQRILE NEKDLE\EAEEYKEARLV\LDLV KLEA |
| 13598 | 43966 | A | 13678 | 1 | 436 | LLACRSMDCYLAIVHATRTL QQRHLVKFICLGLRNLFLLSL RILLFRRTFYPSNVSPVCYEDM GNNTANWWMLLRILPQSFGFIV PL/LIMLFCYRFTLHTLFKAHMG QKHWTMWVIFADVLIILLCWL PYNLVLLADTIMGT |
| 13599 | 43967 | A | 13679 | 1 | 705 | |
| 13600 | 43968 | A | 13680 | 292 | 1489 | |
| 13601 | 43969 | A | 13681 | 434 | 1205 | |
| 13602 | 43970 | A | 13682 | 1 | 390 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13603 | 43971 | A | 13683 | 21 | 479 | TYPEAWKLYYRSR*SRDLRKY HAHSVSP*QDQRYTS*KILKCD EHIQKLGSCITDPGNRETSGNT MHTVFHRDKTKDTHPESCCSSE KGGQPLPWFEHRKNVPQFAEP TETLFGPDSGKGAKSLVELLDE SECTSDEEIFISQDEIQSFMANN QSFYSNREQYRQHLKEKFNKY CRLNDHKRPICSGWVDNGWEA |
| 13604 | 43972 | B | 13684 | 32 | 438 | |
| 13605 | 43973 | A | 13685 | 533 | 1226 | |
| 13606 | 43974 | A | 13686 | 1 | 1566 | |
| 13607 | 43975 | A | 13687 | 215 | 453 | |
| 13608 | 43976 | A | 13688 | 1 | 553 | RRPARAAVIKQPPAPGASQHAA TPTQTPLCTPARPLPPMAHVQQ LEGRWRLVDS\KGF**NTMKE\K GVT\IALRKMGRNAQAQICIITS DG*NPSPLKTESTLK\T\TQFSCT/ LWGEKFEETTA\DGQKKLTNCL STFPDGA\ALVQHQEWDGERKS TITKKN*KDGEISWLECVMNM VTCTPDSMKK |
| 13609 | 43977 | C | 13689 | 11 | 106 | |
| 13610 | 43978 | A | 13690 | 3 | 155 | LCELQKAIDLFTDAIKLNPR LAI LYAKRASVFVKLQKPNAAIRD CDRAIEINPDSAQPYKWRGKAH R*ILAWPFCMPRGVPVSSSNYRS QMLPSETVTEPLK |
| 13611 | 43979 | A | 13691 | 1 | 1732 | |
| 13612 | 43980 | B | 13692 | 95 | 1715 | |
| 13613 | 43981 | A | 13693 | 1 | 446 | |
| 13614 | 43982 | A | 13694 | 1 | 786 | |
| 13615 | 43983 | A | 13695 | 88 | 828 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13616 | 43984 | A | 13696 | 157 | 1515 | RREKMAELKYISGFGNECSSED PRCPGSLPEGQNNPQVCPYNLY AEQLSGSAFTCPRSTNKRSWLY RILPSVSHKPFESIDEGHVTHNW DEVDPDPNQLRWKPFEPKASQ KKVDFVSGLHTLCGAGDIKSN NGLAIHIFLCNTSMENRCFYNS DGDFLIVPQKGNLLIYTEFGKM LVQPNEICVIQRGMRFSDIVFEE TRGYILEVYGVHFEPLDLGPIG ANGLANPRDFLIPIAWYEDRQV PGGYTVINKYQGKLFAAKQDV SPFNVVAWHGNYTPYKYNLKI NFMVINSVAFDHADPSIFTVLT AKSVRPGVAIADFVIFPPRWGV ADKTSGPPYYHRINCMKRFME LIRGQFEQKQGWFPLPGRG/SL HSTMTPHGPADADCFEKASKVK LALKRIADGTMA\FMF*SSFNLA GPKWGLQAPRVLDKNYPKCW EPLKSPF\TPNSRNPAPEN |
| 13617 | 43985 | A | 13697 | 1 | 156 | |
| 13618 | 43986 | A | 13698 | 8 | 306 | |
| 13619 | 43987 | C | 13699 | 1 | 1143 | |
| 13620 | 43988 | A | 13700 | 1 | 1551 | MRKDSCASSMHQQVSRSKKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSSLGADAI AKQRKTSVSAAASVSATIPIRR VQGPTVVGSWARGVSAAASGP RGTGPKGKARSEKGCSLSHGPQ TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSH LIHVRVYAEAITGRRTAPEDKGS LGRDMLAKAGAIHYMNMGKNL PIWCHLLEGIYLEVWALEGQF GRAKNACPVQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPIILGVQKP NGQWSLVQDLRLISEAVIPLYP VVPNPYTLLSQIPEEAEWFPVL DLKDFAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPQGFR DSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLATSSEASCQQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYLGLILARGTRTLGK ERIQPILAYPHPKTLKQLWGFL QIT/GFCQLWIPR*SKI |
| 13621 | 43989 | A | 13701 | 188 | 688 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13622 | 43990 | A | 13702 | 636 | 2628 | SNDRTEDDCGKHPPFMSSPPATEP WVCLIEGQEIDFLDGTTFVS LIPCLGRLLSSRSVTIQGILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTLLGRDILAKAGAIISM KTGNKLPICCPILLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLLSQVPPEAEW FTVLDLKD |
| 13623 | 43991 | B | 13703 | 302 | 619 | |
| 13624 | 43992 | A | 13704 | 1 | 5172 | |
| 13625 | 43993 | A | 13705 | 1 | 2091 | |
| 13626 | 43994 | A | 13706 | 1 | 1754 | GPRGTGPKGKARSEKGCSSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRRTAPEDK GSLGRDMLAKAGAIIMNMGN KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPILGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAWEFP VLDLKDAFFCIPLHYDSHDSQF LFAFEDPTDHTSQLIWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSSEASCQ QATLDLLNFLANQGYKASRSK AQLCLQQVKYLGLILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIARPLYT LIKETQRANTHLVEWESEAETA FKTLKQALVQAPGLSLPTGQNF SLYVTERAGIALGVLTQTRGTT PQPVAHLSKETDVVAKGWPHC LRVVAAVAVLVSEAIKIIQGKD LIVWTTHEVNGILG/AKGSLWL SDKRLFRYQALCLEGLVLQIRT SCGSHLAVTRLWALYF |
| 13627 | 43995 | A | 13707 | 2 | 887 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13628 | 43996 | A | 13708 | 3 | 1750 | GWAVPRPGPRGLTVATEAAAA AAAAAAAAAISSRTRAPQAPEGR NRRLEKMADDIDIEAMLEAPY KKDENKLSSANGHEERSKKRK KSKSRSRHERKRSKSKERKRS RDRERKKSKSRERKRSRSKERR RSRSRSRDRFRGRYRSPYSGP KFNSAIRGKIGLPHSIKLSRRRS RSKSPFRKDKSPVREPIDNLTPE ERDARTVFCMQLAARIRPRDLE EFFSTVGKVRDVRMISDRNSRR SKGIAYVEFVDVSSVPLAIGLTG QRVLGVPPIVQASQAEK\NRAA AMANNLQKGSAGPMRLYVGSS HFNITEDMLRGIFEPFGRIESIQL MMDSETGRSKGYGFITFSDSEC AKKALEQLNGFELAGRPMKVG HVTERTDASSASSFLDSDELER TG\IDLGTTGRLQLMARLAEG TGLQIPPAAQQALQMSGSLAF GAVGRNLFCYRFAKQDFSHQT ETSALSAAAS\VQPLATQCFQLS NMFNPQTEKEVGWDTEIKDDV IEECNKHGGVIHIYVDKNSAQG NVYVKCPSIAEAI\AAVNALHGR WFAGKMITAAYVPLPTYHNLF PDSMTATQLLVPSRR |
| 13629 | 43997 | A | 13709 | 141 | 343 | LHEGLLP*RGHALLSGALHG*C VGSCLFSTPRCLTSSTACGYPSS CTPGSCTAWCPSASRRLSCWT |
| 13630 | 43998 | A | 13710 | 5 | 426 | |
| 13631 | 43999 | A | 13711 | 1 | 1188 | |
| 13632 | 44000 | A | 13712 | 2 | 264 | NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEEDP NCHEQHLSNTATHLGTDQEAVI DGRRKPEESRTTSHICRCRS |
| 13633 | 44001 | A | 13713 | 1 | 700 | |
| 13634 | 44002 | A | 13714 | 3 | 483 | |
| 13635 | 44003 | A | 13715 | 2 | 361 | RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNSLKIIISNA SCTTNCLA/PPASTGAAKAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA |
| 13636 | 44004 | A | 13716 | 2 | 249 | SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13637 | 44005 | A | 13717 | 1 | 1079 | GTRRQSAASSFASPAEPHRSDT MGKVKVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQER\YPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPSADAPM FVMGVNHEKYDNSLKIISNAIS CTTNCLT\PLAKVIHDNFGIVEG LMTTVHAITATQKTVDGPGSKL WRDGRGALQNIIPASTGAAKA VGKVIPEL\NGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVKQA\SEGPLKGILGYTEH QVVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE |
| 13638 | 44006 | A | 13718 | 3 | 483 | |
| 13639 | 44007 | A | 13719 | 2 | 361 | RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNSLKIISNA SCTTNCLA/PPASTGAAKAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA |
| 13640 | 44008 | A | 13720 | 2 | 249 | SADAPMFDMGVNHEKYDNSL NII/SVMKAGPVEKRPAWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV |
| 13641 | 44009 | A | 13721 | 1 | 1079 | GTRRQSAASSFASPAEPHRSDT MGKVKVGVNGFGRIGRLVTRA AFNSGKVDIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQER\YPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPSADAPM FVMGVNHEKYDNSLKIISNAIS CTTNCLT\PLAKVIHDNFGIVEG LMTTVHAITATQKTVDGPGSKL WRDGRGALQNIIPASTGAAKA VGKVIPEL\NGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVKQA\SEGPLKGILGYTEH QVVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE |
| 13642 | 44010 | C | 13722 | 40 | 243 | |
| 13643 | 44011 | A | 13723 | 2 | 2972 | |
| 13644 | 44012 | A | 13724 | 1 | 602 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 13645 | 44013 | A | 13725 | 1 | 325 | MGRNQSRKAENTKNESASSPP KDRNSSPVREQSWTENEFDELT EVGFRKL VITNFSELKEHVLTD HKEAKNLEKS\LEV VAREISQE KEIKVFN*EKRKSNCPCLQMT |
| 13646 | 44014 | A | 13726 | 1 | 981 | |
| 13647 | 44015 | A | 13727 | 1 | 739 | MGRNQSRKAENSKNQSTSSPPK DCSSSPAREQNWTKNEFDELTE VGFRSLIANFSKLKECVLTHR KEAKNLEKSDRENGTKLENTL QDIIQENFPNLARQANIQIQEIQ RIPQRYSLRRATPRHIIVRFTKV EMKEKMSRAAREKGRVTHKG KPIRLTADLSAENLQARREWGP VFNIK\NFQPRIPYPAKLSFISG GEIKSFTDKQMLRDFFTTTRPAL QELLKEALNMERNNQYKPLQK HAKW |
| 13648 | 44016 | A | 13728 | 1 | 1277 | MKEQNGGGGREEDHKDKGIRQ LPSLLPSAGEAKSDKPEHHNRY RKEIASFEDEKRAMGVAKMAE QEQLQSAAPSMTNAEVGTAHG GRAEAGRGVDS PGKRKVLGDF PFLAKGSRDRLPGKAGHSLPKY YAFTKVLATGRQERN SINISKK VIYTKTTSTGHQHQRPKIDKTT KMGRNQSRKAENSKNESTSSPP KGHSSSPATEQSGTENDFDELT EVGFRRSVTTNFYELKEDVQTH RKEAKNLEKRLDKWLTRINSV EKTLSDMELKTMARELRDTC SSFKSRFNQVEERVSVIEDPIYE LSREDKVRDKKVRNKQSLQEI WDYVKRPNLRVIGVPESDGEN GTKLENMLQDIIQENFPNLARQ ANIQIQEIQRTQRYSSRRATPR HIIVRFTKVEMKQKVLRAAREK GPVTHKGNSGSL |
| 13649 | 44017 | A | 13729 | 1 | 1584 | |
| 13650 | 44018 | A | 13730 | 493 | 575 | SHLPMNPANTRSQRNPTKKKQ KKNVC/DNIRELEQQMEDAYR GTKRKMLPSSSSRMRS DGFDEE SQRYYWRPKNEISGTLEDDFLK AKSWNRKFYDYEANMPDRWG\ QVAIKSYTLKNLKQTVVISKILP TGRKHLPR*SHLPMNPANTRSQ RNPTKKKQKKNVCG |
| 13651 | 44019 | A | 13731 | 1 | 655 | |
| 13652 | 44020 | A | 13732 | 2 | 1664 | |
| 13653 | 44021 | A | 13733 | 1 | 2364 | |
| 13654 | 44022 | A | 13734 | 1 | 224 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13655 | 44023 | A | 13735 | 1033 | 7511 | |
| 13656 | 44024 | A | 13736 | 56 | 8669 | |
| 13657 | 44025 | A | 13737 | 42 | 8716 | |
| 13658 | 44026 | A | 13738 | 1 | 5046 | |
| 13659 | 44027 | A | 13739 | 1 | 2298 | |
| 13660 | 44028 | A | 13740 | 1 | 2362 | |
| 13661 | 44029 | A | 13741 | 1 | 2046 | |
| 13662 | 44030 | A | 13742 | 1 | 1503 | |
| 13663 | 44031 | A | 13743 | 1 | 813 | |
| 13664 | 44032 | A | 13744 | 185 | 735 | |
| 13665 | 44033 | B | 13745 | 317 | 910 | |
| 13666 | 44034 | A | 13746 | 1 | 867 | |
| 13667 | 44035 | B | 13747 | 1 | 2325 | |
| 13668 | 44036 | A | 13748 | 1 | 430 | |
| 13669 | 44037 | A | 13749 | 1 | 867 | |
| 13670 | 44038 | A | 13750 | 35 | 518 | CLSRRASPVYLASMSGRGKTG GKARAKAKSRSSRAGLQFPVG RVHRLLRKGHYAERVGAGAPV YLAA\LEVAQPLRVLELAGN AA\RSN\KKTRIIPRHLQLAIRND EEL*KLPGLP*RIAQGSR/VLPNI QA\VLLPK\KTSATVG\PKAPSG GKKATQASQEY |
| 13671 | 44039 | A | 13751 | 1 | 937 | |
| 13672 | 44040 | A | 13752 | 1 | 1096 | |
| 13673 | 44041 | A | 13753 | 85 | 1512 | |
| 13674 | 44042 | A | 13754 | 3 | 2377 | |
| 13675 | 44043 | A | 13755 | 1 | 1134 | |
| 13676 | 44044 | A | 13756 | 49 | 408 | |
| 13677 | 44045 | A | 13757 | 47 | 2603 | |
| 13678 | 44046 | A | 13758 | 1 | 378 | |
| 13679 | 44047 | A | 13759 | 1 | 696 | |
| 13680 | 44048 | A | 13760 | 3 | 401 | |
| 13681 | 44049 | A | 13761 | 882 | 1106 | KLHPYTTRQYCHFRI*TDVMAK RSRNAVKGLSALVWCALSDFA AGFTPDDGCTRATFTTGGWRK RDCRGAVAGG |
| 13682 | 44050 | A | 13762 | 688 | 1100 | |
| 13683 | 44051 | A | 13763 | 476 | 552 | |
| 13684 | 44052 | B | 13764 | 178 | 1107 | |
| 13685 | 44053 | A | 13765 | 1 | 198 | |
| 13686 | 44054 | B | 13766 | 94 | 625 | |
| 13687 | 44055 | A | 13767 | 1 | 732 | |
| 13688 | 44056 | A | 13768 | 1 | 4443 | |
| 13689 | 44057 | A | 13769 | 216 | 575 | PGAGDRYVGKPVSAAGVTAVSC GVWSSMPDATLIASYQAYTSH VGRIRRSRRJR/TNTARADYPAL TALPFNNFRTHNRFNFNAASVL ASIGIGSSLICAARISAHSGAEH KPREPKAANIK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 13690 | 44058 | A | 13770 | 1018 | 1489 | KLPGQRRFVQTPSHVLHTLSY PTAPAQSSYPAPLSPSQDRAPTL AHQTT*FSASYTANAQWQRVA ADHLKSVRETYAHVRQFSPAL GNAPPDQLPLS*ASCVPKSGAR YSSVIRQNRDRDFRATDHMYVT VPTNRPKMWNPVNTQMNSFRA DTCER |
| 13691 | 44059 | A | 13771 | 1013 | 1755 | GSPGLRPGGAAGKALAPSGCT GNSHRAPM*PGAQAQTRPEKW A*QRP/HVSTGARGARVRALAA VAAAEQAQAGAAVRAAALHT RAAVSAGAARAVVQVLAAR TREAGAAAAAQGVAQVQAES AIAAWLQAAPVHPLLTVGALE TGWAVADVGRVRVCTPDTQA AVEAGSICTCHPAHLTPQPVEP TRAGAFKGPGLTTAASIGTRV PVTGPRPRDKASGGSRRAPGA EAAAGGDRDRAEGSSPAL |
| 13692 | 44060 | A | 13772 | 1 | 1236 | |
| 13693 | 44061 | A | 13773 | 1 | 456 | |
| 13694 | 44062 | A | 13774 | 1 | 219 | |
| 13695 | 44063 | A | 13775 | 1707 | 1853 | |
| 13696 | 44064 | A | 13776 | 1 | 615 | QLATFFFGGGLPGGSAPWDPPG EACLWVLVRLPGRTVWVIQFV QLRSFFAPPFAHNGRASSGRVS VHYGIAQTAEWAAEICGVGAR KIRELAAIFHQNTIMHFANGG/N PTRRSVLSMQGSLPGGC\DA VDIHPVARIVEALENPGGAYQH NGMNRHFDPDIRFIWWAGGANF THHQDTNRLIRAWQNDYFRK GRIKAKMGPKLF |
| 13697 | 44065 | A | 13777 | 407 | 661 | ANWIKWRWHRAMHSSSSMWQ TANSLASFISAPVTSSSACRSTL PATRYWCI*WRSSAIWKWVILS GPVATRICTATIWIQLICN |
| 13698 | 44066 | A | 13778 | 1 | 2448 | |
| 13699 | 44067 | A | 13779 | 3 | 1612 | |
| 13700 | 44068 | A | 13780 | 1 | 1626 | |
| 13701 | 44069 | A | 13781 | 3 | 118 | |
| 13702 | 44070 | A | 13782 | 1175 | 1396 | |
| 13703 | 44071 | A | 13783 | 197 | 933 | |
| 13704 | 44072 | A | 13784 | 2 | 64 | IILLNSAPAWM*TFKLGPQVDV NYMLHTQNK |
| 13705 | 44073 | A | 13785 | 1 | 855 | |
| 13706 | 44074 | B | 13786 | 1 | 1605 | |
| 13707 | 44075 | A | 13787 | 1 | 588 | |
| 13708 | 44076 | A | 13788 | 1 | 2769 | |
| 13709 | 44077 | A | 13789 | 813 | 1341 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13710 | 44078 | B | 13790 | 1 | 999 | |
| 13711 | 44079 | A | 13791 | 1 | 281 | |
| 13712 | 44080 | A | 13792 | 1 | 1332 | |
| 13713 | 44081 | A | 13793 | 1 | 1384 | MPITLRRSVEKEQLIEIANTIMPF GKYKGRRLLIDLPEEYLLWFARK DEFPAEARYTHIDLHVPAPLL MFTLDTRQSACDRNPHLPIHVC SSWTSPKCAPRLWTRALLPRTR TPPYATGTTIGSRASWFVTFPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLIHKM VEVNACLKQLDNKDIADYEHN QLMRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSAVVEETR EAVDTSQPVAT |
| 13714 | 44082 | A | 13794 | 1 | 2004 | MTQQITLIKDKILSDNYFTLHNI TYDLTRKDGEVIRHKREYVDR GNGATILLYNTKKKTVVLRQF RVATWVNGNESGQLIESCAGL LDNDEPEVCIRKEAIEETGYEV GEVRKLFELYMSPGGVTELIHF FIAEYSDNQANARGGVEDEDI EVLELVQCGGQIGVPDVLAVF ATGIGFLAMSVTKPRINAQPYP MPWRNLAQLVEHINRTRIHRNL QFTDAFKRRLIDNICRKNNIIGT HTGQSKFSGQTQQIFGEIPQVVP ASELAAAMKQIKELQRLLGKK TMENELLKEAVEYGRAKKWIA HAPLLPGDGERTDDWMDGRRS RHTDDTDVLLRIHHVIGELPTY GYRRVWALLRRQAELDGMPI NAKRVRIMRQNALLERKPA VPPSKRAHTGRVAVKESNQRW CSDGFEFCCDNGERLRTVFALD CCDRLSSRGRNAAAKRQRDDP LRWKFRLPSSGGTKLLMPLDQQ APARFAPFVTCTLTILCGTGHV VYTILPIIYDVAIKNNIRPERPM AASSIGAQMGIASPVSVAVVSL VAMLGNVTFDGRHLEFLDLLAI TIPSTLIGILAIGIFSFRGKDLD KDEEFQKFISVPENREYVYGD ATLLDKKLPKSNWLAMWIFLG AIAVIALLGADSDLRSSF/GGKP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13715 | 44083 | A | 13795 | 3 | 918 | DKTRKRRIRQ*IPNATSFLYQNS PNDLSE*LIPAGTWFAGNAPASS CGFRDRYLIVCSHQTPHVPQQI TVAAPDARAQAILRIVRQLQRF FHRFEGGHRQHRAKNLLEHP HIVLTKQNRREFADALQPDPA WQQGTLSNGLQWQVLTTPQRP SDRVEIRLLVNTGSLAESTQQS GYSHAIPRIALTQSGGLDAAQA RSLWQQGIDPKRPMPPVIVSYD TTLFNLSLPNNRNDLLKEALSY LANATGKLTITPETINHALQSH DMVATLVFRYLKKGWWRYRL KGSTLLSHDPAHPLKQPVEAEK |
| 13716 | 44084 | A | 13796 | 1 | 1368 | MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIILTKTNPASISK NEVFRSGMIAIVAVYGIWMA ETMFAPACYGYIILPTYPDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVSCVFGWIFAAIKRDA AAGRAKENVIFHHFPQSVKAD IATNPFKRPGGAFIRITQTFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNVPLDSSVLSSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTEGAIPFAAADPLR/PSFGG KPLSMVLVIQMFMMLLTGALIIL TKTNPASISKNEVFRSGMIAIVA VYGIWMAETMFAPACYGYI LPTYPDLAAIQFDRSGTTHIGR FVINHSFILPGLIGVSVSCVFGWI FAAIKRDAAGRAKENVIFHHF PFQSVKADIATNPFKRPGGAFIR ITQTFRTVQTFRLSAYRLDFAG DRLRISTPRAKMRTAFKKDHLR QRRRCIRQRAPPARHNLVGA ALPATVAGVNFTFSNVPLDSSV LSSLLTDFSTAVGSIVMLAVIM GLMLAFDMGGPVNKVAYAFM LICVAQGVYTVVAIAAVGICIPP LGMGLATLIGRKNFSAEERETG |
| 13717 | 44085 | A | 13797 | 3 | 2185 | |
| 13718 | 44086 | A | 13798 | 1 | 920 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13719 | 44087 | A | 13799 | 251 | 479 | TQRVDWRSRSSISPGDGLHAFP AFGKEGGKMLDRLRERRDVKT LQQSGSAAGAEFALAGAHPTH GTTA*IQQAINV |
| 13720 | 44088 | A | 13800 | 1 | 939 | |
| 13721 | 44089 | A | 13801 | 1 | 386 | |
| 13722 | 44090 | A | 13802 | 3 | 524 | |
| 13723 | 44091 | A | 13803 | 1 | 548 | |
| 13724 | 44092 | B | 13804 | 67 | 1144 | |
| 13725 | 44093 | A | 13805 | 811 | 974 | VSRRIKLDVTEEFARAGDNKRC ICQ*RHGLAERDIARLLVEIVVI WCDIGVIA |
| 13726 | 44094 | A | 13806 | 1164 | 1262 | |
| 13727 | 44095 | A | 13807 | 2 | 894 | |
| 13728 | 44096 | A | 13808 | 1 | 1587 | MVKEGTFREDLFYRLNVIHLIL PPLRDRREDISLLANHFLOKFSS ENQRDIIDIDPMAMSLTASW PGNIRELSNVIERAVVMNSGPII FSEDLPPQIRQPVNAGEVKTA PVGERNLKEEIKRVEKRIIMEVL EQQEGNRTRTALMLGISRRAL MYKLQEYDATGFFRDGMTIMV GGFMGIGTPSRLVEALLESVGR DLTLIANDTAFVDTGIGPLIVNG RVRKVIASHIGTNPETGRRMISG EMDVVLVPQGTLEQIRCGGAG LGGFLNPTGVGTVVEERQTSID TSTRKRPFELGRPSRNNDKGIRP VDQALDRKNIRE/ALHDSLKRLQ TDYLDLYQVHWPLRPFYCFGK LGYSWTD SAPAVSQDLTDAL AEYQRAGKIRYIGVSNETAFGV MRYLHLADKHDLPRIVTIQNPY SLLNRSFEVGLAEVSQYEGVEL LAYSCLGFGTLTGKYLNGAKP AGARNTLFSRFTSYSGEQTQKA VAAYVDIARRHGLDPAQMALA FVRRQPFVASTL/LGATTMDQL |
| 13729 | 44097 | A | 13809 | 1 | 618 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13730 | 44098 | A | 13810 | 80 | 952 | RPGIVALNAILPLSRTRQSKPTR LKKRAIANCAPTWKKRFVALV YRTA*RFPSITLSVAVT*PASAK NKAIKMTQKIEQSQRQERVAA WNRRAECDLAAFQNSPKQTYQ AEKARDRKLKANLEEAIRRSGL QDGMTVSFHHAFRGDDLTVN MVMDVIAKMGFKNLTASSSL SDCHAPLVEHIRQGVVTRIYTS GLRGPLAEEISRAYCADSHHGP FAMVNNMTDLTAQEPAWQTR DHLDDPVIGELRNRFGPDAFTV QATRTGVPVWIKREQLLEV DFLKKLPKPYVMLFDLHGMDE RLRTHREGLPAADFSVFYHLISI DRNRDIMLKVALAENDLHVPT FTKLFPNANWYERETWDLFGIT FDGHPNLRWIP |
| 13731 | 44099 | A | 13811 | 92 | 735 | RLLRPLPQPRSSVLPGLTTFHAS STSETRQSKPTRLKKRAIANCA PTWKKRFVALVYRTA*RFPSIT LSVAVT*PCVNIITIGCQVKTVT TIATAQIQRFTRFNHFSRFQYFR NSPKQTYQAEKARDRKLKANL EEAIRRSGLQDGMTVSFHHAFR GGDLTVNMVMDVIAKMGFKN LTASSSLSDCHAPLVEHIRQGV VTRIYTSGLRGPLAEEISRGLL AEPVQIHSHGGRVHLVQNGEL NIDVAFLGVPSCEFGNANGYT GKACCGSLGYAIVDADNAKQV VMLTEELLPYTDNPEA |
| 13732 | 44100 | A | 13812 | 1 | 1113 | |
| 13733 | 44101 | A | 13813 | 5121 | 6228 | LRRDSGRLRSCWHPRSPTSMGS LGQREDLQDEDRNSGADPGQR GRCSIHLEGPGQQPCLQRAVQG EGDPVLAKKEIQDQCHPHGQV QLLLVPAAEPVRAVPPRVQPVL PHHHHPAELSGIREE*GNQNDA EN*TISTTRTGSGLESSR*M/SILP LSRTRQSKPTRLKKRAIANCAP TWKKRFVALVYRTA*RFPSITL SVAVT*PYWSGAPGGPCRRPYC HFRHRGARGSGAPGDGGEAPP AAAFLLGGDVGFGL |
| 13734 | 44102 | A | 13814 | 56 | 196 | CRGDGGKLIQCQRRMGI*PCG* LRQRKAELFQHLPLC*FWRPEI GTVCSGSIDNGSDRLRR |
| 13735 | 44103 | B | 13815 | 64 | 2373 | |
| 13736 | 44104 | A | 13816 | 3 | 403 | |
| 13737 | 44105 | B | 13817 | 55 | 1040 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13738 | 44106 | A | 13818 | 587 | 1533 | VLLTAKFFPSMYSPIKTAGGPA ST*VL*MIISIDAEKAFDKIHQPF MLKALNKSENKIPRNPTYNGCE GPLQGELQTTAQGNKRGYKQT QQHDMHMSTKNQYHENGHTA QGMKGITQPSAFIPTAESNSFQP QVKTLPSPIDAKQQLQRKIQKK QQEQKLQSPLPGESAACKSESA TSNGVTNLPNGNPSILSPQPIGIV VAAVPSPIPVQRTQRLVTSPSP MSSSDGKVLPLNVQSHQNCW WTRFNMSSLNVVKMTTISLTPS NSNTPLKHSASFISATGTTEESR SVPQIKNGSVVSLQSPGSRSSSA GGTSAVEVKVEPETSSDEHPVQ CQENSDEAKAPQTPSALLGQKS NTDGALQKPSNEGVEIKATKE RRSSPATEQSWMENVFEEQREE GFRRSNHSQIREDSQTKGKEEK RLKELMELKTKVRELREECRSL RSRCDQLEERVSAMDDDEMNE KREGNFREKRIKRNEQSLQEIW DYVKRPNLRLIGVPESDGENGT KLENTLQDIIQENFPNLARQANI QIQEIQRTP |
| 13739 | 44107 | A | 13819 | 590 | 817 | |
| 13740 | 44108 | A | 13820 | 107 | 410 | KGRNIQLNGPSSRVSLWRSLYF LNLNTGLPC*IGEVLLDNILQSV FQLGSILPITFRYTNQT*IWSFHI VPYFLEALLISFYSSFKLPFSLH FIHFIFHR |
| 13741 | 44109 | B | 13821 | 1 | 3735 | |
| 13742 | 44110 | A | 13822 | 922 | 1137 | HFFLHFNFGESDNYVSWSFSSR GVSLWRSLYFLNLNVGLPC*IG EVLLDNILQSVFQLGSILHITFR YTNQT |
| 13743 | 44111 | B | 13823 | 1 | 954 | |
| 13744 | 44112 | A | 13824 | 3 | 156 | |
| 13745 | 44113 | A | 13825 | 683 | 972 | SHRLLRLLHSSRSSPGLVSSSISS FKHFSVLVILFTLMIVSFAVQKL FSLIRSHLSILALVAIAFGVLVM KSLPTPMSSMVLRS/SFF*GFYGF FRSYI |
| 13746 | 44114 | C | 13826 | 1 | 895 | |
| 13747 | 44115 | C | 13827 | 372 | 1727 | |
| 13748 | 44116 | A | 13828 | 705 | 1072 | LALLVELIPLPLCNGLLCLF*SL LV*SLFYQRLGLQPLPFFVFHLL GRSSSILLF*AYV*LFWHDFAA AGTGCSFPCLALPSGALVGQA WW*QKSLSICLSVKDFISPSLM KLSLAGYEILG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13749 | 44117 | A | 13829 | 1 | 1136 | |
| 13750 | 44118 | A | 13830 | 547 | 675 | |
| 13751 | 44119 | B | 13831 | 144 | 1877 | |
| 13752 | 44120 | A | 13832 | 1 | 441 | |
| 13753 | 44121 | A | 13833 | 27 | 344 | |
| 13754 | 44122 | A | 13834 | 287 | 600 | GPGSLQSSPLLSPWPWRASSPLL LRPSVRGWHLGEP*NCFPSPLA AS/EQAPKRSS*PQCNHR*RETA ARGLAYPPDRPLPSMLSCESPE TPAKAGPGRERGCEKC |
| 13755 | 44123 | A | 13835 | 2 | 226 | |
| 13756 | 44124 | A | 13836 | 2 | 226 | |
| 13757 | 44125 | B | 13837 | 45 | 518 | |
| 13758 | 44126 | B | 13838 | 1 | 699 | |
| 13759 | 44127 | A | 13839 | 3 | 362 | |
| 13760 | 44128 | A | 13840 | 2 | 130 | |
| 13761 | 44129 | A | 13841 | 3 | 96 | |
| 13762 | 44130 | A | 13842 | 1 | 545 | |
| 13763 | 44131 | A | 13843 | 2 | 144 | |
| 13764 | 44132 | A | 13844 | 2 | 91 | |
| 13765 | 44133 | A | 13845 | 1 | 370 | |
| 13766 | 44134 | C | 13846 | 1 | 214 | |
| 13767 | 44135 | A | 13847 | 215 | 310 | |
| 13768 | 44136 | A | 13848 | 2 | 91 | |
| 13769 | 44137 | A | 13849 | 1 | 289 | |
| 13770 | 44138 | A | 13850 | 1 | 997 | |
| 13771 | 44139 | A | 13851 | 1 | 192 | |
| 13772 | 44140 | A | 13852 | 2 | 267 | |
| 13773 | 44141 | A | 13853 | 2 | 181 | |
| 13774 | 44142 | A | 13854 | 1 | 171 | MESYAAIKNDEFMSFVGTMK LETILSKLSQGQKTKHCMFSL TDVIARRRSWTSI |
| 13775 | 44143 | A | 13855 | 92 | 244 | KRRRRRGQIRKMKEEEGNRRT WMKLETIILSKL*QRQKTKHRM FLIGGN |
| 13776 | 44144 | A | 13856 | 146 | 382 | |
| 13777 | 44145 | B | 13857 | 124 | 1215 | |
| 13778 | 44146 | B | 13858 | 1 | 628 | |
| 13779 | 44147 | A | 13859 | 377 | 484 | |
| 13780 | 44148 | A | 13860 | 2 | 220 | WARTSCLKHQKQWQKPKLA NGI*LN*RASAQKKLPSEWTG TWMKLETIILSKLLQGQKTKHR MFLIGGN |
| 13781 | 44149 | A | 13861 | 965 | 1150 | GVDQRAVCSSRIW*SHLFLFHS VVVHLPWAGTWMKLETIILSK LSQGQKTRHRMFLIGGN |
| 13782 | 44150 | A | 13862 | 254 | 571 | YSYKLEIIIGKQPEIYRDP CYRP AV*SQTAVLAISEAPWA*DLPS QVSDTISWWTV C*AHWKSAVL GWE*PGFPGTWMKLETVSLSK LSQGQKTKHHMFLIGGN |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13783 | 44151 | A | 13863 | 62 | 214 | |
| 13784 | 44152 | A | 13864 | 274 | 435 | |
| 13785 | 44153 | A | 13865 | 1 | 294 | ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSL\YIYFFLDEFM YFAGTWMKLETIILSKLSQGQK TKHRMFSLVGGN |
| 13786 | 44154 | A | 13866 | 663 | 1266 | PPLTCQCSHLCVTLVGH/WIKLE TIILSKLSQGQKTKHRVFSLIGG AGALAKECMSLYPGCKITVFDI PEVVWTAKQHFSFQEEEQIDFQ EGDFFKDPLPEADLYILARVLH DWADGKCSHLLERIYHTCKPG GGILVIESLLDEDRRGPLLQLY SLNMLVQTEGQERTPTHYHML LSSAGFRDFQFKKTGAIYDAIL |
| 13787 | 44155 | A | 13867 | 1 | 681 | |
| 13788 | 44156 | A | 13868 | 1 | 247 | |
| 13789 | 44157 | A | 13869 | 2 | 178 | |
| 13790 | 44158 | B | 13870 | 1 | 2042 | |
| 13791 | 44159 | A | 13871 | 1 | 378 | |
| 13792 | 44160 | A | 13872 | 1 | 683 | |
| 13793 | 44161 | A | 13873 | 1 | 972 | |
| 13794 | 44162 | A | 13874 | 308 | 406 | |
| 13795 | 44163 | C | 13875 | 177 | 653 | |
| 13796 | 44164 | A | 13876 | 1 | 465 | |
| 13797 | 44165 | A | 13877 | 3 | 1175 | FFSSQAAALLVVLGSSHTLQRA RKHSAPGLPDTCALLQPPAASA AAAPSMSPGDVETPSAIQICRIM RPDDANVAGNVHGGTILKMIE EAGAIISTRHCNSQNGERCVA LARVERTDFLSPMCIGEVAVHS AEITYTSKHSVEVQVNVMS ENI LTGAKKLTNKATLWYVPLSLK NVDKVLVPPVVSQRQEEEE GRKRYEAQKLERMETKWRNG DIVQPVLNPEPNTVSYSQSSLIH LVGPSDCTLHGFVHGGVTM KLMDEVAGIVAARHCKTNIVTAS VDAINFHDKIRKGCVITISGRMT FT\SN\NSMRFKVLLDPAPV VDS FQKRYRGRQCLSST*VSL SQER QV/PLPVPQLVPETE DEKKRFE EGKGRYLQMK\AKR\Q GHAEPQ |
| 13798 | 44166 | A | 13878 | 121 | 361 | SLFELENRSKFSVATAGLVPSR RLSINCIRRAFITSSNGFPLWFCL HQKGPVDCCVAVY*CGTEDGS WAPTHPGVGPSLP |
| 13799 | 44167 | A | 13879 | 1 | 462 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13800 | 44168 | A | 13880 | 3 | 287 | PCSLSSDCCASNQRDSVGIGPSE PRVGYNILVIRFLSPSEKRSRIV GVTRFSSAWEPSQLAGILPISEP PSNRIFACWGKPAWTACCNSLR ARR |
| 13801 | 44169 | A | 13881 | 1 | 1332 | |
| 13802 | 44170 | A | 13882 | 1 | 753 | |
| 13803 | 44171 | A | 13883 | 1 | 516 | |
| 13804 | 44172 | A | 13884 | 71 | 277 | IYFNTQESFCPPRPLK/LCDGRG CHKGL*NAFKAFSPFSWPLALG SFLLMQISAACLNSFPENGLFFS TT |
| 13805 | 44173 | B | 13885 | 1 | 1095 | |
| 13806 | 44174 | A | 13886 | 1 | 741 | |
| 13807 | 44175 | A | 13887 | 264 | 2880 | WLLQKHKLHVSR*LGL\PDTSW ILPSRPDAGGRFPRTPPCVLVV HKPSRHCREWTANTVLPKGAL AKWLLEPKADLQGWHLPADG QYTKPSISYNIKLYINCYNRTVT TAAQHQQVQRKHGASIFLAEN VAVREKDKEERKVTRAPTEQA WTAGSWIETAYREIKGVGQES VCITVMHLEELVYELAWIIMSA VVEAFDPVAPSSKCRNLNPDPP YCCTPYTLHTSPPPPPSCCTPYT LHTGPPPQTPFCCTPYTLDTSPS PQTHSCCTPYTLHTVPTFHLPA AHPIHLHTIPPPQTQGQGFVSED EYLEISDIKRDQSGEYECSALND VAAPDVRKVKITVNYPPYISKA KNTGVSVGQKGILSCEASAVP MAEFQWFKEETRLATGLDGMR IENKGRMSTLTFFNVSEKDYG YTCVATNKLGN TNASITLYVD HIVGSKALLSKCKRTEITNYLS DHS AIKLELRIKNLTQNHSTTW KLNNPLLNDYWVHNEMKAEIK MFFETNKNKDDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKI DTLTSQLEKEKQEQTHSKANR RQEITKIRAELEIETQKTLOKI NESRSWFFERINKIDRLRLARLIK KKREKNQIDA IKNDKGDITTY TEIQT TIREYYKHL YANKLENL EEMDKFLD TYTL PRLNQEEVES QNRPITGSEIVAI NSLPTKKSPG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13808 | 44176 | A | 13888 | 1 | 629 | AMAGSPPPASLLPCNLISDCCAS NQRDSVGVGPSEPGVGYSLVV RRFLSPSEKRSIRVGVTRFSRCR PSPLSLTQKGNSLTSWASQVLT PAPEKQPDNKLPLPRGRSDPT EYFHGQEVDRDKSDEHVDHVSQ IHSFRDEVKRLGAEDSSNAETP TELHEFNTGGVYRPPNSTSVIQP LDQGVIRTFKPCYTKYSLEKIVS AVEENPDRT |
| 13809 | 44177 | A | 13889 | 1 | 1452 | |
| 13810 | 44178 | A | 13890 | 167 | 309 | |
| 13811 | 44179 | A | 13891 | 3 | 386 | SVGALQKQQGWHQRRCSLHF PSFLCVFSLAKSRRADHNQDPR ASRMAFSLTSSPLARSAASAVA AFGCGTSGNGRFSSVP*AYRQV FQRIAIAYGPLMRDR*AHPVK TPDAIDCRIRQPAIPRLQ |
| 13812 | 44180 | B | 13892 | 121 | 298 | |
| 13813 | 44181 | A | 13893 | 473 | 1826 | |
| 13814 | 44182 | A | 13894 | 1 | 270 | |
| 13815 | 44183 | A | 13895 | 3 | 3706 | |
| 13816 | 44184 | A | 13896 | 1 | 1464 | |
| 13817 | 44185 | B | 13897 | 591 | 729 | |
| 13818 | 44186 | A | 13898 | 1 | 1326 | |
| 13819 | 44187 | A | 13899 | 1 | 1152 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 13820 | 44188 | A | 13900 | 1 | 2524 | MREEFAHRWLRAGEKTPPDA LEKLTDPMLFAAAMVSAGKAD VCIAGNLSSTANVLRAGLRIIGL QPGCKTLSSIFLMLPQYSGPAL GFADCSVVPQPTAAQLADIALA SAETWRAITGEEPRVAMLSFSS NGSARHPCVANVQQATEIVRE RAPKLVVDGELQFDAAFVPEV AAQKAPASPLQGKANVMVFP LEAGNIGYKIAQRLGGYRAVGP LIQGLAAPMHDLSPCIAATDAG SAAAQRIGDLVSVHVIPRPHVD LEQVFPIGLKAYTATCNHPVSL RFTIKSSSDRIKLSNQTLSKLN FIMRFYCFSLCLSLSAFYHCRGV IVNIQAVFWLQKGTEAADILTT CAQLWIMMYALLSVFSLLDVIL NLAQKFPAASQLPLKGIFQGIKL IGAILVGILMISLLIGQSPAILISG LGAMAAVLMLVFKDPILGLVA VRNWDNTITTIPTWSLVSDSK NWSGMSASGGRIKRSISIDVTS IRFLDEDEMQRNLKAHLLKPYL TSRHQEINEWNRQQGSTESVLN LRRMTNIGTFRAYLNEYLRNHP RIRKDMTLMVRQLAPGDNGLP LEIYAFTNTVVWLEYESIQA DHIFAIVEEFGLRLHQSPGNDI RSLAGVTINKAPGDDEILKNTV DFVSFSYYASRCASAEMNANN SSAANVVKSLRNPYLQVSDWG WGIDPLGLRITMNMMDRYQK |
| 13821 | 44189 | A | 13901 | 1 | 2370 | |
| 13822 | 44190 | A | 13902 | 1 | 282 | |
| 13823 | 44191 | A | 13903 | 1 | 714 | |
| 13824 | 44192 | A | 13904 | 3 | 506 | |
| 13825 | 44193 | A | 13905 | 459 | 551 | |
| 13826 | 44194 | A | 13906 | 401 | 492 | |
| 13827 | 44195 | B | 13907 | 479 | 702 | |
| 13828 | 44196 | A | 13908 | 120 | 256 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13829 | 44197 | A | 13909 | 16 | 1249 | SKSGAIEIARLAGRVHGVVVQI TSEIGPLTLLTANFAFSAS*STA WKATSMGDGEVLS*YSTSASAS AERQSTHQ*TGFAPLCR*PLPMI /VAQRADDVGFSFEVHGQVRV RPVAQHAQTDKVFALT VNLGR RVFAALGAELGGARSAVRPVP ECYAVRETLALLQKIFPIRCEN SVYRNRSRPCLQYQIGRCLGPC VEGLVSEEEYAQQVEYVRLFLS GKDDQVLTQLISRMETASQNLE FEEAARIRDQIQAVRRVTEKQF VSNTGDDLDVIGVAFDAGMAC VHVLFIROGKVLGSRSYFPKVP GGTELSEVVETFGVQFYLGQSQ MRTLPGEILLDFNLSDKTLLAD SLSELAGRQINVQTKPRGDRAR YLKLARTYAATALTSNFRSIYR SPATDRACQRVETAGNER |
| 13830 | 44198 | A | 13910 | 1 | 438 | |
| 13831 | 44199 | A | 13911 | 1 | 1200 | |
| 13832 | 44200 | A | 13912 | 1 | 300 | |
| 13833 | 44201 | A | 13913 | 1 | 431 | |
| 13834 | 44202 | A | 13914 | 2 | 1465 | |
| 13835 | 44203 | A | 13915 | 1 | 513 | |
| 13836 | 44204 | A | 13916 | 3 | 535 | RDKILVFKDENFWMIRGYAVLP DYPKSIHTLGFPGRVKKIDAAV CDKTTRKTYFFVGIWCWRFDE MTQTMÆKGFPQRVVKHFPGISI RVDAAFQYKGFFFFSRGSKQFE YDIKTKNITRIMRTNTWFQCKE PKNSSFGFDINKEKAHSGGIKIL YHKSLSLFIFGIVHLLKNTSIYQ |
| 13837 | 44205 | A | 13917 | 1 | 876 | |
| 13838 | 44206 | A | 13918 | 23 | 414 | |
| 13839 | 44207 | A | 13919 | 2 | 425 | QERGPHQVIQRKECLREYSPVV S*AKGTGVAVGQKGT LQCEAS AVSSAEFHWYKDDKRLIEGNK GVKVENRPFLSKLIFFNVSEHD YGNYS CVASNKLGHTNASIML FGPGAVSEVSNGTSRRAGCVW LLPLLVLRLLLKF |
| 13840 | 44208 | A | 13920 | 1025 | 1270 | |
| 13841 | 44209 | A | 13921 | 370 | 701 | |
| 13842 | 44210 | B | 13922 | 1 | 660 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13843 | 44211 | A | 13923 | 1 | 432 | RFSRVDDFVLTMDDGPPRRAR GDLTHSGLWRVCCIEGIYKGHC FRJNHFPEDNDYDHDSSSEYLLRI VRASSVPILSTILLLLGGLCIGA GRIYSRKNNIVLSAGILFVAAGL SNIVGIIVYISSNTGDPSDKRDE DK*NHYN |
| 13844 | 44212 | A | 13924 | 1 | 1093 | |
| 13845 | 44213 | A | 13925 | 1 | 1203 | |
| 13846 | 44214 | A | 13926 | 1 | 1353 | |
| 13847 | 44215 | A | 13927 | 2 | 445 | |
| 13848 | 44216 | A | 13928 | 1 | 227 | |
| 13849 | 44217 | A | 13929 | 1 | 840 | |
| 13850 | 44218 | C | 13930 | 120 | 356 | |
| 13851 | 44219 | A | 13931 | 40 | 342 | |
| 13852 | 44220 | B | 13932 | 403 | 473 | |
| 13853 | 44221 | A | 13933 | 70 | 2169 | |
| 13854 | 44222 | A | 13934 | 1428 | 1905 | RCAATSGYGERVQRTV/PTHTV W*ASLSQSSAHRVVAINSIANK RSSMPPKSWATVALTSTKLKCR FMAKVRNKSFSVLHNV*MTISI/ SPWVILSSGVDEKLFPRAVRVA MTAGASGFLAGRAVWASVVG LPDNELMLRDVCAPKLQQLGDI VDEMMAKRR |
| 13855 | 44223 | A | 13935 | 227 | 342 | VHSWQRYSGR*RGY*PQNQSA TDQTRRWQSLKTAGAVA |
| 13856 | 44224 | A | 13936 | 480 | 928 | FFADLQQPVCADSYPLLQMK LAPHKS*NAVLWQRSATKSFSV L/AQGLNDHINMPWVILSSGVD EKLFPRAVRVAMTAGASGFLA GRAVWASVVGLPDNELMLRD VCAPKLQQLGDIVDEMMAKRR FIPLLRWVDLALTRWLITVSK |
| 13857 | 44225 | A | 13937 | 564 | 1185 | WLHASAALLRW*YQLPGQPHH RRCRSADGSHVPSLCAAVPDQR PLITVRRIGMQAMTTSTTGDRQ RSWQIAMDGSQKLQRM LDSV RWHLAHD SKFDLLALGVAGW MRYVGGVDEQGNPIEISDPLL N RMAANRFVHITQLPVIYRAFRN SFTQVARLQLCHKRFQQRHTSV REQIVTVLSGIRDNHVHFVQTL TGDGVGNQRQLVQ |
| 13858 | 44226 | A | 13938 | 228 | 424 | HRFCPAARH/RSWSGLREMAVS ISMPPRIINSGRYCAICWYKRRS RCARNMLIFPVARSTPIGPS |
| 13859 | 44227 | B | 13939 | 128 | 1670 | |
| 13860 | 44228 | A | 13940 | 2 | 2367 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13861 | 44229 | A | 13941 | 1 | 921 | ELPASAPCARTPQPLGGRWEA ARRKERVLCFLFDVDGTLTPAR/ QGRTLKIGSSHRECHADTPEAE CGVCSSVTEVRAKWRSQTC*KP ECYASPLPP*KIDPEVA AFLQKL RSSYLPVGSQTWSHTLSSSCPLC DPEVIGRDTV PVSGSGSPGHAQ SPVFLGQTIQNHLPGGARFEF RA/CSGSLWLPALPHHRGT FIEF RNGNCVPSQGLAHSRSELPSA PSPLQKEQAALLLALSAPPSRE* QSPPLPTGGMISFDVFPEGWDK QVRSSQCGEGLHLNIPPLPILCV QGGNDFEIFADPRTVGHS |
| 13862 | 44230 | A | 13942 | 105 | 416 | HSVLEVGPWWEVFGSWGQILH SLVSSHVRHWLLPSPSAMTES SLTFQQKPSRCQH HASKAYHS HQLLLVPTAGRLEDRSHH*IPC KHSPAPAWSLAAPVGN |
| 13863 | 44231 | A | 13943 | 191 | 573 | SSSGGYQQLMRVIGTRDTAV NKASNVPSFGA*I/PSGRGQQAK LIALTRALTLAKELHVN IYADC KYAFHILHQHDVIWAERGFLT V QGSSSIINASLIKTL LKATLLPKE AGVIHYKGHQKASAPIA |
| 13864 | 44232 | A | 13944 | 1 | 1065 | |
| 13865 | 44233 | A | 13945 | 321 | 537 | |
| 13866 | 44234 | A | 13946 | 346 | 1260 | GGPARAEFSRHLGCKGHHPLPK DVASEVPAGSSTSVSSLIRTNGC PGLGSWEPP*FFSENKRLSTLMS FTLRDSKMFSPQSGFLGCSAG EHSALRDPTASGLPGTASGVRP GR/RQRVGSDIEASTQGESKPCI LSI* TLPNA*LKTKLTLPLEIAAC TNPHSFSITARIGPAHLAAPRPV TPAGRGGARAPGR*CAAARPPP ASQ*VSGSPAPGGGPSYAPAAR TS*PSSLAPGAKRLRFSRVATFC CSFLAWSSSSNKAFCT*EHMSL LSSWISQSLEKVASCCPCEQFDS WKRLLENILLFS |
| 13867 | 44235 | B | 13947 | 1 | 459 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13868 | 44236 | A | 13948 | 63 | 1263 | VEAAKKAHHAACKEEKLAISR EANSKADPSLRPQAHTYALSPL FLTAMPSV*QGEHVIYTRVRHS DQVSESSGKPLSLPLLEPGIWAF EAAQVPPRWDQVRSLEPTTEW EAPGLKKRRVSQGLNGNEPLSC AWIFL*TKEKYEKSLKELDQGT PQYMENMEQVFEQCQQFEEKR LGWDKG*LAPAF*KSHVSL*FS YKAIYHDLEQSIRAADAVE/DR RGFARK**TFGFSPSAPVA*EWS ADLNRTLRSREKKKATDCQDP HGPLQSWDPLKALSLHSTLNVP SNPAQSAQSQSSYNPRGPHTLC RPVLRALWPPLSCSVSSYEKTQ SYPTDWSDDSNPNPFSSTDANG DSNPFDDDATSGTEVLCSPPSV SYLSWRRLLPLCLAGDELTKME DEDEQGWCK |
| 13869 | 44237 | A | 13949 | 2 | 485 | AAAFGTRLRGRGCGVTGSG GGRRRVPAARRPRSPHQ/P PRRPSRRTPGCGSRGA\PSRGRR LVPPPPPEPPRAAQQRARH\HRTS RPAARQPPRRPPAQRSCPRRV RPTPAWSPPGRRGPRRSRRRRR RGGRARARRPRRGQVPRPQS ATGAGHAR |
| 13870 | 44238 | A | 13950 | 1 | 207 | |
| 13871 | 44239 | B | 13951 | 1 | 5297 | |
| 13872 | 44240 | B | 13952 | 1206 | 1360 | |
| 13873 | 44241 | A | 13953 | 46 | 369 | NEGKNAKGSQRERSGYPQREA HQTNSGSLGRNPTSQKRVGANI QHS*RKEFSTQHFISSQTKLHK* RRNKILYRQANAERFCHHQEGS TKHGKEQPVPAAAKSCQNVK |
| 13874 | 44242 | A | 13954 | 476 | 868 | KYDCCISSTFCRALVHFSRTTFQ VNSPLSPNISAFGYMPLKYSIYF LHHLRPNIL*AASYFLKYKGT KLPAIRGCLS*STRCWCKIHICI *ND/ECLQFLGPWFENEFCLPS TSQFVEFVLDILVLQNEP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13875 | 44243 | A | 13955 | 1770 | 3003 | PANIIMTGSINSHITILTINLVNGI LNAPI*RHRPAIA/S/WLKSQDPS VVCIQETHLTCRDTHRLEIKG WRNIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYIMAK GSIQEEELTILNIYAPNTGAPRFI KQVLSDLQRDLDAHTIIMGDFN TPLSTLDRSTRQKVNKDIQELD SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHIVGSKALL SKCKRTETITNCLSDHSAIKLEL RIKKLTQNHSA TWKLN SLLND YV VHNKMKAEIKMFFETNENK DTAYQNLWDTFKAVCRGKFIA LNAHKRKQERSKIDILTSQKE LKKQEQTNSKATRRQEITKIRA ELKEIETQKTLQKKQPNKDPAM EKNKTDRLARLIKKKREKN EFSAHILYKFSKQNGS |
| 13876 | 44244 | A | 13956 | 105 | 392 | RSRKPRGNPKSHPEDTDPTKAP RKRQISSRGHRSHR*EPGPQSA PGFREQRRRGQMG*IWYLTPTP PGGQRPSSAASPRGFPTNNSR LP AEPE |
| 13877 | 44245 | A | 13957 | 55 | 403 | SEGMSGKASEKQEAFCPRHLT RAVDGPS*SGLLGSRLPPSCSPG KEAPGGSELYLCLMRGLQTL*A RSGTGRL/PNPAEIR*EPGPQSA APGFREQRRRGQMG*IWYLTPT PPGGQ |
| 13878 | 44246 | A | 13958 | 217 | 444 | RSRKPRGNPKSHPEDTDPTKAP RKRQISSRGHQSHR*EPGPQSA APGFREQRRRGQMG*I*TPCRP ALPKSKPRPL |
| 13879 | 44247 | A | 13959 | 309 | 670 | PCPRASSQGLKATHGQR*SSEP PGASFPGLQDGGRRPRRPD*D GPSTGLVRCLGHANVGDPCLK VFVFFKNLSPTYLRASAEQTL LLLPHLHGLCLHQLHLGFTAA WAQLTFWEASQ |
| 13880 | 44248 | C | 13960 | 392 | 760 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13881 | 44249 | A | 13961 | 24 | 915 | HAGRHARGSLFPGARPSETRAH CVRTARPNCKEEDTPMVRGKN SGGEHCTWGPSLAAGG*GIGDP GGLPGT\PHPLQLLLHGFAGP HMASLCCGVSSPAGVRQWPA* GSGNHQVKS WLGLPKNV S*AP SML*NPKMQRLMKAQPHGRCE VRRGRVCSALGP/IGMSGKASE KQEA*DEGHPHLHAPGT*QDQ VDGPS*SGLLGSRLPPSCSPGKE APGGSELYLCLMRGLQTL*ARS GTGLRANPAEIR*EPGPQSAAP GFREQRRRGQMG*IWYLTPTPP GGQRPSSAASPRGFPLV |
| 13882 | 44250 | A | 13962 | 397 | 612 | RPQHHTFCCDGRVMMARQKGI FYLTFLILGTCTLFFAFE/CSFG *VELPDYGYFGSRGRT CFLGSL GLVLG |
| 13883 | 44251 | A | 13963 | 125 | 1298 | FQSWAQPLFLLSCNRKTHFGTR IP\MSVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKGIF\ YLTFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSMAT L\LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGQRPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHC PW VGNCVGKRNYRYFYLFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTVLEVLCFFTLWSV VGLTGFHTFLVALNQTTNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVL CGPLPPSVLDRRGILPLE ESGSRPPSTQETSSSLLPQSPAPT EHLNSNEMPEDSSTPEEMP PPEP PEPPQEA AEA EK |
| 13884 | 44252 | A | 13964 | 44 | 647 | DYSAQH GKASQKHVARLISSGT FQGATVSRPFQLSTSSSSFCSSSS SLSSSSSLSSSLLSCSSES VFLS LSFFFCSEASFLPFC SRLYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFPFI AKLLAQDVAYSTKT LAAREIGAPGLLDVDTVREL R GDRG*AKLPFQHLLPSCPFVRPP RAAHRLLDDPGDHGIGQV |
| 13885 | 44253 | B | 13965 | 158 | 1075 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13886 | 44254 | A | 13966 | 125 | 1297 | FQSWAQPLFLLSCNRKTHFGTR IPIMSVMVVRKKVTRKWEKLP GRNTFCCDGRGMMARQKGIF YLTFLILGTCTLFFAFE/CGRYL AVQLSPAIPVFAAMLFLFSMAT L\LRTSFSDPGVIPRALPDEAAFI EMEIEATNGAVPQGQRPPRIK NFQINNQIVKLKYWYTCKIFRA SRASHCSICDNCVERFDHHCPW VGNCVGKRNRYFYLFILSLSL LTIYVFAFNIVYVALKSLKIGFL ETLKETPGTVLEVLIFFTLWSV VGLTGFHTFLVALNQTTNEDIK GSWTGKNRVQNPYSHGNIVKN CCEVLCGPLPPSVLDRRGILPLE ESGSRPPSTQETSSSLLPQSPAPT EHLNSNEMPEDSSTPEEMPPEP PEPPQEAEEAEK |
| 13887 | 44255 | A | 13967 | 247 | 850 | DYSAQHKGASQKHVARLISSGT FQGATVSRPFQLSTSSSSFCSSSS SLSSSSSLSSSLLSCSSESVFLS LSFFFCSEASFLPFC SRLYASRA SFNGVTNRWNSISSMAESTSLA FSVFRFPFIKLLAQDVAYSTKT LAAREIGAPGLLDVDTVREL GDRG*AKLPFQHLLPSCPFVRPP RAAHRLDDPGDHGIGQV |
| 13888 | 44256 | B | 13968 | 298 | 380 | |
| 13889 | 44257 | A | 13969 | 48 | 252 | QRAGSPHSPRSLAPPLPELPLW RHLRSPSAHRCTVGAPFWDGQ G/LEPAPSAALAAFPRSRARDLQ LA |
| 13890 | 44258 | B | 13970 | 1 | 447 | |
| 13891 | 44259 | A | 13971 | 236 | 559 | MWLEPMQMGLHMMMEKMAA RTSAILD*GTLK*FHFTLTSLK ALSSHTPIFPGTGELQLPVSPSV CLDQGMQLKPSTSSHLLKTVKP RMKRQSLHMKQSFEPKIYL |
| 13892 | 44260 | A | 13972 | 1 | 645 | MKPQTLTVSVTAFKVAHLEFVP SDVQMCSEFLPSGGFVVS LASG VKLQTFVVSFTAHKSSVDPKNS EAQLASPSGFCTRAADGAACQS LPCTCTPQPLGGRWDWALWS RGW/LLVEEAWAAQEPTTELRE RALALASPERGSHSAAVGQRAP QVPPKWEPRQRRRRERARAVR TASTLSPLNPPSKQDTLTAVGN LADDHSSYFLDRGEEGALQL |
| 13893 | 44261 | A | 13973 | 28 | 322 | |
| 13894 | 44262 | A | 13974 | 1760 | 4426 | |
| 13895 | 44263 | B | 13975 | 942 | 3414 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13896 | 44264 | A | 13976 | 1 | 274 | |
| 13897 | 44265 | A | 13977 | 545 | 1150 | RISGPGAVLLPVMPALWRLRHR MFSLTKK*HLP AHRSLAEGYLL YQPQLDTLKARLTQKYQELQV LFEAYQIKKTKLDRQSSASLET LLALLQAEGAKIEEDTENMAEK FLDGELPLDSFIDVYQSKRKLA HMRRVKIEKLQEMVLKGQRL/S TRPWPRCPPGCPNWHLPPPFPT LPQSQWASCRCTSAHPPPTTPG AAGRL |
| 13898 | 44266 | B | 13978 | 213 | 611 | |
| 13899 | 44267 | A | 13979 | 1 | 639 | MEAVTVVPVVGTEEGMGEEEQD SGTTTGCGLP SVEKMLATNPGK TPISLLQKYGTRIGK\TPVYYLL KAEG\HQPNTFWVVGNTSCT AQQPRKKVVKHKA AEVALRHL KVESMLEPAPEDSSSFPLDSSL PEDFPVFTAAAAATPVSSVFLT RSTPMEKQPPLP\QQSECIPVG ALQKL VVQKGWWLPEHTVT*E SRPDQHEELT*RVERFT |
| 13900 | 44268 | A | 13980 | 361 | 894 | AFFPMSTAGVCGNVEGEPETP WSLPLSQVPFSPNA/CPQGTLGR S*AGVAGAPGPGVPGRSPAA\GI PEPAARPGRPALSRLPGLGGAG ARSGAA*G*GSRPGG/PLPAADP VQSWGP*EAPSHP*PGT\ SADSP PSGVSGATGDCLWGSRAELF GFATTSSAAPFPGLPTFFFI PVSP |
| 13901 | 44269 | B | 13981 | 1 | 3842 | |
| 13902 | 44270 | A | 13982 | 3 | 407 | DAWAAARPGRSCALPPPGA/PE EPGHVPGAA*G*GSRPGGRFQL PDPVQSWGP*EAPSHP*PRNFPQ TRRHLGVKQHGCSQSPHGSRA SQAHPGISGLF/GPHHPGPPLFIH GPRCCCAQATASNHLFACGTSS DP |
| 13903 | 44271 | C | 13983 | 127 | 297 | |
| 13904 | 44272 | A | 13984 | 3 | 1920 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 13905 | 44273 | A | 13985 | 3 | 2271 | GQGRRTAGGGGGGGAGVAG AGAMEAERGPERRPAERSSPGQ TPEEGAQALAEFAALHVWSGE GIGVGSPAHTPADGNSGPQVFD AGEVFGIMQVEEVEEEDEAAR EVRKQQPNPLAPPTSLCPMPTR QPHIVACARSIFLIDHAWTCRV EHARQQLQQVPGLLHRMANL MGIEFHGELPIWVPEGSSGGW MGEREVPYVLCLQTAEKMPV WYIMDEFGSRIQHADVPSFATA VPLEEGPQPSVSPPLMGTH/DL GTEEVTRDFAYGETDPLIRKCM LPLSSSHRGMETPCVHTSRASL PLQACELPSWSLLLINEPPRPAF PSLP*PHLYFRCVSF*AIPGLVLE SRLDTWEPGSPSSGSPHRVYTD VQQVASSLTHPALPVRASRHC PPLELAHLPPPCRKLSQERPGVL LNQFPCENLLTVKDCIASIARR AGGPEGPPWWVLGWHHLGTQ APGAPQTALLPRGEDNHWICK PWNLGLCVLGSPRGLCPGHQR ACTCVLQVVSKYIESPVLFLRE DVGKVKFDIRYIVGGTSLAGTR PLKNPYVSAHLSSRAFAQGRRG RGGPTWSGWLLARDPARV*DL LSSLVHSVERCPMQWALSEWQ LHHLSTWSSGLCGLAG**VFQM HRTPTPP**QAACSRPSGGLYR A*WALCLLPGAADPLLRCSEQ AS*LRLPGPQAEIFRAFTLQV |
| 13906 | 44274 | A | 13986 | 1 | 600 | MEEQRVQFTLWLHFSPHGICQF ESGRQEAKKLKSGSQPLKTGEI KTGIQKYRREALLQHYLGPA AGRSKALTGTAERSCSSGSDSSI FTLCVNYNDSRAIMKTLAAIGT GFDCASKAEIQLVQILGMPPER FMYANSCKQMSQIKYTANNGV QMMIFGNEVKLMSVARTHSKQ P/CHISVKSGAMLKASRLLE*A KEL |
| 13907 | 44275 | B | 13987 | 1 | 2040 | |
| 13908 | 44276 | A | 13988 | 205 | 438 | LYFLETGVFCVQVPAQQC*CSV PGSCRRPLEEAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13909 | 44277 | A | 13989 | 284 | 632 | KTGVFCVPGPRPTVLM*CSFVG GKKNQYCLTGDAGCLQEKHSL GPAGV/HLEEAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSPFEP |
| 13910 | 44278 | A | 13990 | 594 | 1003 | VRKGHHA VRGLCGRAQFRCIS GDPGKRPLG/LPGGNAPKSGSL ARRPQPVRI PGSRPQ/RGSVSHL GPAGVH*R/RAGWRGLGLSGRL AGTGLPSGSRGNRTERGERGKL VRGRRGVTRWLSHPQVQRQAD AGTCSPFEP |
| 13911 | 44279 | A | 13991 | 1 | 1500 | VRVAHIPIAAAEIAAIPDRGGHL SVGKRKLTFWFFYGVLPRFDV AIEFSPEEWECLDSAQQHLHRD AMLENYGNLVSLAAGDQSLPG DAAASAVCRQLSPSACGAILGL PPVNGVAPVRLRGEIVTYTWSQ LTGLALALSKDGADGLRRLTRP TRRAPALLLAPQTAERWRG KCDPRHGGGCALALQGWTLYP RESPSRESKELGGLWSFRADLD SRRQGFEEQWYPRPLRELGRG GRRPEARRWEGGSPGPCRLLPL SAPELAPYRKLVNGLRGAGL GDGETGGTGEGRGRRRRKRCC RTLSRDEGFNDICQDWLQRQF VGWVLYEQEVTLPQWTQHRLR TRVVLRIASAHSYATVVSAAARS RQGRGIGGLIYTLGMPFFLSGW QVPEPHAAGYVRECLIAGPLLM P/TTCCPLLISPVSAVGEWGRHA RA*GADSSSLVQNTDFFFNAYA GLQR\SVLLYTTLTTYIDDITITT GVEHDSAEIPFPEYLRVNTGN |
| 13912 | 44280 | A | 13992 | 2 | 307 | |
| 13913 | 44281 | A | 13993 | 220 | 427 | MSTLPFPSLQMFRRPPYGSPSTC RSQDNRSYSRVTEELQERRRW NSGDAN*DQSPEARRRQRPRHIE EAA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13914 | 44282 | A | 13994 | 1 | 2832 | MGKYYTQGDKVLMLPLAIQVH HAVCDGFHVGRMLNELQQYC DEWQGGAYPKGYFVQNTDFDF FNYAGLQRSVLLYTTPTTYIDDI TITTGVEHDSAAAPMVDSLIAR VGVMARGNAITLPVCGRDVKF TLEVLRGDSVEKTSRVWSGNE RDQELLTEDALDDLIPSFLTGTQ QTPAFGRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDEQ MAALSRLGNDYRPTSA YERGQ RYASRLQNEFAGNISALADA |
| 13915 | 44283 | A | 13995 | 1 | 2934 | MITFDFMSHIQVTLMQEVSFHG LGQLRPCGFAGYSPPPGCFHRL ASSVCSFSRCTVQAAVDLPFWG LEGTSPLLAASLGSAVGTLCG GSDPTFPSWTALADVLHEEGHT PASNFCLRNLAGESQSWRKE GLGTPRPTASSTEELQTLNEDSR LMTSPHNLEETRDCDEL PKKS LGWKEIRVYGQNKTLGFWLQA QLLICDGGNLRMFLLPYGSPS TCRSQDNRGYGGVTEELMERK RWNSTDGFHIQGVLE |
| 13916 | 44284 | A | 13996 | 68 | 425 | SHILPGAPGAPAWWTRWPSTLP EPFPRGRGSPAGTSPISRPGLVQ SS*ASRGSDSRLPV/GPASCQAS GPGPDSRRPPCTPA\GPHHGSL PSAGRVGASAAAAGPPSPAVPL PPAERPAP |
| 13917 | 44285 | A | 13997 | 324 | 723 | TAFSLNFQGGVEGEVWAGTRA ARGACAGERGLGGSRTSGW/P GTAGPGQAGHGTCSLPCPSLPP AMGSCVSEPPRQAPPPAPWRLV PSTAQGLRSVGTQCGTGGSSAC GPC\GDPGF*THQSAPCQNGPIS SL |
| 13918 | 44286 | A | 14000 | 39 | 383 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13919 | 44287 | A | 14001 | 181 | 1446 | EDLLQEAQALAEVTAQGKGLG QVRSLDLSLEACAGSPPLQVLD LQDREPRSLTSLPSSAANRGKL EKAQSNPCGHRRHQAAGLKLP LFSAQAPQQQPTPA PRFRAATR KPGTAQSHAPLWSPAMSFFPEL YFNVDNGYLEGLVRGLK/ALGE LSQADYLNLVQCETLEDLKLHL QSTDYGNFLANEASPLTVSVVID DRLKEKMVVVEFRPHEGTPMPY EPTSPSFP*TSITLQFT*FDNVI/L WLIHRARLHQRSIAELVPQVAH PLG\SFEQMEAVNIAQTPAELY NAILVDTPLAAFFQDCISEQDLD EMNIEIIRNTLYKAYLESFYKFC TLLGGTTADAMCPI\LEFEA\NR RAFINT\INFFG\TKTVPKKDRCP AFFPH/CGAGFFPEGPAAMGFG LNNLLTGAKKRGPNFPEVQL AFLRGDG |
| 13920 | 44288 | A | 14002 | 1 | 1182 | |
| 13921 | 44289 | A | 14003 | 26 | 342 | ARFLAGP*LPSRRTGLRDLQPA MPEPP\PTPWAPVRPEPPRRAPP PAPRRPVPSTGKEQTTQGLRSA GAGHRDWQAAPPAAPVRDPLG EASWAPESGGDVESLYV |
| 13922 | 44290 | A | 14004 | 66 | 463 | |
| 13923 | 44291 | A | 14005 | 3 | 1446 | |
| 13924 | 44292 | A | 14006 | 221 | 852 | NSFLMVGFPPFFSL/CAAFDTKT GLRVAVKKLSRPFLRPDGYYTE FNIYLLFNFYILTSSAV*VVLSH SVVIECLLSIRHCSRYFRKSSD KNFLRGSRLLCNFSLSRYLVTH LMGADLNNIV*RYR*YK**FFK MNSPFLPLVGGELIMHHKVDP VCFVFFSLPVSKS*QFVCSSAL *ILD FGLARHTDDEMTAKGQPE CFVRWACAS |
| 13925 | 44293 | A | 14007 | 55 | 784 | RHIQDPASQRLTWNKSPKSVLV IKKMRDASLLQPFKELCTHLM ARGAGGGHDARSLTAPVSRE PPCRRVGSAGGMSRLALCFQEN MIVYVEKKVLEDPAIASDESFG AVKKKFCTFREDYDDISNQIDFI ICLGGDGTLLYASSLF/QGNAA VVLRSRLKVRVVKELRGKKT VHNGLGEKGSQAAGLDMDVG KQAMQYQVLNEVVIDRGPSSY LSNVDVYLDGHLITTVQGDGVI VSTPTG |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13926 | 44294 | A | 14008 | 155 | 1592 | PESRHQCFSDRSANFLTMEMEQ EKMTMNKELSPDAAAYCCSAC H\GDETWSYNHPIRGRAKSRL SASPALGSTKEIRRTSLHGPCP VTTFGPKACVLQNPQTIMHIQD PASQRLHVEQRPPRTVLVIKKM RDASLLQPFKELCTHLMEEENMI VYVEKKVLEDPAIASDE\SFGA VKKKFCTFREDYDDISNQIDFII CLGVDGTLTYASSLFPGQPSPP VMAFHLGSLGFL\TPISFENFQS QVTQVIEGNASCCSSGSRLKGQ GW*RSLRGKKTAVHNGLGK G\SQACRPGTMDVGKA/QAMQ VPRS*NEV\VIDRGPSYLSNVD VYLDGHLITTVOGDGKARSTV LGP*ASLGRE*RLRLSLSGVIVS TPTGSTAYAAAAGASMIHPNVP AIMITPISRSVLPTAGGPHLSLL DPQIMLSPEARNAAGGPFWK WLRLLLSRPSISITTSCYPLPSIC VRDPVSDWFESLAQCLHWN |
| 13927 | 44295 | A | 14009 | 327 | 466 | |
| 13928 | 44296 | A | 14010 | 2 | 196 | |
| 13929 | 44297 | A | 14011 | 923 | 1776 | WRKCGCETAGSASATRAAATE KMEAPRNKMCRDQENSAWRN AVPGP*E*RQPEEFRTTSILAEP TVLSRRKCRPSEKRGSAATEKFG ATSAVTENPPLGAAGERANKTL GAATVTPTLGPRPRMEKGGTR CPSTL*PSVQERQPESPSGNHPE TQKIEFAGRRVTFQHRWATTLR TRISGTGASPRDRSAFFGFPWC G/AAQPSDEESTPATQEEAQAQ AGVAAAASSEEPGHCAPRPPHA PRSALFEDWSREPERSDDGDL ECRRPATEPWRPPGSAWRLPCA A |
| 13930 | 44298 | A | 14012 | 568 | 1223 | SARGLLPGSGPLSHAGPQLQVE WFGCLPPDSTLELVCGTVAI SRVRMSAVCVLRTWS\RNAG\Q LI\CFTVFQPCSNVHVL/KGPNY VCFFG\YPSFKYSHPHNFKTI NAVCGQLVQFRFPDTEEGIRK VTV/KCYVKEGDTV SQFDNIGK VQSDKASVTIASPYDGI/RKL* HSLDDIAYVGKPLVNIETEALK GTVNLFYQIDYCPPFVIGSQLK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13931 | 44299 | A | 14013 | 5 | 296 | LFSRVPSKGPPIRYHHTSSRG*TR AD*LISS\GNS*AHCIPSLQGM LNLLPTPRAPVRPEPPRRAPPA PRRPVPFDHPRACGTGRQLHLQ PRCGIH |
| 13932 | 44300 | A | 14014 | 1 | 376 | MQAVLLTVLQKHNSVIYWY MKYIYYEGLVIMDDYDYVIMD YMTMETEKSHDLQAGGPGKPV VQFQFKPKILQASRNGVKSWS KSKGLRTRCANVQQQENREGP AKHSPFLCLFVLFGSSTGRMIPN HTGDTSKVIAGTEERGVPKKVT LKFDACAAIDRPWAHQDLCTY HFKGSNDEHDSRLHTNAG*L*L C/RLWIT*LWRLRNPICRLEA QESQWYSFSSSPKSCKPVEAMA LSPGSPKA*EPGVLMKGRKI GRAQLSIHLSSAFLFFSAPQQVE |
| 13933 | 44301 | A | 14015 | 1638 | 2289 | VEKKKKPMSAPALRLPDLTKLF TLYVSETKKMAVRVLTQTGVP WPRPVALLSKQLDEVSKRWPP CPKSLVAIALLAQEADKLTLRQ NLNIKSPCAVVILINTKGHH*LM NARLARYQSLLCEHPRITLGS QHLNPATFLPVSESPVKHNCVE VLDSVYSYVGNHRDHPLNISR LGAVTWMGSSFHQPLQSDTLK KTTSPGSSHTRKLTGPRTAEA |
| 13934 | 44302 | A | 14016 | 1 | 675 | MAPPLRPLARLRPPGMLLRALL LLLLLSPLPGLREGIGELITPIGT SLPDLDPARRRWEGGIGRVGSE VADLCPGKEGKVPAAEKEGV WCFSELSFVKEPQDVTVTRKDP VVLDCQAHGEVPIKVTWLKNG AKMSENKRIEVLNGLYISEV EGRRGEQSDEGFYQCLAMNKF *AILNQKAHLALSRIGST*RRRP DRP*EDEAFVMTTHCFQDLLTS |
| 13935 | 44303 | C | 14017 | 18 | 329 | |
| 13936 | 44304 | A | 14018 | 391 | 895 | WASSDTPGTGFTQRWRPDWAGG GGGEERGDGTGVVWEGEKVY RFRRVTGGSSFPSPAVLVRAPN TGMPKLTYYQT*GPLGERGKEP VPPN\PTLPQTGGLLNASVVRK TEIPSPSPPPVCYLASAERQ/PA GGSPQAKWRRRAASSPPPLPPVH LPPPPPPRPPPPPP |
| 13937 | 44305 | B | 14019 | 1 | 1110 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13938 | 44306 | A | 14020 | 282 | 710 | YPEPQGWRVAHTVQYPIHIQPL KPGPRGR*SIMDIQVPPKEGGV LILKN\SSRLLNSWTQGCLQISA FSPTSSTLPGTPWSNVGPYKIAP ITSFGEAPFIRVIWKQLPSWISIIQ V/SHKQ*QIHRSDIGWSPGQEC GPKGCFV |
| 13939 | 44307 | A | 14021 | 1 | 1416 | MIILIDAEKAFDKIQQPFMLKTL SKLGTGTYLKIIRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCPL SPLLFNIGLEDLARAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPR DIDQW/NRTEPSEIMPHTYNYLI FDKPEKNKQWGKDSLFHKWC WENWLA VCRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGVGKDFMSKAPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTTWEKIFATYSSD KGLISGIYNELKQIYKKKTNNPI KKWAKDMNRHFSKEDIHAAK KHMKKCSSSLAIREMDIKTTMR YHLTPVRMAIIKKSGNNRCWR GCGEIGTL |
| 13940 | 44308 | A | 14022 | 1 | 3450 | |
| 13941 | 44309 | B | 14023 | 1 | 3171 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13942 | 44310 | A | 14024 | 1 | 2433 | MRTKTQHTRISGTHSKPVCRGK FIALNAHKRKQEKSKIDTLTSQ LKELEKQEQTHSKASRRQEITKJ RAELKEIDTQKTLQKINESRSW FFERINKIDRPLARLIKKKREKN QTDTIKNCKGDITTDPTETIQT REYYKHL YANKLENLEEMDKF LNTYTL PRLNQEEVESLNRPTG AEIVAISSLPKESRTGWIHSRI LPEVQGGTEKEGILPNSFYEASII LIPKGRDATKKENFRPISLMNI DAKILNKILAKRIQQHIKKLIHH DQVGFI PGMQGWFNIRKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQRFLKTLNKLIGDGYF KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPLSPLLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSGYKINVQKSQAF LYTNNTQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKDDTNKWKNI PCSWVG RINIVKMAILPKNWKKTTLKFI WNQKRAHITSILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMLHTY NYLIFDKPEKNKQWGKDSL FN KWCWENWLAICRKLKLDPFLT PYTKINSK WIKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLKSFC |
| 13943 | 44311 | A | 14025 | 1 | 1023 | MGAIDYDKPTANIILNGQKLEAF PLKTGIRQGCPLSLLLFNIVLEV LARAIRQEKEIKVIQVGKEEVK LSLFADDMIVYLEDPIISAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNI PCSWVG RINIVKMAILP/KAICRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMDKDFTSK TPKAMATKAKIDKWDIKLSF CTAKETTIRVNRQPTWEKIFAI YSSDKGLISRIYNELKQIYKKKS NNPIKKWAKDM/NRHFSKEDIY AAKRHM |
| 13944 | 44312 | B | 14026 | 1 | 2206 | |
| 13945 | 44313 | A | 14027 | 1 | 1689 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13946 | 44314 | A | 14028 | 1 | 2523 | MKQFLLYLDESNALGKKFIIQDI DDTHVFVIAELVNVLQERCHTR LGYTEFLVAWRVTFGLCVEAV TLHLKYQILIRGLLEMMSFSDA DILKQLPVTVPGLFPASLSPSSL LGNSPPSWLRHNSESKVSAVSS PSATKTLSTGIGKLDPGHKEMA EESELLKNKMQAPLSRCPESQ KCQHQLRLHHWKPSVRHQVKR RSPAVLRSAMPADCPAVLEAT TATHPEKGTALSKHLPSSDSMS LKVDVEALENSPGATYIWKGG KVTRDSQPKEQGKGDLLKKKKK GKLPKNYDPKLTDPERWLPM QECIFYQGRKKGKKKDQMGK GTQGATAGASSELDARKTVSSP PTSPRPGSAATLSASTSNIIIPRH QRPAGAPATKKKQKQKKKKG GKGFPVLREITVVKVDTLVVFQ ILEERLSVFHIQYDTSYPFSTVDI EDHECAVWLLLRKSKSDDKTT RLEAVREMSETHHWHDAEKAF DKIQPFMLKTLNKFVGDGT LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNTV LEVLARAIRQEKEIKGIQLGKEE VKLSLFAGDIIVYIENSIVSAPKL LKLISNFSKVSEYKINVQKSQAF LYTNNRHTESQIMSKLPFTIATK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNEWKNIPCSWVG RINIMKMAILPKVIYRFNAISIKL |
| 13947 | 44315 | A | 14029 | 1 | 2868 | |
| 13948 | 44316 | A | 14030 | 1 | 3099 | MGELITPLSTLDRSTRQKVNKD TQELNSALHQGDLDIYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIITNYLSHSA IKLELRIKNLTQNRSTTWKLNN LLLNDYWIHNEMKAEIKMFFET NENKDTTYQNLWDAFKAVCR GKFIALNAHKKRQERSKIDTLT SQLKELEKQEQTHSKASRRQEI TKIRAELEKETQKTLQKINESR SWFFERJNKIDRPLARLIKKKRE KNQIDTIKNDK |
| 13949 | 44317 | A | 14031 | 2 | 3419 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13950 | 44318 | A | 14032 | 1 | 2685 | MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFPSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRKINLTQNRSTTWKLN NLLDDY WVNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLELEKQEQTTHSKASRRQ EITKIRAELEKETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHL YANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKKSPGPDG FTAIFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCWSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNLY IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLD PFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD |
| 13951 | 44319 | A | 14033 | 845 | 1616 | ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLLKLISKFSKVSRYKINV QKSQAFLYTNNRQTESQIMSEL PFTIATKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLA ICRKLKLDFFIPYTKINSRWIKD LNVRPKTMKTLEESLGNTIQDI GIGKDFMTKTPKAMATKA/KKS FCTAKETTIRVNRQPTWEKIF AIYPSDKGLIS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13952 | 44320 | A | 14034 | 707 | 2878 | TLMQKSSIKYWQNESSSTSKSL STMIKWASSLGCKAWFNIRKSI KVIQHINRAKDKNHMIIISIDAEK AFDKIQQPFMLKTLNKLGDGT YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLIRNFSKVSGYKINVQESIQ AFLYTINRQTESQIMSALPLTIA SKRIKYLGIQLTRDVKDLFKEN YKPALLKEIKEDTNK\WKNIPCS G\EGRNIVKMAILPKNWKKTTF \RFIWNHAKRACIAKTILSQKNKA GGITLPDFKLYYKATVTKTAW YWYQNIDIDQWNRTEPSKIIPRI YNNLIFDKPDKNKKWGKYSLF NKWCLENWLAICRKLKLDPFL TSYTKINSRWIKDLNVRPKTIKT LEGNLGNTIQDIGMGKDFMSKT PKAMATKAKIDKWDLNNLKSF CTAKETTIRVNMQPTWEKIFA IYPSDKGLISRIYNELKQIYKKK TT\NPIKKWAKDMNRHFSKEDI YAAKKHMKKCSSSLAIREMQI KTTMRYHLTPVRMAIIKSGNN RCWRGCGEIGTLLHCWLDCKL VQPLWKS\W*FLRNLELEIPFD PAIPL\GIYPNDYKSCCYKDTCT RMFIAALFTIAKTWNQPKCPTII DWIKKMWHIYTMYYAAIKND EFVSFVGTWMKLEIIILSKLSQE |
| 13953 | 44321 | A | 14035 | 869 | 3869 | RHKKPFFKLTNPGAEIQTIREY YKHL YANKLENLEEMDKFLNT YTL PRLNQEEVESLNRTITGSEI EARINSLPTKKSPGPDGFTAIFY QRYKEEMVPFLLKLFQSIEKEGI LPNSFYEASHILIPKGRDTTKKE NFRPISLMNIDAKILNKILANQI QQHIKNLIHHDQVGFIQGMQ WFNICKSVNVIQHINRTKDKNH MIFSIDA EKAFDKFQQLFMLKT LNKLGIDGMYLKIIRAIYDKLT ANIILNGQ |
| 13954 | 44322 | A | 14036 | 2 | 99 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13955 | 44323 | A | 14037 | 1 | 914 | TVTVIHTVARVGNLDIQIRKS ELFLSLVVCEAIKNEMNVMKLS SPVDLVTATDQKVEKMLISSIK EKYP SHSFIGEESVAAGEKSILT DNPTWIIDPIDGTTNFVHRFPFV AVSIGFAVNKKKKVDETYLGL VKETCFPLQIEFGVVYSCVEGK MYTARKGKGAF CNGQKLQVS QQEDITK SLLVTELGS SRTPETV RMVLSNMEKLFCIPVHG\IRSVG TAAVNMCLVATG\GA\DAYYE MGIHCW\DVAGAGIIVTEAGGV LMDVTGGPFDLMSRRVIAANN RILAERIAKEIQVIPLQRDDED |
| 13956 | 44324 | B | 14038 | 91 | 1959 | |
| 13957 | 44325 | A | 14039 | 28 | 152 | LPSPSSKDTDS/AASCCAPRGRA KGSVSNRSLFPPSSVPLP |
| 13958 | 44326 | A | 14040 | 35 | 879 | GSQCSSPPPASRCGSCSSAPSRH CPCRD FEP AVAGLARTPVLT TK TNPSPPARTGLNAPSMGTSLI/P ALCCFPLYQGSTELQCKAP**LP SPSSKDTDS/AASCCAPYFLVLL KVLSSVDNSSIWCSAGPPAQS/S SLYTIPMSSMSAKNCSVLRSGT WASFTCS*GSQRVSLGTPEALG TEDHTSRSLGHSHVCHVDLSPA TASCSFQTASSEVSPPATASCSF QTASSEVSPPATASCSFQTASSE VSPAATASCSFTFSFFVCALWF GICPSCSAAVLST |
| 13959 | 44327 | A | 14041 | 3 | 159 | EHQCENPQ*NTGTPNPAAHQK AYPP*SSGLHPWDNQRQKPHD YLNRCRKGL |
| 13960 | 44328 | A | 14042 | 54 | 245 | GGGGGEAEDRLREPETEKALSS SL/RRAPDQC/RALIMQLFQAHC FFLST/QATAALQAHYAHIFPSK |
| 13961 | 44329 | A | 14043 | 903 | 1205 | WDVSQNNKSYL*QTHSQYHTE WAKTGSIPFENWHKTGMPSLT TPIQHSVGSSGQGNQTNREPNH E*TIHNCFKENKIPRNPTYKGC EGPLQGELQTTAQ |
| 13962 | 44330 | B | 14044 | 1 | 339 | |
| 13963 | 44331 | B | 14045 | 1 | 1547 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13964 | 44332 | A | 14046 | 807 | 1440 | NTGKPNPAAHRKAYPPRSSRLH P*DLQQTPTDLQLSDLTPGRKT NKQKGIASPSTKRTSTPKPHLQ ANAQRFCHHQACVTRVPKGST KHGKEQLVPATAKTQIVKNIN AMKKLHQLTEIQITIREYHKHL YANKLKNLEEMDKFLDTYTLP RLKQEEVESLNRPIMGSEIEAIN SLPTKKSPGPDGFTAKFYERYK EELVSFLLKLFQSIEKEGILPNSF YEASIIIPKPGRDTTKKENFRPI SLKNIDAKILNKILANRIRQPIEK LIHHDQVGFIPEMKGWFKKCKS INVIHHINQTNCKNHMIISIDAE KAFDKTQQPFMLKTLNKLGTIR QKKEIKGIQLGKEEVKLSLFAD DMIVYLENSIVSAQNLLKLISNF SKVSRYSKINLQKSQAFLYTNNR HMESQITSELPFTIDTKRIKYLGI QFTRDVKDLFKENYKLLLNEIK EDTNKWKNI PCSWIEESIS |
| 13965 | 44333 | A | 14047 | 603 | 764 | LPLFLIEYPLFLSLA*LPWPKLPT LC*IGVVREGIPVLCCFSKGMLP VFAHSV |
| 13966 | 44334 | A | 14048 | 1566 | 1865 | MQSIRKTIGIHAKYDKACRNGE DICLRETNSAADTQAKRV*SGP PANSNRPA AEGPDC*KEN*QTE RTSTPKPHLYVTIHKDQRGQTLL TNNGTKLDRE |
| 13967 | 44335 | B | 14049 | 1 | 1932 | |
| 13968 | 44336 | A | 14050 | 711 | 1575 | TRKFRRNG*IP*HIHPPKTKSGR SRI\FNRPI TGSEIEAIINSLPTKKS PGPDGFTA EFYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFI PGMQGWFNIRKSI NVIQHVNRTDRCKNHMIISIDAE KAFDKIQPFMLKTLNKLIGIDG MYLKII RAMYDKPTANIILNGQ RLEAFPLKTGTRQGCPLSPLL FN IVLEVLARAIGQEKEIKGIQLGK EEVKLSLSADDMIVYLEKPIISA QNLFKLISNFSKVSDTKSMYKN HKHSYTPITDKQRAKS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13969 | 44337 | A | 14051 | 1 | 1579 | MQGWFNVRKSLNIIHHINRND KNHIIISIDA EKA FDK IQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRQ GCPLLPLLFNIMLEVLARAI RQE KEMKGIQLGKEEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKINVQKSQAFLYIINRQTESQ IMSELRFTIATKRIKYLGIHLTR DVKDLFNENYKPLLNEIKEDTN KWKNIPCSWTGSINIVKTAILPK VIYRFNAIPIKLQLTFFTELEKTA LKFMWIQGYSNQNSMVLTLV IPRKMRS AVELQQTSTD LQLRD LTVRKKTNKRKATASTSQKGH LHQNPICRSPTSKTKEVGFRRSV ITNFSELKEDVRTYHKEAKNLE NRLDEWLTRINSVEKTLNDLKE LKT MARDLHDACTSFNRRFDQ VEERVTVTEDQINEINDGENGT KLENTPDIIQENFPNLAISRPTF KFRKYREHYKDTPREEQPQDT* LSDSPRLK*RKCC*RQPERKVE LPTKGSPSD |
| 13970 | 44338 | A | 14052 | 50 | 1105 | TRKSRRNG*IPGHIYPPKTKVQE EGESLNRPI TGSEIEAI NNLP TK KSPGPDGFTAKFYQSTNNKNH MIISIDA EKA FHK IQQPFMLKTL NKL GIDGTYLKHRAIYDKPTAN IILNGQKLEAFPLKTGTRQGCP SPLPFNIVLEVLARAI RQEKEIN CIQLHNEEVKLSPFADDMIA YL ENPIVSAQNLLKLISNFSKVSGY KINVQKSQAFLYTINRQTESQI MSELPFTIATKRIKYLGIQLTRD VKYLFKENYKPLLNEIKEDTNK WKYIPCSWIGRINIVKMAILPKV IYRFNAIPIKL PMTLSSQNWKKT TLKFIWNQKRARIAKSILSKKN KAGSIMLPDFKL |
| 13971 | 44339 | A | 14053 | 1 | 764 | MQGWFNVRKSLNIIHHINRND KNHIIISIDA EKA FDK IQQPFML KTLNELGIDGTYLNIIRTIYDRP AANIILNVQKLEAFPLKTGTRQ GCPLLPLLFNIMLEVLARAI RQE KEMKGIQLGKEEIKFSLFADDII VYLENPIFSAPNFLKLISNLSKFS GYKI*FPLFLIEYPSFLSLA*LPW PALPTLC |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13972 | 44340 | A | 14054 | 1 | 344 | MGINQRRKAENSKNQSASSPTK DCSSSPAKEQSWTENDFEELTE VGFRQANAERFCHHQVCPKR APEESTKHGKKQ/RSISHCKNM PNCKDHRCYEETASTDSLAETQ QQKREF |
| 13973 | 44341 | A | 14055 | 301 | 370 | DDGVF*IDNHVICKQRQFDLFS |
| 13974 | 44342 | A | 14056 | 1 | 1418 | MVREGFPEEVTFELKNELEISK GQQMGKNIPDTGASSAKALGE RELGTLDKMKNPSDGSKKDIR THRKEAKNLEKRLDEWLTRINS VEKTLNDLMQLKTMARELHDA CTSFNSQFDQVEERINKIDVRLA RLIKKKREKNQIDAIKNDKGDIS TDPTEIQTIREYYKHLIYANKL ENLEEMDKFLDTYTLPRLNQEE FESLNRPIIGSEIEAVSNSLPTKK SPGPDGFTAIFYQRYKEELVPF LLKLFQSIEKEGILPNAFYEASII LIPKPGRDTTKKENFRPVSLMNI DAKILNKILANRIQQHIKKFIHH DQVSFIPRMQGWFNICKSINIHH HINRTNDKNHMIISIDA EKAFDR IQQPFMLNTLNKLGIDGMYLKII RTIYDKPTANIILNGQKLEAFPL KTGTRQGCPLS/ATPVQHSVGS SDQGSQARERNKGYSIRK*GSQ IVSVCR*HDCIFRKPRLSPKSP |
| 13975 | 44343 | A | 14057 | 1240 | 1596 | CYSFLFVRCPSDSQVPQLQVC/C EFAGGPLQTVFAWVSPA EVVE MFLQG*RKPFYMSY/TSFEMAL MKVWTMVRTSASPVGDFVGR GWSPFPTSTVGALT VFGVSPGS CRSSPLPSERLWV |
| 13976 | 44344 | A | 14058 | 507 | 971 | PANQKKSRTRRIHSQILPEAQR GAGTIPSETIPINGKRGNPPKLIL *SQHHPDTKA WQRHNRKREFY TDIPDDH*CKNPQ*NTGKPNPA AHQKAYPPRSSWLHLWDARLV QRTQISKRNSSYKQNQRQKPHD YLSRCRKGLQQNSAALHAKNS |
| 13977 | 44345 | A | 14059 | 561 | 758 | |
| 13978 | 44346 | A | 14060 | 2364 | 2663 | DGQLTLVSILNHYS LAQSCEY* DGEFCFLHCSASPFL*EGAQST ACTAPPECFASDLGAV*LPQHS WCSTLLLEGAPWPGTLGTAPQF QHRKLGTNLAG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13979 | 44347 | A | 14061 | 1 | 64 | MPIGKVGEYYIKGTLRATKESE QQSSALELSSDRVYLNEKEPGD QPWNAAFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSLTLIIQGCKQEGFYS PSMRPRVVPKRGSAPKVRAEEN AALPSRCPPGPLPVAQP/TGPAD GGSCSEQCPCGCGCCQLPPPLP WFPR*TPCDKRV |
| 13980 | 44348 | A | 14062 | 1 | 774 | MFVWSNVEGHSVAMFPWYSIP FLNPPCSHTRPSNLPVTQWPPT ENNLPWSQLLLTSHQAQFLSA LHKEQGSSEKDGRSPNKWDK DHIRCPMS\AVMIFSKRHQAL/V RAHQGHPNQDNWTVSQMLSK WWYTLGPNERQKYHELAFQAT AALQAHYVHIFPSKGRWELLH GSQRLDWGRCQLKLLGQQGQ DVLHTNLGKEENSSCWGYKME CEEFGFPQGGDCGLGGVHAPL LSPEGLDSEQNTLIMGDIFHCA KKLP |
| 13981 | 44349 | B | 14063 | 1 | 753 | |
| 13982 | 44350 | A | 14064 | 2 | 1457 | YPRRRPSRAGVLAGPAVLGAPP SSPGRPRRAAFFAEPFSARRS PRRAAVLAVPPSPRRRPRRAA VLAAPRVLAAPPSSPRRRPRPP PSSPRRRPRRAAAGSLPGAELP QSSRLAAHL\AAD*PDS*IAAGA VPRGWEGLTIMAEGKEEQVTF YVDGSRQRAYAEKPPVVKTIRS CTV/SGHSRHNSSSGM*/SSPNSP /IPFQFTFQIPSLQAALWLCL*V TWHFFVR*PVLSSRHCFSPGGLF SLSLQSAGCPAGSLQAEFVALP PGGQSRLHRTRAS*VPGAFAQEK CPLERVWPFHPSKQHPRNLAF PLP*APQRTQPAEDTLPRHP GLILSQGTAG/PGRECQATQLPA QHSHAEVLHFGGAMSGQLSLV GPQDSKRTARLTDSQHLGSPT* QPPGLTEGTSLEQG**S*MGWM VGVIAGAPSGWSGSSGPSEGTP LFSSPA*LPWPELPTLC*IGVVR EGIPVLCQFSKGMLPVFAHSA |
| 13983 | 44351 | B | 14065 | 72 | 1235 | |
| 13984 | 44352 | B | 14066 | 1 | 2715 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13985 | 44353 | A | 14067 | 50 | 1304 | TRKFRRNG*IP*HIHPPKTKSGR SRI\FNRPI TGSEIEAIINSLPTKKS PGPDGFTA E FYQRYKEELTNIL DEHRCKILNKILANGIQHDIKKL IHDDQVGFIPGMQGWFNIRKSI NVIQHVNRTRDKNHMIISIDAE KAFDKIQQPFMLKTLNKLGDG MYLKHIRAMYDKPTANIILNGQ RLEAFPLKTGTRQGCPLSPLLFN IVLEV LARAIGQEKEIKGIQLGK EEVKLSLSADDMIVYLEKPIISA QNLFKLISNFSKLSGYKINVQKS QAFLYTNNRQTESQIMSELPFTI ATKRVKYLG IQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNI PCS WIGRINIVKMAILPKCKTVGLLS NISTHKS AVHALVEAGGIPSLIN LLVCDEPEVHSRCAVILYDIAQ CENKDVI AKY |
| 13986 | 44354 | A | 14068 | 1 | 1155 | MFVWRNVEGHSVA VFPWYSIP FLTPPCSHMRPSKLPVTQWPPT RENNLP SWQLLLMSVHQAQSL SALRKEQDSSSEKDGRSPNKW DKDHIWWPMS\AVIIFSKQHQA L/VRAHQGH PNQDNRTISQMLS EQWYTLGPNEMQKYDLAFQN VEARIRY/CHRPKRARFLSHAS PPWRQLPAAGAEASGAWNLP GGG*HDYNRCSVPVFRTEVSTR PRPSEICGLTQE*TLLSAKSQVG NTFGFAGHTISDTTTPCGLCTSK AAIEVPEADTLPHICSWHKGEE CGLRGPEPSSPPPRPSLAARVSA GRGALRRRRRPEVPP\SRAPRSA ATATPANEQRAVADV GQWAR ARGGRVRAAGRSGLLRVKMM KMKTVMIH FHLMKDEYIFSS |
| 13987 | 44355 | A | 14069 | 1331 | 1584 | SLQRKAARFASSTVPRRPQGIL PIISFSNVPVGSRRLLKAPLVFIGP G*ITLNRIPYLP HSAARDPFTWN TFSFLLPCEEVPST |
| 13988 | 44356 | B | 14070 | 1 | 1248 | |
| 13989 | 44357 | B | 14071 | 1 | 459 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13990 | 44358 | A | 14072 | 1 | 2156 | MGKKQSRKTGNSKNQSA SPPP KERSSSPAMEQSWMENDFDDL REEGFRQSNYSELKEEV RTHGK EVKNLEKKLDEWLTRITNAEKS LKDLMELKTTARELHDECTSLK RVSVTEDQM NEMKREEKFREK RIKRNEQSLQEIW DYVKRPNLH LIGVPESDRENGTKLENTLQDII QENFPNLVRQANIQEIQRTPQ RYSSRRATPRHIIVRFTKVEMK EKMLRAAREKGRVTHKGKPIR LTADLLAETLQARREWGPIFNI LKEKNFQPRISYPAKLSFIDRST RQKVNKDTQELNSALHQADLI DIYRTLHPKSTEYTFFSAPHHTY SKIDHIVGSKALLSKCKRTEIIT NCLSDHSAIKLELRIKKLTRNHS TTWKLNNLLNDYWVHNEMK AEIKMFFETNENKDKTYQNLW DTFKTVCRGKFIALNAHKRKQE RSKIDTLTSQKGLEKQEQT HS KASRRQEITKIRAE LKEIETQKT LQKINESRSWFF EKINKIDRPLA RLIKNKREENQIDAIKNDKGDIT TDPTEIQTAISEYYK HLYANKL ENLEEMDKFLD TYTLPRLNQEE VESLNR PITGSEIEAIINSLPTKK SPGPDGFM/RRILPEGQGGAGTI PSETVPINRKRGNPP*/PHFM/SA SIMLIPKGRD TT KENFRPISL MNIDAKI/RQ*NTGKPNPAAHQ KAYPP*SSGLHPWDARLVQLTQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 13991 | 44359 | A | 14073 | 3 | 1794 | AMLPMELGCGPLPEPLPVGCSR FSLFK*QTCISTVP/GYMVTAQS MSSTPPPPSPSTLPSSPSPPPPLPQ PLPPPPSPPTLSSLSPSPRPPL VSPSTLPSPQPSSPQLLPPSSSP SLSPPPSPPLPSPSAIPSLPPP SPQPLPPPPSPSPSLPSLLPPP PLSSSPSSPLSPSPSPSPSLPPS PPPSPPPPPQPPSPSSPLSSPP LSSSQPSLLPSSLPLPSSPSPL LPLSLPLSISPP*LSLLSPLPPSPS LPPSSFQST*TIGQCFSL/VMWH VAPCTYLALAGNTLMAWPLMS ASSKASGGVSMFVWRNVEPCS VAVFSWYSVPFLTTPCSRVRPS NLPVTQWPPTRAKNLPSRQLLL TSVHQAQSLSALCKEQDSSSEK DGRSPNKWDKDHIWWPMSGG HDLQQAAPGPRAHQGHYPYQD NWTISQILSERWYTLGPNEMQK YHDLAFQHMAGEDIASDEEHM VIHEEEGVMVSLLMTALAPLTL ISSSRIFGKVYGPPTSSSYTYSD ASSSTLAPTSFLLGPGAFKAQES GEEAEDGLRELETEKALSSSL/R RALDQ/*LALIMQLFQAHCFFLS T |
| 13992 | 44360 | A | 14074 | 1 | 2496 | MLLSIDAEKAFDKIQPFMLKT LNKLGHGYESHHLHTTNDVDE EDLSDAASKGDDFALSEQSQD AHFLQPEAYGLGEGAETATGT AHQGNHVRVEECGRSLCGCVP LVLHPLPDPSLQPHEAQQPASH SVACNQRKQPAKLPAVAHERP PGGTGSVDPGRPPGATCPESPG PATPHTLGVVEPGKSSPPTMEE EPWAPQGSPCWTAQSLSALRK EQDSSSEKDGRSPNKWDKDHI WWPMS\ALMIFSKRHQAL/V |
| 13993 | 44361 | A | 14075 | 4317 | 5099 | KMFVFLCISAQLSLQCFRGSFHF IKIYDFSQFLFLFELPYLLLLN HFKMLELVLQQGHPNQDNWT VSQMLSKWWYTLGPNERQKY HELAFQVKVAH\CNKD*KKFSS EAKPTSQGLAG\GNKGSWEWS MSETGTATAPGVSSSELLSVAQA TLQSSDTK\SSFCGAEWGHP*GI GCDDVIADDDGFSTTDLDKFKE WVTDAESGDNSGEEPEGNGKFG GKVFAPVIPSSFT/HCRPLLDPE/ PPGSPDPPAAFGKVYGP TLSSSY |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 13994 | 44362 | A | 14076 | 1 | 637 | MSRVGSCRWVCGLADFKNGAT DLCDKSLHNRELSAERPLNEQI AEAEDKIKKTYPPENKPGQSN YSFVDNLNLLKAITEKEKIEKER QSIRSSPLDNKLNVEKDVDNFQ EFGKLIDGYDSTKEWDVWHKF QDIPNVLVGTA FNVDGNGGF VVHWLNNKEFHFTSSTEVMH QLRKLSDKQVDHENDDADRED EEHSQEDRERGLHMKLDH |
| 13995 | 44363 | A | 14077 | 448 | 464 | KKRA*GSVSQRFP AET*LAD*VI NTGSQEA KRREQR |
| 13996 | 44364 | A | 14078 | 179 | 382 | NTPNQRSVASNR FVKCTHQHS VKCTQSALCKMHQSAGFLKVD NHRED*KKGHSDRAKTEHGRG QIRE |
| 13997 | 44365 | A | 14079 | 697 | 1654 | PKPSVGRMGFLGTGTWILVLV LPIQAFPKPG\GSQ\DKSL\H**ED LSAERPFELNRLLEAEGRTRFK KTYPPENKPGQSNYSFVDNL NLL\RAITEKEKIEKERQSIRSSP LDNKLNVEDVDSTKNRKLIDD YDSTKSGLDHKFQENETADNSF SQEEEPVVAGEDLPPSPQESD VQPVQPEEVSARDLQRLDLQI KLSTQA AKKLKEESSLERMRE ETSLSPTVPTKRWDTRILLIGAF YRVLIGAFYRVL MGAFYKPIAS YRALIGVFYRALMGAFYNPLV RQKSSPRPHSTQEVQLASPLTN TQITYYVIFTV |
| 13998 | 44366 | A | 14080 | 72 | 1117 | ILENHLSDRVAEGG PLQGLRLG VQGEAVPPGLVHQRGGLGPLD GELIGSVGQQVSDVEGAGSHR G*RHTGRTPAVSAGPAA*SATH TAPMWLAGWYEP AQPGPVLV SPPTPFGQTRQASWCSA*ARCA GSWWH*HQTPGGA*RVAAPAP SWSRSCP*RPTRSPAAAPPAPSR PGRAVGLATGAGHPAQHGHGR AVPTGPRAAGAGSWSELCPSS CAGTSRGR*AGTRR*AAPAGSG RPGPGA WAGPRCSRSTYAAAA CGRGGA*AGADSGPRSGTHAG HCGARCRSSTPLVPAAAGHLPP PGPGRTGDCPASSCPGPGLPHG CSLSGSWGEGWVSAARQAGLP WAVA |
| 13999 | 44367 | A | 14081 | 2 | 269 | |
| 14000 | 44368 | A | 14082 | 1 | 591 | |
| 14001 | 44369 | A | 14083 | 2 | 477 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14002 | 44370 | B | 14084 | 237 | 419 | |
| 14003 | 44371 | A | 14085 | 2 | 1220 | LPPGFVMAAAAARWNHVWVG TETGILKGVNLQRKQANFTA GGQPRREEAVSALCWGTGGET QMLVGCADRTVKHFSTEDGIF QGSETLPGVGEPMFRGLAQTG TLITCVDSGILRVWHDKDKDTS F*PTPGTESGPWGCVCAKTQA HPHVVCHRLGKRMLLKIWDLQ GS\GNLCFKAKNVRNDWDLR VPIWDQDIQFLPGSQKLVTCTG YHQVRVYDPASPQRRPVLETT YEEYPLTAMTLTPGGNSVIVGN THGQLAEIDLRQGRLLGCLKGL AGSVRGVAV\HPSKPLT*PPVRL DRVLRHRIQNPRGLEHKVYLK VSIE/RALLLSGRDNLGG*APEP SKTQTRCP*EDTEDR*TLGDPW RQLPSGKLFVWSSPKELSKRD GERRSGLGPPAPDAPVPTL |
| 14004 | 44372 | B | 14086 | 96 | 592 | |
| 14005 | 44373 | A | 14087 | 102 | 612 | HCAGSPHSPRSLSGTPLPL WRHLRSPSAHRCTVGAPFWAG QDRSQLP*LAGRCGGRGPSGNP GCA\PACGPAGVPGGRGLGGPR TRSSQPALPAPGNEGLSTRASG CRGRTGSPSSASPPLGLSCLPAG QGWGP/GSPPCVSLPPTPWAPV RPEPPG*AAPPAPRRPVP |
| 14006 | 44374 | C | 14088 | 1 | 636 | |
| 14007 | 44375 | B | 14089 | 31 | 612 | |
| 14008 | 44376 | A | 14090 | 234 | 504 | SFYHLGAGE*PGKSRVPIQFQS PWGPYCQGRARGGEVCHLQAV PPRGAGAARTLSGHPLGSPEQL PQGPAAELPGGVVPRSTPPCP |
| 14009 | 44377 | B | 14091 | 1 | 924 | |
| 14010 | 44378 | A | 14092 | 11 | 354 | RLSTSPDSSGAQLASPSGSHTRA AGGAACQSRAVRS/PFPSPWVV DGTGCGGAGGGARWGGSGCT GAHGVGGR\PGMAG*GPEPCP EGRQLRPLAPVGCQG*REP\G*K NSMGETTT |
| 14011 | 44379 | A | 14093 | 147 | 513 | GSASGVVRLSRWARGLAGFRS EAADLRGECYSS*GSASGVVRL SRWARGLAGFRSEAADLRGEC YSS*KQRGPKELRSPAGFT*WIP /LPGLQVELPASPAPCAPTPQPL SG*WD\GRRGAGGGARRGGSG RTGALGVG\GGSGMAGCRSRA LPPREGS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14012 | 44380 | A | 14094 | 418 | 1026 | WNPHQGCRWSCLPVPRHALAF LSPWVIDGTGRHGAGGGALWG GSGRTGAHGVGG*GMAGCR SRALPHGKAAKAR*EIERSASG/ TGTAGGPSTPSAATGPGAKSLI ARGQQGWPAAPSAGPAKPTPT GNSSWPASAAGSSGSCSRLS/SP HLPAS*GSLQPWPAQKGAPT VQQQAEGLPPIRLPEEWISLPFLG HQGEHSGMA |
| 14013 | 44381 | A | 14095 | 897 | 2111 | PLLQSSPNFFLICYPWHNSHE NTHRTGRRGAGGGARRGGSGR TGAHGVGGRLRHGGLQVPSPA PWECS*GPARNRAQRRYHCSCP GLQSGLPHYSGYHT*PDEKEKN GREGQKLER |
| 14014 | 44382 | A | 14096 | 1304 | 1922 | KLNIGVIYSSEIPDSGAQLASPS GSGTRAAGGAVCQSCALRSHSS ALGWSMG/PGRRGAGGGARW GGLGRTGAHGVGGRLRHGGLQ VPSPAPREGS*GSVRNPAQRRW AGTAGGPSTPSAATGPGAKSLI TRGQQGWPAAPSEGA KPTPTR NSSWPASAARSPGSRSR/RLPPH LPAS*GSLQPWPAHYFEFFLPI GQNAQTEVSY |
| 14015 | 44383 | A | 14097 | 318 | 533 | MVCFDGDGPWVVDGTGRRG AGGGAHRRGSGRTGAREAGGR LRHGGLQVPSPARREGS*GPAS PAGCLAHL |
| 14016 | 44384 | A | 14098 | 346 | 957 | ARYTLHIPTRLGSPAGFTQWIPH RGCRCWSCLPVPRRALAFLSPW VVCSPVDGTGRRGAGGGARR GSGRTGAHGVGGRLPGMAGC RSRALPRGKAAKARREIERSAG G/TGTAAGPSTPSAAAGPGAKS PFARG/LAGPAAPSARPAKPTST RNSSWPASAARSPGSRSWKMS LYMKKSASGQSQAQWIAKMW KSPRFKPLWLTS |
| 14017 | 44385 | A | 14099 | 124 | 663 | SCLPVLRRLTFLSPWVNGTG RRGVGGGARRGGSGRTGAHGV GGRIPGMAGCRSRALPRGKAA KARREIHSAGG/TGTAGGPGT PSAATGPGAKSPIAPGQQGWLA ALGINGAGERLFMKVAFSLKTC SLSCSYLRRLTSLRGGSVHVLRG NLTVCQPQALLRVVFHHQRQ ADCGALPVP |
| 14018 | 44386 | C | 14100 | 1 | 672 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14019 | 44387 | A | 14101 | 3 | 1759 | RPLRGWRRTRDARAPRRRCRG SHGARRCLRKTAATSRCGGAP GPARSRPPSTGQAAEAGDW/PAG CNP*GGLRAADGPGSRPPRGS GLLCGQGGQGGSSPWVHGTG RCGAGGGAPWGGSGRTGAHG VGGRLRHGGLQVPSPAPQEGS* GSARNRAQPRWAGTAGGPSTP SAATGPGRDGEGG\ETGAHVSA LKGTGTEWPAHGLVPYSIGDQ TCLIFKVTFAVVLKCGPQTTS STSISCPGSAN/SPPSPAG*/GSSG CGSSSLCSAHSVQEDSQPQ*KR TGLQS\TYGRSGSSSNEPRYHSD LPTSRSKLRNEDTFFGRRKKLS EVQRTGQDPA*SHHTSSYTLPG L*TAEGKDRVENAA*KGSPNFQ RSGTFNPKGGARKTRQAWHPR APNCQAGTPPREGSSGPRTSL AAFRIPQEVVNFISGPITRAQR HGEPEsprGQTGSPPLGKTGSE GDRKSTGADKKSTGDRQEV EPTESQGLDRKPTGMDRRSTG NRQKVRRQIGSPLGLNRKPNGT DKKSTRNRQEVRRRQSAGARQ ERAGSSTFLRLSALCGLLDVN REQVAKQKWDLYSSRFTSGNR |
| 14020 | 44388 | A | 14102 | 1879 | 2607 | GKPSLSLHPGHKCGISRCNGNV SSRLRSPAGFTQWIPHRGCRWS CLPAPRCALALLSPWVVDGTG RHGAGGGARRGGSGRTGAHG VGGRLRHGGLQVPSPAPREGS* GPARNRAQRRWAGTAGGLSTP SAATGPGAKSPIARGQQGWPA APSGGPPSPSPPGTPAGPQAPH AAPVPA\PLPPHLPAS*GSLQ PWPAQKGAPTQGGG*RAPQM PPKWEPRQRRIVAFTEVGVL |
| 14021 | 44389 | A | 14103 | 2 | 272 | GHWGMVNSPCRASATVSRGSP LPGVLTPSPSATSTCRMCHPR RCPLPFRRLSPPSLTPP/PGKPPL LPRPHSMPLGLPLGGLPVFHP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14022 | 44390 | A | 14104 | 101 | 1815 | QSARQLRPCGAPSLAGVENRR KKTNTLTS AAPDTQSTCGQSC GCLHSMGSSCMQHSYYTGFLR SLWPCRCHRSASFSGQRRSEKD SKSVRERSGRSQNVPARPALTS PLTQSPGPLAPGAGWSRSQLG TGTGVLWWQRESATGDFRTES ARSSDPSRRDWP GAKRKREEG AATVLWACATASTAIICQDNAI SPLKSGNSPSNHLWRPQGQLPP VLGLAQPKRWRPNRLTTSPPSPS RMMARPVD PQRS DP TFRSSTR HSGKLEPMEATAHLLRKQCPSR LNSPAWEASGLHWSSLDSPVG\ PCR P*GLRPSTHGAR\TFSGARP GLGGYSPPEEAMPFEFDQPAQ RGCSQLLLQVPDLAPGGPGAA GVPGAPPEEPQALRPAKAGSRG GYSPPPEETMPFELDGEGFGDD SPPPGLSRVIAQVDGSSQFAAV AASSHQCLSHHIPMSPSVGRNG LLTKPPSTSRRGKLT KRDDMY Y FVPFRSLNDMMHMLPFIEDSR WTHNLDINREQTNPLAGPKG RPISRTQAAASTSNSKTESIQIE KTEEAPFSLRYININNRSM DPLN |
| 14023 | 44391 | A | 14105 | 39 | 877 | AGPGPPRPLPPRSSEGPPGASISL CSEVPGPSCQGRFRGGRDAMS MPWREEERSLLAGE*PS*GG*S GRGVSRKCS*PGPRGVPRPRPL RSRPRAASSE\DQNSPLDQSLHR TRKTIPSSGGSTAIMPRGSSSE TFFSAPSKTWVLGIPGETFISGP AAFP\APGGPRAAPRPSPLNSL *SGGNGGPGPRLHFSSCGKGP PRPSNSRN\GGQSACQGGSHLV C*SHRGS LGEGHAYQGDPCSPG HPAKAPSRAHAQARRSAHAAS LTSGPCDASCQAW |
| 14024 | 44392 | A | 14106 | 358 | 546 | CFPSRI RLALS RAPK WPAKRSPS EPEMS/PPVWSPHPDPNNTAPPK EQPPSSPGRVGRHGNWSV |
| 14025 | 44393 | A | 14107 | 22 | 549 | DHCLCSVVRNKRDSVYPLPIPP CCKTSTISPP/LVDAVRP*DISVS KRVTS CAPLEPQPHCLPTINAG R/TLARPQGAPTPNKEEGQAPG RATASGQAAPATTVLGD TTK/G PQGRHRGTSASAAGPAPFAVA DQLPPEDRAASA EGRK*AAAFP FCHRLVQDGGPPPPAAGVPGA GES |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14026 | 44394 | A | 14108 | 146 | 2616 | LAAVGMASHCFRQRRQSQSPA\ GLRGAGSAYSPA\EGARSSHGQ/ PPWRGRRRGPGDPVRGAARCR RPRAAAQPARPAARPPARPRPA P*AACCE/VPSAANSVAPSAAM *SSAGRDGASSQRSRRPHAAPP RSSALPANGK/PPSPVTRAARTC GARSSNTGA*SAARPKHSAASS RHPPPA/MPLPARHA/PGGTSG RPLPTPQGSAPTSSASPRGPATP PPAGPRAPPPSPRRAAAPRPPGR QLSPAPGTPAAGGGGPPFPALR *SGSVFGRQLVGDGERGRACG ARGSAVPALRTFVVPSTVVA GAACPLAVALPAPDPLPCSE*A PLRSG*VPQPASLFCSQFRPQA WQHP*LLRAPCRLGAAVPCV WCHSRALDSATPRWM*G*RLP AVWLPAFPSPFFNQAFVPPCQQ NCSLQNRQTLASAKIGTEEWD IAIKIPENVEVTLELGNEQRLEE FGGLRRRQEDEGKFGTPTDWL NGCDQNADSNMDSEGQGEDG GCSFGGAGLRGSGWGDQTRET FLALKANLRWFRSSAQSQTSQ EGAAGARSGLKGGKKNPLKLP KKQAKKMNAFKQKQEKERK KHKELKAKASWKGLRPQVEFK NLAERRGEAAVPGCPVVAGHS WRLLSLARGCAKRARQLLPSE KLLAALREGSTRGGGAASQPQ RKLRVCMRVLDSVEDFHMDG |
| 14027 | 44395 | A | 14109 | 1 | 885 | MIISIDTEKALDKILHPFILKTLN KLGIDGTYLKIIRALYDKPTANI IMNEQKLEAFPLKSNTKQGC PF LPLLFNIVLEVLARAIKQEKEIK SIQIGREEVKLSLFADDMIVYLE NPIISAPNLLKLISNFSKVS GYKI NVQKSQAFLYTSNRQTEIQMM SELPFTIATKGIKYLGINHPLTRD VKDLFKENSKPLL/KELEKTTLN FIWNQKRAHIAKTMLS KKNKA GGVMLPDFKLYYKAAVTKTA WLGDDQVFLIPRGHISDYHMG KNLGQYPAFQDRGPCGFQCIV PLVYRD |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14028 | 44396 | A | 14110 | 453 | 891 | LIHLSTDALRVSGWGTVRSFSS HEAIFQTIAWGETLDNTLLSRA EVPAAFHGALCPWFIETREWQ* LLQSILLVNIWLTRHVLHSPRSL KP*FYTT*VFVCSKLGQSGWGK VAGAKLQMNNISAKQLFKVQV LFKIESLMSSLST |
| 14029 | 44397 | A | 14111 | 452 | 2922 | KMGLAREWILRFLVLILQEIRS MRQKENKDIQDLNSALHQADL IDIYRTLHPKSTEYTFFSAPHC/ RTYSKIDHTLGSKALLSKCKITE IITDSQTTVLSELRIKKLTQNR ATWKLNS/YLNDYWVHNEMK AEIKMFFETNENKDTTYQNLW DTFKAVCRGKFIALNAHKKRQ ERSKIDTLMSQLKELEKQEOTH SKVSRRPITGSEIEAINSFTNPK RVPGPDGFDEPNFYQRYKQEL VPFLLKLFQSIEKDILPN*FYE ASILIPKPGRTTK/EENFRPIS LMNIDAKILNKILANRIQQHIKK LLHHDQVGFIPGMQGWFNICKS INVIQHINRTSDKNHTIISDAEK AFNKIQQLFMLKTLNKLGTNG MYLKIVRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLAIRQEKEIQGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINLQ KSQAFLYTNNRQTESQIMSELP FTTASRKIKYLGQLTRDVKDLF KENYKPLLNEIKEDTNKWRNIP CSWVGRINIVKMAILPKV TYRF NAIPIKLPMFTFFTELEKTILKFR WNQKRAHIAKTILSQKNKAGGI RLPDFKLFYKATVTKTARYWY ENRDIDQWNRTEPLEIMPHIYN HLIFDKPDKNKQWGKDSL FNK WCWENWLAICRKLKLDPFLLTS |
| 14030 | 44398 | A | 14112 | 3 | 3349 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14031 | 44399 | A | 14113 | 294 | 1107 | RRHRLNYIPRTAQSPHPRKAL ARSESKRDGGFKNWFSFDHEE ESEGDTDKEPGPLDAPPRP/ESG PRAPGKGL*RRSRSPGPSEGRSA ARLTAEPEARNPAASTLLRRGP SSRRARRRCGPWIKKEAAWEE EDGGRQERRLGQDLRTRTLNK SKGGIDSRIISLGQHSHPHAKL WLDQSLREMEVLKIIIGALIMKK KVKEIQIKSRARSTPLHDQIGTT SPRERTIASKRHPYYITPKGIRY EQDTLSRTPITTIRSRQRPLGPLT ASPPPSFPTLAPPTQAIKPSLHLR EGKPTPTPGERSTRPHHPEPPRK EYALSSLYPPTYLLAPTSTDLG NAHPTQEPQFNVDATHPRQNR FIPVAGNSPKRSSQFPIVFAPKK NTTPPYLDFAAILGLHRRPPRSR FRTSYPPKEFRSSPPPERTAPRN |
| 14032 | 44400 | A | 14114 | 2 | 297 | VQKSVLCSFQAGTMEGVVEEKK VPAVPETLKKKRRNFADAIQFL QTVFLAF*YTLLKGRQ\VYWL EE*HQFYKISYRKKMVQRIRQH PQSCTVQKSWWP |
| 14033 | 44401 | A | 14115 | 3 | 754 | GTMEGVVEEKKKEVPAVPETLK KKRRNFAELKIKRLRKKFAQK MLRKARRKLIYEKAKHYHKEY RQMYRTEIRMARMARKAGNF YVPAEPKLAFVIRIRGINGVSPK VRKVLQLLRLRQIFN\GTFFVKL NKASINMLRIVEPYIA*EYPNLK SVNELIYKHGYGKINKK*VALT DNTLIARPLGKYGITCMEDL/IH EIYTVGKCFKEANNFLWPFKLS SALSGMK/KKTTHFVEGGDGG NRVDQINTLNRRMN |
| 14034 | 44402 | A | 14116 | 1 | 388 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14035 | 44403 | A | 14117 | 1 | 1145 | MTRNYEWLLEAESSQPPIAFQK MEPQPYNSKELNSANNQCLLE KPKLRQRLKDKEYDQGHTAVQ CQSWVYVLT PDSFCQQLILLPS TENFHECSRSDTAGHLRTGHVA SNWLSEHSPQTMPAAMQWDK KMQNTSSWFPQKAPEKVKPMS KLWQTPSQNDTLYKAVKALTL SSPERNSINTNKKDVHTETSSK GHQHQRPKVDKSMKMRKNQH KKAENSONQNASSPPRNHNSSP ARERNWSENEFDELTEVVFR WVITNSSELKEHVL TQCKEAKN LEKRLEELLTRITGLEINQAEERI SETEDQLNEIKHEDKIREKRMK RNEQILQEIWAYVKIRPKLRLIG VPENDRENGNKLENTLQDTIQE NFPELAR*ANIIQ |
| 14036 | 44404 | C | 14118 | 291 | 551 | |
| 14037 | 44405 | B | 14119 | 1 | 1308 | |
| 14038 | 44406 | A | 14120 | 82 | 367 | ITLSSPPHSFIGHKTPASGPPQKI PPQPSQ/CKQWGDPTPVEAC/CV SCPTQGFISPTRGGPPCKHESLV VPLVGT PRRNQPGGHIQHSQR WAPVLT |
| 14039 | 44407 | A | 14121 | 999 | 2661 | VHLTGC GGPGQPVPEPAPPRGL RSMRC/GP*GFSPGAEA*TEP/C HYGGRGFPCGPFSLGCLATNSP WLPGRPPCSPWAGPCGLCPLP AAAAERQPALSVPGASPSRLL PLVVLCHGSHLNGGRVLLRPG GSPCGHCHNCAGARRGLGHVL QGGAQARQREQLQR |
| 14040 | 44408 | B | 14122 | 164 | 1042 | |
| 14041 | 44409 | B | 14123 | 320 | 566 | |
| 14042 | 44410 | B | 14124 | 1539 | 1674 | |
| 14043 | 44411 | A | 14125 | 185 | 780 | QKAKKGKLRSKQNSFPGLKK TVPSQLVQYCPSF*ISWKPMVY QKVPA*PRPPRTPDHHPDPGPA PHPRQHHPSPDAEP/SPTTPT RRRPPTQPPDHPKRPPPHSKPH PPQQPPTPTATPTEQQRHTAPP TPRPPTTHPPSTPKHPA\ PHTAPP PTKNTKPPTPQRTTQDKGRQKK PRRQPHHSEPNKKSPKAHI |
| 14044 | 44412 | C | 14126 | 1 | 1128 | |
| 14045 | 44413 | A | 14127 | 319 | 536 | |
| 14046 | 44414 | C | 14128 | 231 | 425 | |
| 14047 | 44415 | B | 14129 | 1 | 1431 | |
| 14048 | 44416 | A | 14130 | 75 | 393 | |
| 14049 | 44417 | C | 14131 | 174 | 371 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14050 | 44418 | A | 14132 | 79 | 164 | |
| 14051 | 44419 | A | 14133 | 343 | 775 | |
| 14052 | 44420 | A | 14134 | 554 | 724 | SEGPSKEPTHRRMKFSHHDDL FLDLSN*QPPNSPEPHPPQSP*KP WPQNPSSRQM |
| 14053 | 44421 | A | 14135 | 20 | 242 | VSFLSMGSGHCIRSTRGSKMVS WSVIAKIQEI*CEEDERKMARES LAESMSTYVMMNHTYDS*GK THILIMKK |
| 14054 | 44422 | A | 14136 | 229 | 366 | |
| 14055 | 44423 | A | 14137 | 131 | 505 | |
| 14056 | 44424 | A | 14138 | 1 | 1317 | AGCSCGSRAMAEQGRERDSV PKPSVLFLHPDLGVGGAERLVL DAALALQARGCSVKIWTAHYD PGHCFAESRELPVRCAGDWLPR GLGWGGRGAAV\CAYVRMVFL ALYVFLADEEFDVVVCDQVS ACIPVFRLARRRRKILFYCHFA DLLLLTKRDSFLKRLYRAPIDWI EEYTTGMADCILVNSQFTAADF KETFKSLSH\KDPDVLYP\SLNV TSFDFSCS*KAGMT*SPRGKNS WLLSINRY\EREGKIWTLGTK ALVQLRGRLTSQDWERVHLIV AGGYDERVLENVEHYQELKK MVQQSDLGQYVTFRLRSFSDKQ KISLL/RQLARVCFYTPRQ*GTL GIVPLGRPCYMAVPQFICCLIRV GPFSSSI*PQCSQGFCVEPDVH FSEAIEKFIREPSLKATMGLGWE EPE*REKFSFGSILQEQLYRYVY |
| 14057 | 44425 | A | 14139 | 1 | 648 | MESKEEQGVADHQAATRGIP TPQPREVVSERATQRGNRAFST KLCNPKTNRKQQQQYQQQQK GRTKTLPGQHPQRSKLDKLTE MRKHQQKNTKNPKGQSPCSPP NDCNVSPARVHNWTGDEMEEL TEVGFKKWVRKNCAELKEHVL TQCKEAKNLDRLEELLTRKTS LERNINDLMELKT/RA*ELCKA YTSINS*IDQAEERISEFEDHLAE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14058 | 44426 | A | 14140 | 1 | 1365 | MPVKGGTKCIKYLLFGFNFIW VSEDCRALLSGPTCSRAPDTG RGRECRQLALPAPGRHRAGRES ALRLPAGSKAGSRAGRDGRDG RIRVGVS GTLFGSTTGLFNQSL AETGFTPYTQKSNDLVKSLKI WHTYFKNFHQEARLYIRTSPGS NWNWFCTLGIESPEQPGVYEG QRPRVVTKS FASLT LKRVGTVL LLAARINADVLYVLQLAGIAVL AIGLWLRFDSTQKSIFEQETNN NNSSFYTGVIYILIGAGALMMLV GFLGCCGAVQESQCMLGLFFG FLLVIFAIEIAAAIWGYSHKDEV IKEVQEFYKDTYNKLKTKDEPQ RETLKAIHYAVCRLGKDTLLRF LRIVSAHRLNCCGLAGGVEQFI SDICPKKDVLETFTVKSCPDAIK EVFDNKFHII GAVGIGIAVVMPS FRSNHPDPHVSSYLLNIFGMIFS MILCCAIRRNREMV |
| 14059 | 44427 | B | 14141 | 98 | 1064 | |
| 14060 | 44428 | A | 14142 | 560 | 964 | KRLPRILGIRGKPCCPDTSRAGR RVRGRAAAPCREAARGRGQRR FLPPTWRCETGAATMFPSPALT PTPFSVKDILNITVRPRS/LGQAA LTKRLSASLSPQSCARCRRRWS CVILSAVRGN*YAGSRAHRDCT Q |
| 14061 | 44429 | C | 14143 | 189 | 452 | |
| 14062 | 44430 | A | 14144 | 1 | 647 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14063 | 44431 | A | 14145 | 890 | 2905 | LRLSLKFPMQWTPPEYNELTYL KVDMKSEIPSDAPKTQESLKG LLHPEPIGAAKSFPAGVEMINSK VGNEFSHLCDDSQKQEKEMNG NQQEQEKS LVVRKKRKSQQAG PSYVQNCVKENQGILGLRQHL GTPSDEDNDSSFSDCLSSPSSSL HFGDSDTVTSDEDKEVSVRHSQ TILNAKSRSHSARSHKWPRTE ESVSGLLMKRPCLHGSSLRRLP CRKRFVKNNSSQRTQKQKERIL MQRKKREVLARRKYALLPSSSS SSENDLSSESSSSSSTEGEEDLF VSASENHQNNPAVPSVTYGGP WSKNIKEKTLEINSSQALTA YE CLHSAHVINLISPFYHHFPSSQE RSYLSTLSTLSNKTGVS WFTR SPKVTQFFPGGAI TGLSQRPER EILRPLALPGKGNTPPYFCSPSM GCTHCPTSPNEMNQGIS EDTAA APVRDIYIKPPSPWDRA PGGRG GCGHSFSRLKSPYL RALKSAAD FPAQHSSSDKGQAASSSGSLTP VYPVWVTPPSRGRQTPHRGEL WLASDGCPSGRKLPEEGTGSNL CCSAASAGDTQANRDHNSSPA REQTW TENKFDKLTEAGLRRW VINSELKEPVL TQCKEAKNLE KRLDESPTRITSSEKNINDLMEL KNTAQELHEEHTSINSQ/DQAE* |
| 14064 | 44432 | A | 14146 | 1 | 737 | LNRGEQRAVRYYS HMKLNMA EEEDYMSGFLH*CP RRYQTRIA NAKANPRSPSKRÆKQ QEANLK NRQKSLKEEEQERRDIGLKNAL GCENKGFALLQKMGYKSGQAL GKSGKSGIGHEASLRKAE EKL ESYRKKIHMKNQAE EKA AEQF RMRLKNKQDEM KLEGDLRRSQ RACQQLDVQKNIQVPREAWY WLRLEEETE EDEEEKEQDEDEY KSEDLSIKKTYLQIVQDQLLQI MTKIIPNKVET |
| 14065 | 44433 | A | 14147 | 1 | 1860 | |
| 14066 | 44434 | A | 14148 | 1 | 1203 | |
| 14067 | 44435 | B | 14149 | 1 | 1119 | |
| 14068 | 44436 | A | 14150 | 1 | 1407 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14069 | 44437 | A | 14151 | 1 | 1731 | ERSSSPATEQSWMENDFDELRE EGFRRSNFSELKEKVRTHHKQD KNLEKRSWFFKINKIDRPLAR LIKKKREKSQINAIKNDKGDITA DPTEIQTITITEYYKHLIYANKLE NLEAMDKFLDTYTLPRINQEEV ESLNR/LNNRL*N*GNN**LTNQ K/NVQDQMD*QLNSTRGTRRS WY/RFLCLKFQSIEKERILPNSFY EGHILLIPKPGRDNTKKDNFKPIS LMNMDAKILNKILANRIQQHIK KLIHHDQVGFIPGMQGWFNICK SINVIQHINRTKDKNHMIISTDA GKAFDKIQQPFMLKTLNKLIGID GMNLKIIRAIYDKPTANIILNRQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPV SAQNLLKLISNFSKVSGYKISVQ KSQAFLYTNNRQTESQIMSEIPF PIASKRIKYLGIQLTRDVKDLFK ENCKPLLKEIKENTNKWKNIPC SWIERINIVKMAILPKVIYSFNAI PIKHPMTFFTELEKTTLKFIWNQ KRARITKSILRQKNKAGGITLPE FKLYYKTTVTKIAWYG |
| 14070 | 44438 | B | 14152 | 1 | 906 | |
| 14071 | 44439 | A | 14153 | 3 | 553 | EHSSSPATEQSWMENDFDELRE EGFRRSNYSELKEEVRTGKEV KNLEKKLDEWLTRITNAEKSLK DLMELKTTAREICDECTSLSSR CDQLPRPDGFTAIFYERYKEEM VPFLLKLFQSIEKE/VNPP*LTL* GQHHPDTKAWQRHNKKREF*T NIPDEH*CKNPQ*NTGKPNPAA HQKAYPP |
| 14072 | 44440 | A | 14154 | 1 | 909 | MKAEIKMFFETNENKDTTYQN LWDTFKAVCRGKFIANVHKR KQERSKIDTLTSQLEKEKQEQ THSKASRRQEITKIRAEKIEIET QNTLQKINASRSWFFERTNKID RPLARLIKKKREKNQIDAIND KGDITDPTEIQTITIREYYKHLIY ANKLENLEEMDKFLDTYTLPRL NQEEVESLNRPIGAEIEAINS PTKKSPGPDGFTAIFYQRYKEE LECSSSPAMEQSWTENDFDDL EEGFRRSNFSELKEEVQTHRKE AKNLEKRLEKWLTRITNVEKS LNYLRELKTMARELC |
| 14073 | 44441 | A | 14155 | 1 | 969 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14074 | 44442 | A | 14156 | 377 | 687 | LLEGKLTNRKDIHTKTPSV/SPP SSKTKEHSSSPAMEQSWMEND FHELREEGFRRSNFSKLKEEVR THRKEVENLEKRLDEWLTRITK VEKALNDLMELKTMARE |
| 14075 | 44443 | A | 14157 | 1 | 711 | |
| 14076 | 44444 | A | 14158 | 1 | 831 | |
| 14077 | 44445 | A | 14159 | 1 | 744 | |
| 14078 | 44446 | B | 14160 | 1 | 1479 | |
| 14079 | 44447 | A | 14161 | 1 | 810 | |
| 14080 | 44448 | A | 14162 | 3 | 651 | |
| 14081 | 44449 | A | 14163 | 2 | 1067 | |
| 14082 | 44450 | A | 14164 | 2 | 2063 | |
| 14083 | 44451 | A | 14165 | 1328 | 1639 | PTNAHETSGRYIAGSSEKRTSA RTCGGTSAARPAGTSMQTRC RQPPSS*HAVPRVAQSSDGL KATHPQAYQPCGHTPTRLPQES NCIEHERGLGKKKKKKK |
| 14084 | 44452 | A | 14166 | 1 | 620 | MTLGYGQRGANKDLRTGFDPD LCTMDNFAEGDFTVADYALLE DCPHVDDCVFAAEFMSNDYVR VTQLYCDGVNDSFLIGLLRIG CKIENERSSSPAMEQSWTENDF DELREEGFRRSNYSELKEEVRT NGKEVRNFEKKLDEWITRITNA EKSLKDLMEKTTARELCDKC TNLSNRCDQLEERVSAMEDEM NEMKHEDKFREKE |
| 14085 | 44453 | A | 14167 | 1 | 514 | MGKKQNRKTENSKNQRTSSSP KERSSSPAEEQSWMENDFDEL REEGFRRSNFSELKEEVRTGK EVKNLEKRLDKWLTRITNTQKS LKDLMEKTTARELHDECTSLT NQFDQLEERINNIEDH*QD**R RKERRIK*MQ*KMIKGISPLIPQ KYKLPSSENTINTSMQIN |
| 14086 | 44454 | A | 14168 | 1 | 366 | MDTFLQAERKDYMEAYELIEQ EEQGEREPVAVNNILSTEALMA NAKSTLMFYAVGFLWQPGGGR GHKAASNPGVTRDVVGLSSLT FLRGERSSSPAMEQSWTDNDFD ELAREEGFR*SNFS |
| 14087 | 44455 | A | 14169 | 1 | 1026 | |
| 14088 | 44456 | A | 14170 | 1 | 3906 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14089 | 44457 | A | 14171 | 1643 | 2721 | IKPTKMGGKKQSRKTGNSEKQST SPPPKERSSSPAMEQSWMENDF DELTGAGFRRLVITDFSELKED VQTHHKEAKNLEKRLDKCRTN G*LEWMNG/ITRITNAEKS LKDL MELKTKARELHDECTSLRSRFD QLEERVSVMEDQKKVMNEMKR EGKFREKRVKRNEQSLQEIWD YVKRPNLRLIGVPESDGENGTK LENTLQDIIQENFPNLARQANV QIQEIQRTPQRYSSRRATPRHIIV RFTKVEMKEKMLRAAREKGQ VTLKGKHIRLTVDLSAETLQAR REWGPIFNILKEKNFQPRISYPG KLSFISEGEIKYFTDKQMLRDFV TTRPALKELLKEVLNMERNNR YQPLQNHAKM |
| 14090 | 44458 | A | 14172 | 351 | 898 | SGVTAPWRPNGTLLITAATASH PVLAI PAHLCSRPCSFLT TVTC SGPQHHAARGRVPFHC/SEC GK SFRYRSDLRRHF/ARHTALKPH ACPRCG/KGFKHSFNLANHLRS HTG/ERP YRCSACPKGFRDST/G LLHHQVK TITT*PD/CGGCLVSN IVGSYSRPPWPCTRGPRRPLGSP SPAPGSVCLC |
| 14091 | 44459 | A | 14173 | 1 | 551 | |
| 14092 | 44460 | A | 14174 | 3031 | 3207 | TIHGCWWDPLSSIF*PFWGRGFI SHKICQAQISFRVISGTVLSLDK LLIMFHKAIFASP |
| 14093 | 44461 | A | 14175 | 3555 | 3957 | ENGQKTWTGTSQRRYTGDRM AQIQNPDTKCW*ECKATGTRI CWWECKMVQPLWKS\WQFLT KLSILLPYNLA ILLGNYPNALK MYAHTKGFTCMFIAASFIIAKT WKQPRRPSVGEW/INNL*LVQT MEYYSAL |
| 14094 | 44462 | A | 14176 | 3 | 883 | CQPYPRPRPTGTHGSCQPPSQ GSAEP*G*CLPTLLRMALKAQP TKVNPRTLLDSDPDVC/S*AAHS RVLITSPSRAPWRLPSP*RRCPA GTCMPSTAT SAR*CSQRPGSSW *T*TGSSLGSQACGPSSSTAPPSS SWSACTCGCAAAARCSCAASS TRSGPTCGSSPPASSCASSTPAP GTTPSSTLT SWASSPWSTPCPGS AGPSSWSSSSSATPSASASTRTL SPGSPAAP*PWPTALSRLTEQEA VWGA WGISHGNSWDKETKLV RLPHPCSKSPCFRPSLQPYRAHR AP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14095 | 44463 | A | 14177 | 3 | 395 | SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL\GILLHL ESELAQTRAEGQRQAQYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH |
| 14096 | 44464 | A | 14178 | 2 | 1044 | AKTSSQMPSQPQEGMCGKACTP ALSQADSLCPLLRLASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALSSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTNG\GGLA GMGGIQNEKETMQSLRDRLAS YLDRVRGLETENWKLESKIQEH LNVTRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAMTLT ELRHRVQSLEIDL DSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14097 | 44465 | A | 14179 | 1 | 2040 | MPVPQLPPPVSRLAATAAASVT EPGPNPEAVRSASAEPEVKEGF PSQNHSGVGHSLIPSGGVSAPSS GRSHYGYASEDGTCSKLRVRPR LAAAPAAPFAFVADLASCCQG LSFFEGILLVRGPYRRLRATVV RDLVAVRMAEEQEFTQLCKLP AQPSHPHCVNNTYRSAQHSQA LLRGLLALRDSGILFDVVLVVE GRHIEAHRILLAASCDYFMSFT TRSTFSTNYWSLGSVLATTYGA RLVSSTARVYAGAGGSGSRISV SRSTSFGGLESGLAAGMAG GLAGMGGIQNEKETMQSLNDR LASYLDRVRSLETENRRLESKIR EHLEKKGPQVRDWSHYFKIIED LRAQIFANTVDNARIVLQIDNA RLAADDPRVKYETELAMRQSV ENDIHGLRKVIDDTNITRLQLET EIEALK*ELLFMKKTPEEEVKG LQAQIASSGTLTVEVDAPKSQD LAKIMADIR\AQYDELARK\NRE ELDKYWSQQIEESTTVVTTQSA EVGAAET\TLTELRTVQVFGD STWTSMRNLK\NLENS\AGEV EARYAL\QMEQL\NGILLHLESQ LGQTPRTEAQRQAQE\YEALL\N IKVKL\EAIEICHLTRPPSWKIGE DFNL\GDS\LDERNMQTIQKTT TRRISWIGQSGVLRPIDTKVLEA LSQQEASGTLLGKQEANKKFQS |
| 14098 | 44466 | A | 14180 | 275 | 550 | |
| 14099 | 44467 | B | 14181 | 729 | 909 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14100 | 44468 | A | 14182 | 1 | 1415 | MGTQCDLLAKSLEDPCVDEVE DAFQQLGKEDEEIEQFSDKTFG SGAIDDDWREAHECLAEEVK QPVAVIEQTGNGERDEMDLLD DHEENLAERLSKMVIENELEDP AIMRAVQTRPVLQPQGS LNSSI WDGS/VSSEANPRTTACSGNAY SVCIRICFASEA/SPRVQKMIGTF LNEHYQGGQLHLSLAVLLELS P*APHLNRWLYPASPNRFCVRS LSMFGP/QMPPRYPAPYGERMS PNQLCSVPNSSLLGHPFPSVPP VLSPLQRAQLLGAQLQPGRM SPSQFARVPGFVGSPLAAMNPK SQAPMFRPDTTHLHPQHRLLH QRQQQNRSQHRNLNGAGDRGS HRSSHQDHLRKDPYANLMLQ REKDWVSKIQMMQLQSTDPYL DDFYQNYFEKLEKLSAAEEIQ GDGPKKERTKLITPQVAKLEHA YKPETIICQALCRALHINYLTKA FQQAFEVSASIIYR |
| 14101 | 44469 | A | 14183 | 204 | 560 | QGYWRGCTSSGGDGGCRGCW SPGKRR*GLSRTASGPPAAVAS PGRPRSPPSARTG*S*PGA*ARP CSRTW/PPPRCPLRPPSAARASA SRV/APL/GEPAPANTNIYCAAL THRATKSSTREF |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14102 | 44470 | A | 14184 | 59 | 1695 | DMPWWPVL PWIKDSSPSSLEM NPDNTSGLRQKSVEAEPCLW MVHRYTPQSTGEACTMAKAA GPSSP\GSCPPRPLGADPWMSR LSH*EC*KTGTTASGYRRHQET APPESSGSPVGLSAGLWLSWA WPVSPACLHPGPPLCP/GPPALG LGPRSPAAS/C/PPLPEAPPACSP FCP*GEISSSGPLEVPVQV*LPGD LSEPLGTSP LGRAPGLCSLLRA P/RPGAACPPASPSRPAMLLS*E APRRPGPSGETSPSPSLAPSEASP G\PPR\HHNGRDSEGAGTRTPGA SGSSKG/LGGQPAPHGPGGR*G GGRYRGSAAAGSVHSAPGGCSP HAPGCA/CDVRG/AKPSHFHSG CQSG*GHQTSGGCPHLGLSPCS TCLCAGQLQQK/PGSSSGNL* GQGHSSGDLGSAPPHLVPG\PG PLTAGGHG/SLVGDSEWGSPAP GAVLGQNSSGPDQQRAGRWC SRAEKSGCYTAPPLG*LSAQFQ EEKASWVPPGSGQLED SHPDPY TALPLAAPPWGTGTGCPPAWP RL/EPDDCGPRHLSPTCSTLPS WGGCAGS |
| 14103 | 44471 | A | 14185 | 264 | 643 | RCLRPGEGRSRQGRRSRTGRGK AEEGGARTRQQRRAALLPERS ASQPGPRDSPRWRRRRQTTRGR ARPASSGGT*GSSWLTAWPPR EP*RLRSASAQG/CRRQLQQR RRGLYQPHRPATCGPRAAD |
| 14104 | 44472 | A | 14186 | 114 | 1039 | QSQRLRPLADTPRRSNRPCSAA GLLFPQSFWSQELSQGAFLPPS SPCLHCLPGTAAASRHQRSPT RPSVQERRETHGLCAHRCEWR AGSPAHP*AHRFVSRAGSPA GP*AHRCISRAGTPARGPYSR* VSEAGSPA/AVVSAPCSLSS*AC VTG\CSPAHSP*AHRCASRAASP EHTSREDAEQAP*MQGLCPVH QEQPPSRKSVVTSPHIPPETDCR LLPKNPCANKHQPTATGGRAV PPEVQHVP PRSGMTLGSHQPLA LQFQM QATDAARLG LSPQGG SPPGPRSTLLGLCLSLFQLSLLR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14105 | 44473 | A | 14187 | 1 | 1629 | MIIYVENPKQSTSKCVRAYTFS KVAGHKAIEKRLEKLAVDPHR DRAQMLKVENVQQA WQQWIN KLPPARREDEDVKEIRWMIEEL RVSYFAQQLDHTGVD RGQPGA STWSASLMCSVTQPKLKTRKP GFLGLGERNCFSVYGAGRSW GRGLGSCGFWLPPRTRIRAADV CLARWGWRAHRVRVLAKNS RAESMLWSFHKAIEAARTNII QAQTRVEAAQATERRJAADIDD SELKAPRDGRVQYRVAKPGEV LAAGGRVLNMVDLSDVYMTFF LPTEQAGTLKLGGEARLILDAA PDLRIPATISFVASVAQFTPQTV ETSDERLKL MFRVKARIPPELL QQHLEYVKTGLPGVAWSFLYSI NQTICLR LDSIEAKLQALEATC KSLEEKLDLVTNKQHSP IQVPM VAGSPLRTTQMCNKVR/CVNP* ATVVPPVPQPTTQQYQGLDA GATTRVPRSLLRSEGSQTQKSP SCGSHSQDNSGGRKAVGARRD RWWLGAGKGPDCRGAKCGLP LSGQKCPTLDPYQVVGCTSKTG |
| 14106 | 44474 | A | 14188 | 3 | 1010 | GLQTQLVPLSSPVASLDNFSNL FGADLHVEKGQVPSSDQHLSQ RCHFPKAPPWSVCKALLPRSNP ATSLSGTSKPNSSGDFNSVTKS QPHCELNSFVL TGHSPVLWMM SEHDLADV VQIAVEDLSPDHP VQSCGTVVVLENHVV TDEDEP ALKRQRLEINCQDPSIKSFLYSI NQTICLR LDSIEAKLQALEATC KSLEEKLDLVTNKQHSP IQVPM VAGSPLGATQTCNKVRCVVPQ TTVILNND RQN/DHCSQDGRPL EQQGTGFPGKMSLASQ*HGTNP TFPCHCAESHENKSTSLSQGT QHTLHLCGHRVEPGRHRPSSLR SGRAGWAMLNA |
| 14107 | 44475 | A | 14189 | 1 | 1710 | |
| 14108 | 44476 | A | 14190 | 52 | 457 | |
| 14109 | 44477 | C | 14191 | 1 | 838 | |
| 14110 | 44478 | A | 14192 | 92 | 514 | |
| 14111 | 44479 | B | 14193 | 1 | 531 | |
| 14112 | 44480 | A | 14194 | 1628 | 2008 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14113 | 44481 | A | 14195 | 2 | 1616 | CPPRRRPRPRAPPHHRPPAAGARTAAAGDRSRHGPPASRVGTGGQMRKTYCRNSEPSDLDQGGSRGGPRRQSKCVRNWWVLGLTDFKNEAADPHDSGAQLASPSGFRTRAAGGAACQSRAMRSYSSALGWSMGLGAVEQGVVLVGEAQAAQEPMEWVGSGMVGCRSRAPPAGRQLRPDKKLSTAPVGRHRWRPSTPSAATGLGAKSLIARGQQGRLAAPNKTDKFARAVKDKKEGHYIMIKGLVQKESITIINIYAPNTGAPKFTKQLPLDLRNKTDSENTIIVGYFSTPLTALNRSSRKVNKETMDLNYTLEQMDLTDIYRTFYPTTAEIFYSSEHGTFSKTDRMIGHKTSLNKFKKIEIIPSTLPDHSGIKLEINSKKNLQNQTNTWKLNNLLSDHWVNNEIKMEILKFFKPNDNSDTTYQNLWDTAKAVLTGKFIALNAYIKKSERAQVDNLRSHLKELEK*EQTKPKPSRRKEIMKIRAELENEIKT/QKIQKINKSQSWFCEKINKIGRPLARLSKKGREKIQISSIRKK |
| 14114 | 44482 | A | 14196 | 1097 | 1686 | APRPLALRFGPLPSNSGAQLASPSGSCTGLQVELPANSCTVRWQVSALGWSMGP/GPGAGGSADQGGSGGTGAHGGVGRFRHGG AAGPEPCPMGEVAKAPARNRAQRQWAGTAGGPCASS/NSC*PGC*APYCPGWGQPAAPSAGPPSPRPPRTRAGPQAPWAAPVPAHASP/PHLPAS*GSPLRPGIQGSKTYQKSH |
| 14115 | 44483 | A | 14197 | 647 | 1496 | FLNLLSWQNMLCGLKKKRKQFKDYEKKVKELNEERDKYRKGSVYIYTFGKEPTLNKVLDACDGKFQAIDFITPGTQYFMGCRWSCLPVLHCALAGLSPWVVDGTRRPGAVGSAGRGGSGGTGAHGGVGRFRHGGQLQVRSPAHEVLRPSEKSSAAQWAGTAGGPCASSTADLGAKPLTARGGGPAGVPPSAGPPSPRPPRTRAGP/PSTVGSPPG/SPPTPLPHLPAS*GSPASGLGQPRKGLPQCSGGLKGWLLKHRQSGCPGRGGAQSERGLRGLPARC |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14116 | 44484 | A | 14198 | 1 | 560 | MAALLLVGASWL/LLLLVGASWLLARVLAW/TYAFYDNCHRLQCFQQ/PPKRNCF*GHLSLCGA/TEEDMRLMEDL/VPLFRDVQLWWLGSFYFVL/SLVHPTFTAPVLQASGG*PGFTTTMGLSFKRAKWQRLA/SEGSVRLEMFEHISLMTLDSLQKCIFSFDHSCQMVSPGSCTTSRGPRIPGALPTGGARAPENGDPKEIE |
| 14117 | 44485 | A | 14199 | 175 | 2225 | RWSSVSFASGMPSAPCCWGHPQCPASAAQPTGPSWAGCRGLTMPNGQASPAS*VPPGAFPFCLIKQPLWENLMTGVGKFSREAATLEGPTLPTR/GVGPQCRQIADLPLERTEGWRGD\GNPVRGVROKRKQLVAGETAASLLPCQASGESCSVP*QARGPPVLFLPQ\WGRRWAKGCASRSCF*PDRPSHAVPGA REGAGLAAAPKRVARLSPAVPPACC\GLQGGSSSAAQAL*PQLSGPRLPREK*GA/PCWRGGPRCCPQNSAPETLEYVEPRGTGAPGTTHITGLPSPSQGCRAEGW/WGLPGLPGPRAGSSPQPRGRAWRPRARTPPPASWAAKGRGRPLAAGGLARPRDPGPGSGVAPAGSLRPHSSGRGWGRRRLRARPTGGNRGSEWPR/RPPGYPGARPGAPSVPRPQP/PAA*TRPLPVGCGARPFHPVPATV\VPHAGPP/SGMGRRRGRYPRPASARPAGRCGAGSAEPGRGTDKGGDCGEGKTKRGGG/LGGGAGAPKAAPGAAEPMGGRGAGAGGGGAIR*GGGGGGSGTTGSGSSSRPPRTRAPPETDPAAPRPRPGLVRAAGGGAASGSGTGRGAEGCGVRAARGVPASLRAALARGAARVLVSGPAPGWA EPRPAGGARGVGWGPVLAGPGRGPRGGAGRGPRALSRGCAA*AWTPGRGAGQRPGPSGRGSG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14118 | 44486 | A | 14200 | 1 | 2850 | MHPQERTAAATNAAIIITDGAA TQMGVTSTPAPGHPRDGYQGG KDVSLLAHTHSFKISAAIEAKTT WVGMCRWGCKVALDVTDFDVH QGKPEGAGRNKQIPFIQDFPFAL RSEKRPSLPATISGKTLPLNTKT CPQLLQCKREGHSLQCLIWLQ MVPQLGRLAVGGCHSNAWFPS KKAVIWEKFKHNLSGLVSDKG GKRTGKGLGECLLMRMKMS ALEALTTFDSSLQHHPRTFPVS ALEALNPGKPRQLVTPA |
| 14119 | 44487 | A | 14201 | 1 | 1570 | MQSATSDAGSAPKKQKKVMTL QEKSGIAWYFFTAQEWPNTPP KLRTCTESMGCCLLDCCCTGQ GDWTRVTLYCRYPFILFGTNA WVANFERPRMNANSLASPTG LSPYLRFGCLSCRLFYFKLTDL YKKTTLGSLPDAAMAFVNCHG AGGTVAVRTSRGHSRCHFGFG VSGTRYHYLTPQVWVERQQQK VDSLLGTQQMLEAQGREF/PGP CIPLPVPTNAPAAKTTPQPPSPD L*PPNYLFLCVDGHRPIC*EPKQ NKSDSFTSQA*SQDG*YCGCS/C RAPRPHGTSATIPMSSCKRFQP SSPF/CKGPYHFRFLEERPLASRP SIHPSCGSYWLRLGCVAVGRTG /SRLNLQLHSASGLQALSKQR*R YCQSAGAGSPEPPRGGTR*CCR EAAPGCRAGTCPSAANLPSLR RK/PGTC*PQNPPGRCGSCGASA AVLAETPARIRRSFPRARQSCPR TWMAAGAPGSSRRQGTHVT* *SSTLEKQLDNPTATYFSVPTRK PVH*NQQKDL*VTG*LQIFHL |
| 14120 | 44488 | A | 14202 | 11 | 356 | VSGPPR*APWCPCLAAPTGSTS HGSTARDSSTACKVS/GGATCV/ SGCGPGLGVLGRGLSSTRSCCM PAG*CPSSKDTCEKSGGRTQPV PPFEWAAQDASLVRRCRILAHR PCRGTS |
| 14121 | 44489 | C | 14204 | 333 | 473 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 14122 | 44490 | A | 14205 | 344 | 1035 | QSAAQWFWWPGRSASLGGA GMQPPSLASWPHPRSIRCLRAP AP*QFTNATDPRFRSAPRRSGQ QQPRGSSGPAALASPSRQPNR AGALRTGGAGWATALDTWSC PRTRRRAPMGSL*AAAQQCV TGATWPPPSAIA*QSAAQWFW WPGRSASLGGA GMQPPSLAS WPHPRSIRCLRAPPCSGPSASS AAVQVACCCSLACCGSRPASQ GHLDTGTPITSPETCTTSLWSPQR RRAAGPPKVVDIPD*RGSRRLPS GRGAPNTTCIPYGGSPGAKWIE GCPAQ/RPSPPGLHPAMRASAL LLMPFLQRRHRSATRLLLRPGS DCTGKK/GKGFLAGPETKRQKR LCPSPKTLGRALGQQEALPANV RC |
| 14123 | 44491 | A | 14206 | 41 | 292 | |
| 14124 | 44492 | C | 14207 | 480 | 1637 | |
| 14125 | 44493 | A | 14208 | 3 | 410 | SPPCGAPPPPVCAPAPRAPAPP RAPPLAEALPGFASAAGSAPA RSGPAGAG*GSRSRPRARASAS LAPASAGDHLGYPSATAAAAP ASRPWLWRPSLNAARLGDPAC GWQASQWAAGSA*RAGSQWA AGEARA |
| 14126 | 44494 | A | 14209 | 1 | 1274 | FFFFHPLRSLGLDLGLHSQERSA PEIKPGALESTWSQARGAALRL AEAR*RAAPAAGTACSAGGAA SSPR*GSRATRRRRRGPTAPSRA ATAPGRGAAASAAPAARPART ALMASARGPP\TAASPAQALTR SAPGHLPPMSELGAVTALCESC PVT/AAPRSGGGEAGGTLASEW GRTCRNYG/PAPGIWPRPPLSAA RPAAASPPARRIWSPPAPVHSA ASPIGLRVAAPCSSGSAVPLRSR RASPPCGAPPPPVCAPAARAP APPRAPPLAEALPGFASAAAC RGKLRLALQGGLGRSGSRSRQE GPAAGS*LRTGKSWSPPPGSA PLPLAQVLQALVEAGSRSPRA RASASLAPASAGDHLGYPSATA AAPASRPWLWRPSLNAARLG DPACGWQASQWAAGSA*RAGS QWAAGEARG |
| 14127 | 44495 | A | 14210 | 2 | 335 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14128 | 44496 | A | 14211 | 344 | 1062 | TRAEVTQQKLSRFASPPVLRRL RSYVSPPAAPTADPRWRPSWST SLRWVVKPNVSA YRIPPRASNR GYRASDWKLDYA*WTGRLRIT SKGKTAYIKLEDKVSSELFQA PVEQYPGIAVETVTDSSRYFV\I RISDGTGRSAFIGIGFTDRGDAF DFNVSLQDHFkWVKQSEISKE SQEMDARPKLDLGFKEGQTIKL CIGLCSKPGTTAIQLGPVLNGIG RTLRTDLRNKNDLEGTNL |
| 14129 | 44497 | A | 14212 | 573 | 1017 | TDQGVGSPHCPRFQGGPPRSR FQQRSPHSPDSSRG/PPHSPRFQ QGSPHTPDSSSG/PPYSPDYSSG HPTP/HTSQQGIPC*DGHWLPC GPVFLWSEAPHLNPLGLVWGQ PRAPALPGNSAESKLWPHDRPA RPETPGAGTAWAHQALRV |
| 14130 | 44498 | A | 14213 | 707 | 836 | |
| 14131 | 44499 | A | 14214 | 724 | 927 | SFMDFRFVLLFFHLVPNPK*RP VS/SPPGSKLLVPPWGPKT\VPVP HPSPPPPAHGEPGLPPPPPPPLPH |
| 14132 | 44500 | A | 14215 | 29 | 157 | |
| 14133 | 44501 | A | 14216 | 1 | 363 | |
| 14134 | 44502 | A | 14217 | 770 | 952 | |
| 14135 | 44503 | A | 14218 | 1053 | 1995 | KSSEPDLSHSFIFCSNFPSSSL KRPHVFQSSILACVFCITADSSRA PCVLRVCDGFAGLTRSSAPSSK EKPCGFSLPEFTPLAVSFPQAAL CSLGTVSCLRRPQLTPSWCEP VLLAGAVCPGLPCAIGCPWA GEEGCPGATSQLDQVSWPSLQE APEVLWPCLDSWGWFWAPSTV IPLMASPRFGFMGRSQQPVLIN HLIKEPKAKFSNKNHSIRCCQG QRKWRRGNAAGMCCQPQIPGK GEVKTEFQPVSNRSVNYGCTM HFQETLWTPRLGLGDGDSNNN NNNNNNNRITANPGKEAEKPE HPHLLVKM |
| 14136 | 44504 | A | 14219 | 482 | 833 | THQGARGCTHARVSVREMRT RGRWATGMRVPAPCSSVHTTA VQRQQVADQLQTAEISME/IL N/KWDQDPEAFVRKVATSYET WIS*YYPEDKAQSKQWLPRSGS GATLYSATNQYP |
| 14137 | 44505 | A | 14220 | 195 | 367 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14138 | 44506 | A | 14221 | 989 | 2210 | LLVSCAILLSVSFLHSSSFVRSRS NRDSPACVDATYRGCSQEGEG VCGEACSCFPDLNQPGVHAG EGVLPCSGWEDTFGKNTCLVS YQQIPNKRRPCTCEECGKAFGQ RSHLVQHTSEKLYACQECGCTF SNNSSLVKHWHVHTGEKPYMC GHCCKCFRESSSLAKHQRVHT GEKPYVC/GESTHLVQHW*FHT GEKPFAC/HR/CSKAFADFSALL ACHGTYTGERPYECRVCKAFS PSLSLAEHIRCHTGEKLYACQE CGKAFSHSSSLSKHQVHTECG KAFSQGSYLTQHLKIHSGEKPYI RGEHPYACGKCGKTFSHSKFLT QHEQVRMGEKPFMCGDCGRAF MQTSSLALHQRTHNGEKPYKW NECGKSCIQMShLTEYYQNLPE KGSKDPHTDATVHSPVMD |
| 14139 | 44507 | A | 14222 | 1 | 245 | PPFRKQQAQHRNKTVLVSRSQP VPVTVPE/PSA*RSTPEGPRRAG CDPRP*PCPAGPELPAQMKVLA IEQLLSLHFKKALLF |
| 14140 | 44508 | A | 14223 | 477 | 947 | LCSLSSLPPPPPPPPPPPPPPPP PFPPPSPVPLPPSPRSPVSPPPPH SFQGRSPSELGSSAEPWLRPGT WV*/PPPLTFSQQEAASSAQK*N CPGES\QPVPVTVPERQPDAA NHSLLLPGQQCFWCQGPHPPY WMGPVDASSSGFLSQSFY |
| 14141 | 44509 | B | 14224 | 438 | 1437 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14142 | 44510 | A | 14225 | 584 | 2866 | WHFAKLSRNTQDHTRPTLGAA QAVPATGQPAAPGPAGAGPEW VPFLAVYKEQLVRNDSVLKVFF FPPIFYREGWVCCSVVESHLE GFVWLFSLQL*PPKLRSLFSLSY CLSP\SDIEISRGQTPKAVDVLA KEIGLLADEIEIYGKILVSSAGF A*VVWEIL*NSLSPPELRITPTPL GEGKSTVTIGLVQAVSLGLCPS WQLYLVTALQPGQQSETLFLK INK*KDILFL*FNLHLTGDIHVVI SCELSKFMDN*LLCGLIFVLCFF RGIILVTLCLFLLKLLTFLLNH *KLGINKTDPIRTMPDTHQVAG PYLST\DD*SVLFQ*SPAPCGNG HPTGTVADHYLCLGW/YQAQF DIAVASEIMAVLALTDSLGREV PRG*PLPG*YFVRNLMFFSHLPQ IDLGFHASVCLLGF*FAFSL*G TPVVFVHAGPFAADRDLCPYQFL LCQTHIYKIHVIMAEYFQRYKL MMYAKQTSPLCDLEQAISLSGC VPCRHSCLKNEKFSCGTC*QYL PKLSLPNSDPLTLPFSADYGKFK ESNHANHSGDCQNLPLFLEDNS TYSTCFPTVTEAGFGADIGMEK FFNIKCRDVVLSFRSVV*AFLLL AV*LGRFGGRQYTGWVLLFS FLQNIQLVADGV*MVSLSLKT* LNGYRCKTTNIFFTRTDTRAEID LVCELAKRAGAFDAVPCYHWS VGGKGSVDLARA VREAASKRS |
| 14143 | 44511 | A | 14226 | 3 | 587 | YPASAGLMLQNFVIGLRYHF AIHSPAAGLLDGLHAVAAIQG ITKIETTPNHQRAHAHTLLTQ QAHLPSPHLFNLPLTLCLMHC PTAIPHCFAADARTWVNLPTSSLI GHKKENLKEFISGSLIVHEILEE VLQAEQDFQPFTRVTVHWGKG NDQTFRGLLDTGSELTLIPGDP KHHYGPPVKVGAYGAQLL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14144 | 44512 | A | 14227 | 2 | 1256 | CHCGPP/VKVEAYGSQVLKGVLAQVQLTVGPGPRTHPVVIFPVPECIIGIDMLSSRQNPHTGSLTGRVWTIMVRKAKWKPLELPLPRKIVNQKQYHIPEGIVEISATIKDLKDAGVVIPTTSPFNSPIWPVQKTDGSRWMTVG YCKLNQVVTPIAAAVPDVVSLLEQINTPPGTWYAAIDLANDFFPIPVHKAHQKQFAFRWQGRQYTFTVLPQGRWEINMTKIQGPSTSVKFLGVQWCGACQDIPSKVKDKLLHLVPPTTK/EAQCLSGFRREHIPHLPIYRVSRKAANFEWSPEQEALQQVQAAVQAAWPLGPYPADPMVLEVSVADRDADWSCWQASI/GHKVGHAQQHSIIKWKWYIRDWARADPEGTTKGQGQRRWWQLAERQDSRDREA AIGERQETA VGKTARDGEAVCD |
| 14145 | 44513 | A | 14228 | 155 | 531 | GNLWSVDLRPGTPLRQNFRTIRQQHSRFTKNHCSQTPLLI PRQTGSGVDLSKLQQTCS*GSCLVCTIDLANAFFSIPVHKA/HQKQFAFSWQ\YTFTVLPRLTWLQPC*V PNLPA AETNTEPSNGT |
| 14146 | 44514 | A | 14229 | 1 | 518 | MTVDYCKLNQVVIPIAAAVSDVVSLEQINTSPGTWYAAIDLANAFFSIPVHKAQQKQFAFSWQQQYTF TVLPQWYINSPALCHNLIRRDLCFSLPLDITLVHYIDIMLIGSTIKWVHSS/DSIIKWKWYVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG |
| 14147 | 44515 | A | 14230 | 281 | 1140 | VRVLSPVEKELKLWKNT HKLLSYPTVGAAVTQLQNL TAMGVIGSHGARGQVVALNRQRQGDLPFTRVTVHWGKG/NMQIFGGLLDTGSELTLP GDPKHHCGPPVKVGAYGGQVINGVLAQVQITVGPQTHPVVISPVPECIIGIDILSSWQNP HIGSLTGIMVGKAKWKQLELPLPRKIVNQKPYCIPGGTVEISATIKDLKDAGVVIPTTSLFNSPIWPVQKTDGSRWMTVG YRRLNQVVTPIAAAVPDVVSLLEQINTSPGTWYAAIDMANAFFSIPVH |
| 14148 | 44516 | B | 14231 | 1 | 1521 | |
| 14149 | 44517 | A | 14232 | 3 | 202 | |
| 14150 | 44518 | A | 14233 | 2 | 367 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14151 | 44519 | A | 14234 | 1 | 553 | MTVDYCKLNQVVIPIAAAVSD VVSLLSEQINTSPGTWYAAIDLA NAFFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLCFSLPLDITLVHYIDDI MLIGAPRQLLACY/WALVETEHL TISHQVTMRPELPIMNWVLFDP SSHKVGCAQQHSIHKWKWYVH DWARAGPEGT |
| 14152 | 44520 | A | 14235 | 3 | 728 | |
| 14153 | 44521 | A | 14236 | 1 | 635 | |
| 14154 | 44522 | A | 14237 | 3 | 266 | |
| 14155 | 44523 | A | 14238 | 1 | 1245 | |
| 14156 | 44524 | A | 14239 | 2 | 837 | CHCGPP/VKVEAYGSQVLKGV AQVQLTVGPVGPRTHPVVFIPV PECIIGIDMLSSRQNPHTGSLTG RVWTIMVRKAKWKPLELPLPR KIVNQKQYHIPEGIVEISATIKD LKDAGVVIPTTSPFNSPIWPVQK TDGSRMTVGYCKLNQVVTPI AAAVPDVVSLLSEQINTPPGTWY AAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEI NMTKIQGPSTSVKFLGVQWCG ACQDIPSKVKDKLLHLVPPTTK K/EAQCLSGFRREHIPHL |
| 14157 | 44525 | A | 14240 | 1 | 533 | |
| 14158 | 44526 | A | 14241 | 1 | 1043 | MTVDYHKLQNQVVTPIAAAVPD VVSFIEQINTSPGIWYAAIDLAN VFFSIPVHKAHQKQSVFCWQG QEYTFTVLPQVHINCPALCHNPI LRDFDHFSLPQDITLVHYIDDI LIG/PV*NMLLHLVPPTTKKETQ HLEVLFQFWRQHPIHLATPSSP NGPMNKVTMMA/ANVGAWD QKHGLPLTKANLVMAIGECSV/ SPAAETNTEPSIWHHSSGQDSQ VQESKGGNGSGTTHHHP**STS KIFASCSDITFCWPRGLSSRGR NAATTRHNNFIKPEVKIAFWT LWDPPTFKSTG*ERS*SVGWW D*HELPR*NQSTTPQGSVSIIPH GQPPHQLFGVAKARTFGIT |
| 14159 | 44527 | A | 14242 | 1 | 336 | |
| 14160 | 44528 | A | 14243 | 3 | 1885 | |
| 14161 | 44529 | B | 14244 | 1 | 1423 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14162 | 44530 | A | 14245 | 1 | 1361 | MIISIDA EKAFDKIQQPFMLKTL SKLEETASPSPVVATYTPQPML PSAFPPLSEEINPVLPETTVMAS PEA VTRQDNVDSPQKPPPTPMF ASRPITRLKPRRAPSEEGIQRLK KIGMVEWISHFRPTPLSMEGPE HILLTNTLLNRYVKAAPASLKS PLTALLFMSDLTVGTTFSQLQN LNTMGIFGSSCDRSQVAALNHQ RQVPECKIVIDILNIWRIPHIGSL TGRVREIMVGKAKWKPLEQPP PRKIVIQKQYHIPGAITEISATIE DLKETGVVILTTSFVKSSIWPLQ KTDGSRWMTVNYHKLNQVET PIAAAVPDVVSLLEQINTSPGT WYAAIDLNVFFSIPVYKAHQK QFAFSWQQQQYTFTFLPQGYIN SPDITLVHYIDDIMLIGSSEQEV ANTLDLLPARVASWGVYPDQL T/GGRED*GLLHRWSCRICRHH PQGSWIQES |
| 14163 | 44531 | A | 14246 | 1 | 1795 | MRKCGKPOFKLGQTNKANSRI QEELIHSKSLIEQEGEKPQVQFSA FHRMWQPADSQCDIIDSADIWA DPLVRHREIITGSGGINRRRTRG GRGRGGEAAGGAENCGSREER ERAGVGTA VTQLQNLNTIGIIGS RGGRGQVA AINHQRQGGHSHYC KGQKQNSNQNSVTHVELWH WLNHSVPRSEIDRKPTTFLLNL YKQKTSRDLWPFTRVTLHRGK RNDQTFQGLD TGSEMLIPED TKHHCGPPVKVEAYGGQVING VLAQIQLTVGPVSGTHPVVIY PVPECIIGIGILSSWQNP HIGSLT SRKTDGSRWMTVHYHKL NQM VTPIAAAIPDVVSLLEQVNTSPG SWYAAIDLANAFFIPVHKAHQ KQFAFSWQQQQYTFTVLPQGE TLVNFSLPQDITLFHYIDDIMQI GSSDQEVANTLDLLPRKSTTPS G/LYGFWRQHIS/HLG LLLTPIY* VTQKAA/SFEWGLEQE KALQQ VQATVQASLPLGVYDPADPMV IEM/SLSDPSSHKVGCAQQHSII KWKRYVCDQA*ASPEGTS*LY CTSFIMEKEEVC/LSLEQTLTD MGLPILHAMLLWIHLWIHGLPY PSSWYSTQQCL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14164 | 44532 | A | 14247 | 55 | 1241 | NRFVRAAPASLKR SAGIGLLCM PDLTVGIVVTQLK NLNAMGITG SELTLP GDPK*HFGPPVKV GAF GGEIVNKYLAQLGL TDDPVGPR THPVAIFPVPECH IGIDLSSLQNP HIGSLTGRVRAIMK GKAIMKGY YEGKGKAKWKILEL PLPRKIIN QKQYRIPGGIVEMSA TIEELKY AGVVIPIPTTFPLNS PIWPVRKT DGCWRMTVDYCELN QVVTP T AATVPD VVSLL EQINTSPGTWY ADIDLANAVFSIPVH KAHQKQF AFSWQGGQYTFTVLP QGWTV NSPALGHNLI GRDLDRFSFPRDI TLLVHYVDDIM LIGSSEQEVAN ALDLLVFS DHLAIKWVMHSSIA SSSGSGICVIRL KKVLKAQPAP MASWGVLYDQLTE EEKIRA |
| 14165 | 44533 | B | 14248 | 1 | 346 | |
| 14166 | 44534 | A | 14249 | 485 | 717 | |
| 14167 | 44535 | A | 14250 | 1 | 345 | |
| 14168 | 44536 | A | 14251 | 300 | 689 | TKRAPCSPAAGSR GRARSLALL TLYHGHYPALPPG PTPAQQPGR GLAEAAEPRGSEGG NGSNPCG RA*DGRSRREGRG RLGGWRPC CEPQPWRQAHDPA GPDRVDGG ERRGAGVLRGQDQ DEKKKPK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14169 | 44537 | A | 14252 | 1 | 2430 | MAVLQPSRHRLRPQLGLEPDN WHSQQDEVSSVATARA VVPSG RGAAWMGPPSGNIGGSGLV SHE CGEGTGAAGSTQLQEGMHFCR QSRWAF LTALCEVYTQSLQDT VQWLQLCQWSAQQGDDHTLIE WLMGATWTVWNDAREIPETG TGQDAWLCGSWGVDDQRPHV ELAIHCSPTNVQ RVLALVDTGA DCSLVFGNPVRKPDGTWQMTV DDWELNKVTPPLHAAVPSIMD LTDH LTMELGQYHFVDYVHSP TICRGLVAMELAAWKCPKGVL LFHYIDDIMLTSDSLADLKVAV PLLWQH LAACGWAINKSKVQ WPGLSAKFLGVIWLSKTKA IPE AIIEKIQAYPRPTTMKQLQTFVG LLEYWRPFVPHLAQMIKPLYGL SKKGATWDWDNEAGTDLLAA KWA IQQTQALQVIDQGCPFELD VHVTTDGF GWVLWQRMECFR TPVGFWSQLWKGAELQYSLIQ KELAAAYAALQAYETVTDWA TVIVQMSYPIVGWTGTAQT TTL AKRGAYLEQQSMLTTTPLAAE LQEALGP IVLMEDKAMGPEAPL DPEPSLLKKGYP LVPDGAWYT DGSSQGA AAAWTAVAIQP/ITD TI*FDTGCGQSTQWAE LRVVE\ MDILEACQKCPACAQAYLRQR QLPNVTQQVTVGQMPLTRWQI DYAEPLPKLQGYTYALMAADI |
| 14170 | 44538 | A | 14253 | 2 | 239 | |
| 14171 | 44539 | A | 14254 | 3 | 211 | VVYYSPNEVKVVAEGFDSANG INISPDDKYGPL*NIFLQLWC WPNSLLCFLCQCENSFLDIYGIL |
| 14172 | 44540 | B | 14255 | 13 | 87 | |
| 14173 | 44541 | A | 14256 | 42 | 854 | VLVFLTAALFILPTFSNSMMILQ VSGGPWT/VILRRGVLLGVAPP PSLPALAPENSVYQERQECYAFN GTQRVVDGLIYNREEYVHFDS AVGEFLAVMELGRPIGEYFNSQ KDFMERKRADQLPDCRDPLMP D*GVWISPLGQQVPNLTAQKTL QHLPSKKEPQQHHDLLVYHVT DFYPDSIQVRCFLNGQEETAGV VSTNLIRNGDWT FQILEMLEMT PQQDRT*AGVQLLEVTLNLSLF FLEAQSDSVQSKMLTGARGLFI NYLQLNLCTP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14174 | 44542 | A | 14257 | 3 | 571 | QGRATPENYLFQGRQECYAFN GTQRFLERYIYNREEFARFDS VGEFRAVTELGRPAAEYWNSQ KDILEEKRAVPDRMCRHNYEL GGPMTLQRRVQPRVNVSPSKK GPLQHNNLLVCHVTDFYPGSIQ VRWFLNGQEETAGV\VSTNLIL NGDWTFQIVVMLEMTQP/QGE DVYTCQVEHTSLDSPVTVEW |
| 14175 | 44543 | A | 14258 | 1 | 1677 | |
| 14176 | 44544 | A | 14259 | 2 | 430 | |
| 14177 | 44545 | A | 14260 | 821 | 1428 | QVTDVQDFPLKCKIQWRRTVR GDLQ/PFTRVTVHWGKGNDQT FQGLDGTGSELTLPDPRHC GPPVKIGAYGGQIINGVLAQVQ LTVDAVGPWTHPVV/I/SPVPECI IGIDILSSWQ/NSHIGSLTGRVRA TMVGKAKWKPLELPLPRKIVN QKQYHIPGGIAEIGATIKDLKDT G\VIPTSPFNSPI*PMQKTDGSW RMTVDYL |
| 14178 | 44546 | A | 14261 | 507 | 910 | |
| 14179 | 44547 | A | 14262 | 1 | 2898 | |
| 14180 | 44548 | A | 14263 | 1 | 2580 | |
| 14181 | 44549 | B | 14264 | 159 | 2657 | |
| 14182 | 44550 | A | 14265 | 142 | 377 | NHLLRRQQWQTPFPPPSWS/SPR SSSDCCGSSSENFKPVDSLGLSV GVGPTEPDHLDPWLPQPPFGSE RFCLAGVPGATG |
| 14183 | 44551 | A | 14266 | 363 | 638 | EVWKESGWHLAGAPLGQS FQ RKEQAVIFAVLQPLLVIKQTGS GVDLQQTPAHLQQRGLSGCLQ SLCSLTSS*PQRHPQNSSLVSNC VVS |
| 14184 | 44552 | B | 14267 | 1 | 2424 | |
| 14185 | 44553 | B | 14268 | 446 | 623 | |
| 14186 | 44554 | A | 14269 | 245 | 690 | APSRSTWGSSTAARRNLKTR KLRTPRTPPHQKPRNPHHGPPR TPSG*TPRNPDRPPGPVQVGQ PGCWAPSQGPRGWGLGC*RE EVPGGGHAGRHSTPVGG/DFFL QAGPWPPDASLPTNPFVLRGAS TPPHPLSENNKDKFLLQK |
| 14187 | 44555 | A | 14270 | 223 | 365 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14188 | 44556 | A | 14271 | 1 | 687 | MSEYIRVTEDENDIEPIPSDD GTVLLSTVTAQFPACGLRCRN PVSQCMRGVRLVEGILHAPDA GWRNPVYVVNYPKDNKRKMV LGLPWKTTEQDLKEYCSTFGD VLMVRQSQDEPLRSRKVFVGR RTEDMTEDELWEFFSQYGDVM DVFVPKPFRAFAFVPFADDQIA RSLCGEDSMKGISVHISNAEPK RNSNRQ/LRSGRFGGNPGGFGN QGGFESYQRCERKAV |
| 14189 | 44557 | A | 14272 | 1 | 833 | |
| 14190 | 44558 | A | 14273 | 3 | 447 | RGTAGGQPNGPALAQSP*WC RLGSGGT*GKSPGTSQGRALPW CSC/SVSTWATAAPGSQQRASP CSWAQPGPLASRLMLPRLR* GHLGHLAWLQLFAAPCPVIHV AVMWSLLGIALRKVHGDWAPL AILSLVVCASNKLNKKKKK |
| 14191 | 44559 | A | 14274 | 988 | 1803 | RAARVPRAPEAVAHRWASAS EDDGTVLLSTVTAQFPACGLR CRNPVSQCMRGVRLVEGILHAP DAGWRNPVYVVNFGDVLVVR QSQDEPLRSRKVFVGRRTEDM TEDELWEFFSQYGDVMDVFP KPFRAFAFVPFADDQIARSLCG EDSMKGISVHISNAEPKRNSNR Q/LRSGRFGGNPGGRLOQTRY PAPAPGSPGRAQGLGAG*SRPS GSWLSGHLQRPEQSVGRAPAA PRHAVRRSLRRLAALCRRTAR CRAQLHVSPQRRRH |
| 14192 | 44560 | A | 14275 | 3 | 184 | |
| 14193 | 44561 | A | 14276 | 1 | 352 | KAAMVRFKHYLLCELVSDDP RCRLSLDDRVLSSLVRDTIARV HGTFGAAAC\SIGFAGTIRTCQK FLIQYNRRQLLILLQNCTDEGER EAIQKSVTRSCLL*EEEESC EAAKAME |
| 14194 | 44562 | A | 14277 | 1 | 456 | PTRAVEAAMVRFMHRYLLCEQ VCDDLRCRLSLDDRVLSSLVRD TIARVHGTFCIAIALALARA LNEEGNPEGWRDVAGASAGGR KKGHECPSPCTVFCTL/RYPNA YTVIGLLRCKKELYQVWWSVL YLMTYLENKGHRYPCFFNTLH |
| 14195 | 44563 | B | 14278 | 34 | 267 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14196 | 44564 | A | 14279 | 3 | 395 | SAEVGAAETTLTELRRTVQSLEI DLDSMRNLKASLENSL\GILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRILLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH |
| 14197 | 44565 | A | 14280 | 2 | 1044 | SSQMPSPQEGMCGKACTPALS QADSLCPLLRLASEVEGYWQM ACAEPYVQSEMNDHLSVWSLQ HGSTTLASMSFTTCSAFTNYWS PGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHFTSF\GGLA GMGGIQNEKETMQSLRDRLAS YLDRVRGLETENWKLESKIQEH LEKNRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAAEMTLT ELRHRVQSLEIDLSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV |
| 14198 | 44566 | B | 14281 | 247 | 857 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14199 | 44567 | A | 14282 | 1 | 2104 | LRGSELAGGVAAPDPSSRARAP GRGQGSEPPRRS*GRGRAPPRA HTPLDDFPPGRAALSPGRGLSS RRPDPGSAGRPLLLCLRPLHSP PPPRGCQAPAFQSLPSFHLALRL RSSGEEKLWGPRRAPAAP*SQR RKPDPARPGLA AAVPLRPV*AS D*GAAQVPPPSPLRDGGQPGGR EGVGRRTPHRAAAWLLGE*AA DAAAFHWGGRPPAAPARLLP GAPHHREDRVHHQPRGHPLQH QSPGDPTPAGEQHASRH*LCRN PETQKL RH*TSERRDGHREEEH TG TAGVPRSRPATQRPHAVPAG GLQPHRMLPALSSGAASGGEA EHGQLSGRGREEDGPVWPQLP AGLQGHFRGESPRWPPCLGDGS EN*PGPVQAEFSGG*DPAVSESE DNQPRSRQFLRLQREEKAKPD QRFTYLPANVPIIKTEPTDDYEP APTCG/RGEPGVKSSPKTILQPA ARDATRPQLLPRGRLPALSAEK HPDASSPWREPQAPRPF SRCLH QGR CQPGPLSPRTPAAGR RGPR RPG\VPRPVATHPGSPGQPPPAL LPQQ*MK*YEMTSPARAPTSC HIGALSSAGVC*LQQT KTFE*IN *THTWYHSEPPTD*MPGA EH*Y VQRLALQQEGKQGGRETTVSP GGEVIS*QKGGGRAEHGRPTV QGP/SHGN GPHAV*PHAQPFWH PWGSILEVPYLTRPSGHHRIEH |
| 14200 | 44568 | B | 14283 | 41 | 4224 | |
| 14201 | 44569 | B | 14284 | 1 | 1332 | |
| 14202 | 44570 | B | 14285 | 140 | 215 | |
| 14203 | 44571 | A | 14286 | 234 | 657 | VQQPGRGLDLSTDGPGGRSQV GLIWSCCLH*AASGEPGGRCP GS/GAPGPAGSALEFRARDGVP GVGGPSWESHSPAAATPPPAEC RPGPTPSPAPGEAAPEDREDG AAPGRAEPASIVAPADGSQGG VLATQAGALGA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14204 | 44572 | A | 14287 | 134 | 789 | PDSSQAPSRNSTRPAASTRKSSS PPAARS\AGNELGSSRGDADPPP QNPTGPAPQSAEVPRCD/SSSA WASNGSSISPSFFSLRPWPSST/S KVPGAGHHTPPEGAGGASAR\S SSLAPSAGAPVPS\A*RSQLGTW LSVLRPRSL*QSRVRSPSSHVSS PGSMQAPNSPSSFQPGMNGAWI WWL*THIPLARWPGPPGILVITC PTVTWIKWSFICSFHPT |
| 14205 | 44573 | A | 14288 | 465 | 1541 | GPPKRKLISNFSKVSQYKINVQ KS*AFLYSKK/QTESQIMSELPF TIASKRIKYLGIQLTRDMKDLF KENYKPLLNEIKEDTNIWKNIP CSWIGRINIVKIAILPKVIYRFNA IPIKLPMTSFTLEKTTLKFIWN QKRAHIAKSILSQKNKAGGITLP DLNLYYKATVTKTAWYWYQN RDIDQWNRTEPSEIIPHIYNHLIF DKPDKNKQWGNDSL FNKWCW ENWLSICRRLKLDPFLTPYKKIN SRWIKDLNVRPKTIKLTLEENLG NTIEDIGMGKDFMTKTPKAMK TKAKIEKWDLIKLKSFACTAKET TIRSFQSEQKSHTLV RATRLVSD HSQSFEAWLQFLGDTRFGTQKL RDS |
| 14206 | 44574 | A | 14289 | 1921 | 3199 | GYLAAGQVTSRIHTGRRHFSGP ARCPVCVSCRRPGC*PQPAVRP SG*HCRKTAPSHGPSIWQTR**P GSWPNL RPG*GWRWLRAQPRG RGIPVGCRSNLQLHPTKNPGSH *GSGSPWQCPGVLL*ASGRQPG SPSGGCT*SSGKAGLEPQWHPA IPGHCRNKPAAPASWERAPRPR AHALACGWWRYSSC*SWRS*S SPETPGAQV*CHRPCAAWW RCHS**TAQFL*D*FS*FLQTIGE PCICPKPISVPH*PMKQSHRGIG GCLQYSSHPGIESSLGMSRGF/D RRDL*TLQIGS*RHPRAGPEGA AL*CLAGESSLRTPSAPCPGSPH TPGSSASGNTSPV**ETGCGSRQ GSARLVLESLLSR**CLSGPSRP SCLLRGISWQCGTAGRLSSSGPP AASGAGADAAPGGFPRLPCLEF GTV |
| 14207 | 44575 | A | 14290 | 3 | 626 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14208 | 44576 | A | 14291 | 1 | 1065 | MRGSCERSGEDEEQKEEAMVA CGRLSGVPEAEQGPEANWDS LETEGTDGLGELVRDTLYLRSC RAHSVVPISCFLRQGS AQELNL RHRGLGPQGARALASSLSSNPY VKRLDLRDNGLCGAGAEALAG AL/QQKQQHP*CGPVGEPAGSG RSPGP/RVPPSQ/CNQAMRKM LSGNGLLEEQAQHLAELLAH TDLKSLDLSYNQLNDQAGPAPS LRAFPQANIFLKVLDISYNGFG DPGASAVGEALKANNVLEELN MSNNRISAMGALSGLGLRVN QTLRILVLCVRVSQVSRNPMRS EGCFGLLSVQDNPALELLD FSDIQVNAEFDGLASSVRGILPG LGIKDWRLQSGV |
| 14209 | 44577 | A | 14292 | 1 | 416 | |
| 14210 | 44578 | A | 14293 | 2 | 384 | ELWVVT SFMAYGSAKDLICTH FMDGMNELAIAIYLQGV LKAL DYIHHMGYVHR/DLQGYDAKS DIYSVGITACELANGHV PFKDM PATQMLLEKLNGTVPCLLDTST IPAEELTMSPSRSVANSGLMTA |
| 14211 | 44579 | C | 14294 | 142 | 474 | |
| 14212 | 44580 | A | 14295 | 1 | 1470 | |
| 14213 | 44581 | C | 14296 | 91 | 471 | |
| 14214 | 44582 | C | 14297 | 195 | 480 | |
| 14215 | 44583 | A | 14298 | 121 | 1130 | SRSTQYELMSFLTNDASSESIAS FSKQEVMS SFLPEGGWYELLTV IGKGFEDLMTVNLARYKPTGE YVTVRRINLEACSNE MVTF LQG ELHVYKLFNHPNIVPYRATFIA DNELWVVT SFMAYGSAKDLIC THFMDGMNELAIAIYLQGV LK ALDYIHHMGYVHRSVKASHILI SVDGKVYLSGLRSNL SMISHGQ RQRVVHDFPKYSVKVLPW LSP EVLQQNLQGYDAKS DIYSVGIT ACELANGHV PFKDMPATQP/M VLVLSSPDAARETERHSALPVG YQHHPR*GADHEPFALSGQLW PE*QPDHQHPALQR*LALPPLP PNLLPPLPLC |
| 14216 | 44584 | A | 14299 | 304 | 412 | |
| 14217 | 44585 | A | 14300 | 2 | 350 | |
| 14218 | 44586 | A | 14301 | 191 | 299 | HRPATAVLHVPTSPSPGSRPS *PPPAALLWTPA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14219 | 44587 | A | 14302 | 537 | 5523 | LARYYKFMHQDRQGVARNLL CQKEKRR*YTTKCEDNTCHWT GRTSS*PRSV/SNLNSQCGPRLW PPVTIIRQANIKTGEKAH*TSKL LPPVQLKFPARDDTLWPWGYIP* QLRRPSPR*SILSMLPRKVVPCL *QKP*TVCWKF*EPLSYIHSLV LKMMIPMPMTLLGA*CLTQAL K*SRMERKKGRAAQRSSTLGC QSPRGSPGGGPGPPGPPGAGKQ QSNSVQTSRLLARTLI*SFSSST VKDKELARNTAP |
| 14220 | 44588 | A | 14303 | 2868 | 3095 | PGWAGGLFGPSAGMRAWATK PSLTPPAPAGQRC PQGHRG*SG PGIYAVQPPSVPAWAAHATTQ ARLCHPRSPPLR |
| 14221 | 44589 | A | 14304 | 693 | 821 | SDRQT*RQEKRLTRRQSCCLPC N*SFQPETTFLHGPDTFHDN |
| 14222 | 44590 | A | 14305 | 338 | 645 | |
| 14223 | 44591 | B | 14306 | 181 | 480 | |
| 14224 | 44592 | A | 14307 | 155 | 543 | |
| 14225 | 44593 | B | 14308 | 1 | 1260 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14226 | 44594 | A | 14309 | 1 | 2025 | VINIINAAQESSMPMPVTEALDRV LEILRTTELYSPQFGAKDDDPH ANDLVGGLMSDTGLEIHKDGEE EGESRTAQQYPGLSESTRQPWR RSRTPRTTWGWKATEQQCPDF PPPGPHPHLELLIFHCEGQGTGQ KHSTSYPTLMSEKRGLMNVFF AKYTGPMARKSSGLTPSLLHLY CADPLHSKPLFNCPPPTTSKTEI LGSCNCSPSESVRGAEKGDQEL LANIKQAEKHEKNHPEVTAM ALTDIDLQLQFSMSQPEALLL AAGPADHLLLQLYSGHLQSAT GIYGEGRASSATLEDLESQYQE LAVALDSSSTIISQLTENINSLVH TLKEEKHEIHQVQKLGRNLFKL KNQTAEPLAPEPPARPSKVEQL QDET NHLRKELESVGRQLQAE VENNQMLSLLNRRQEERLQEQ EGWQEEQERLLDKNNENKSAL QLEQQVKELKL\ENLEATSQ*K QQL/TAQLSLMALPGEGDGGG HLDSEQEAPRPMNIPGDLESR EAMVAFFNSAGANAQEEQVC CQPLAHPVASSQKKPEVAAPAP ETGGESVCGETHQALQGAMEK LQUESTSARGQCQRRSTGRGGHR QAGPGPGGDEEMLCTCTQVSS AGRGMGMLTVVLVVSLLMMLS ASFSTWCMRSISSCHCAYS AHS SISVFWFPREYILASGSEMMNS |
| 14227 | 44595 | A | 14310 | 3 | 564 | SLRVSLKAVVDRAGSRILSYIA GLGVDLGFGGGS RVAGGIADL GRSGGGKATRSRRGS RAGGGR LRSRHHEEALQLRETPGPGAPE\ PMDQEYAGPGYDIRDWELRKI HRAAIKGAAG/VWSAAMTRR FRDL DARDRKDR TVLHLTCAH GRVEVVTLLLSRR CQ\IDICD\N* NRTPLMKAVHCQEEA |
| 14228 | 44596 | A | 14311 | 515 | 778 | GQAQGTGDREGAVLFTARAPD QCRP*SCSSSRPTASSCPLGHSC SPGPLCTHLP LQGPPQAPTVP ATATCWFSWNQCRCRAVSSYP |
| 14229 | 44597 | A | 14312 | 411 | 608 | EAEIP*TGLPGHSRPPGPLCTHL PLQGPLGAAAWVPEAGLGQVP TEAAGAARAGCSAHKPWKRRK |
| 14230 | 44598 | A | 14313 | 2 | 338 | |
| 14231 | 44599 | A | 14314 | 1 | 390 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14232 | 44600 | A | 14315 | 237 | 488 | PWKTLDSSEAEILRGVSESSAV TLHCMEGQAVGPRQVKRIVHC *ASSA*NPHAMLLLQNR*LALC TSVPQGA AVL CGGWD PGN |
| 14233 | 44601 | A | 14316 | 358 | 616 | |
| 14234 | 44602 | A | 14317 | 13 | 1155 | IKLPPPGCRRRGGRHRRHRYRG RAEPLAPRRRLPPAPEQPRARP PASRFLKNTMSNGYEDHMAED CRGDIGRTNLIVNYLPQNMTQD ELRSLFSSIGEVESEAKLIRDKVP GHS LGYGFVNYVTAKDAERAI NTLNG\LR LQSKTIKVSYPSS EVIKDANLYISGLPRTMTQKDV EDMF\SRFGRIINSRVLVDQTTG LSRGVAFIRFDKRSEAEAEITSF NGHKPPGSSEPITVKFAANPNQ NKNVALLSQLYHSPARRFGGP VHHQAQRFRFSPMGVDHMSG SGVNVPGNASSGWCIFIYNLGQ DADEGILWQMFGPFGAVTNVK VIRDFNTNKCKGFGFVTMTNY EEAAMAIASLNGYRLGDKILQV SFKTNKSHK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14235 | 44603 | A | 14318 | 1 | 2340 | MFVWRNVEGHSAAVFSWYSIP FLTPCSHTRPSNLPTQWPTR ENNLPWQPLLMSVHQAQSL ALRKEQDSSSEKDGRSPNKSDK DHIRWPMGAHDLQQAAPGPG GAHQGHHPNQDNRTVSQMLSER WYTLGPNEMQKYNLAFQNV ARIRYVIVRGNEQGFFRMHHLR GVSSLQLGRRRPGPGTYRLEV DMITIDARYRCSGLRSPDPDH LKSVDLHRNEHFFLQKARWEIH LVLQATPSQIQLLHVAFVLAKQ PLRCRKQTLFLISVVGTKEN ASEGRNPVRPLRGHRWLPASPP AAEHFAGGADRKSRLSRAPRSA ATATPANEQRAVADVQWAR ARGGRVRAAGRSGSCALRRSR CRRRRRRHRRHRYRGRAEPLA PRRAASGQPGKLRRRGINCNA SSIPMLQVVRIKSISKHCQMAR VAGEGSLPLSHAQLTHCVFGN KQVQRTIAYLPPQQQGVQGF KNTMSNGYEDHMAEDCRGDIG RTNLIVNYLPQNMTQDELRSF SSIGEVESAKLIRDKVAVGLLSL CVPIRNVEIVASTSWWSLPLAP YVPRGIRRSQPSTLMDDLSCRS HQAAAPFTASVLLYISGRVKAH TAAQGFNHIPEEGVSQEAGSG WSQAWKDGWLTNVFMFSCTG HSLGYGFVNYVTAKDAERAIN TLNGLR/PPVKNH*GRPLQLGFL |
| 14236 | 44604 | A | 14319 | 701 | 1050 | LIVHFCLQVGCGVGNTPFPIQ TN/NTNSEYDPSRCFAFVHDL DEEKSYVPKSSLDIIILIFVLSAI VPDKMQKAINRLSRLKPGGM MLLRDYGRYDMAQLRFKKGIL KVLNPNH |
| 14237 | 44605 | A | 14320 | 701 | 1519 | LIVHFCLQVGCGVGNTPFPIQ TNNDPGLFVYCCDFSSTAIELV QTNSEYDPSRCFAFVHDLCD EKSYVPKGSLDIIILIFVLSAIV DKMQKAINRLSRLKPGGMVL LRDYGRYDMAQLRFKKGQCLS GNFYVRGDGTRVYLCHTRCNW TRFSPTAGLEKPKPVDRLQ VNRGKTTDNVPGLDVQILQAP SVQHQLRGYLLPTRCKPVVVS GLFLKKKIVALGVV/RCL*SQPL RRLRRGGSIE/HQQSNLGKIVRD PVSESNDKIKRI |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14238 | 44606 | A | 14321 | 756 | 1334 | PGKFVLMSFLDPQPPTRILEVGC GVGNTVFPIFTNRTMTQDSL VYCCDFSSTAI N ELVQTNSEYDPSS VF A AFVQGPV**RESVTQCPRAV LDIIILIFVLSAIVPDKMQKAINR LSRLLKPGGMMLLRDYG RYDMAQLR F KKEELDTLFTTAGLEK VQNLVDRRLQVNRGKQLTMY RVWIQCKYCKPLLSSTS |
| 14239 | 44607 | A | 14322 | 249 | 474 | VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQL\TRDV KDLFKDNYIPLLKEI*EDTSKW KSIPCSWI |
| 14240 | 44608 | A | 14323 | 1 | 5796 | |
| 14241 | 44609 | A | 14324 | 1 | 2721 | |
| 14242 | 44610 | A | 14325 | 1 | 3438 | |
| 14243 | 44611 | A | 14326 | 1 | 3306 | |
| 14244 | 44612 | A | 14327 | 1 | 2364 | |
| 14245 | 44613 | A | 14328 | 1 | 2091 | |
| 14246 | 44614 | A | 14329 | 1 | 2334 | |
| 14247 | 44615 | A | 14330 | 1 | 1986 | |
| 14248 | 44616 | B | 14331 | 1 | 2559 | |
| 14249 | 44617 | A | 14332 | 1 | 1671 | |
| 14250 | 44618 | A | 14333 | 1 | 1845 | |
| 14251 | 44619 | B | 14334 | 1 | 2055 | |
| 14252 | 44620 | B | 14335 | 1 | 1554 | |
| 14253 | 44621 | A | 14336 | 1 | 2559 | |
| 14254 | 44622 | A | 14337 | 1 | 1714 | |
| 14255 | 44623 | A | 14338 | 1537 | 2204 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met bod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 14256 | 44624 | A | 14339 | 2004 | 3751 | YQSLAETQQQKKNFRPISLMN IDAKILNKILANRIQQHIQKLIH HDQEGFIPGMQGWFNHKSINV IQHINRTKDKNHMIIISVDAEKA FDKVQQHFMLKTLNKLIDIDGL EVLARAIRQEKEIKGIQSGKEEV KLSLFADDMIAYLENPIVSAQN LLKLISNFNKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTI ASKRIKYLGI\KLTRGVKDLFRE NYKLAPLIKEIREDTNKWKNIPC SWIGRMNIMKMAILPKVNYRF NAIPIKLPMTFFIGLGKILLSSY GTTKRAHIAKTILRQKNKAGGI TLPDFKLYYKATVAKTAWYW YQNRDIDQWNRTEPSEIMPHIY NYLIFDKPEKNKQWGKDSL FN KWCWENWLAICRKLKLDPFLT PYRKINSRWIKDLNVRPKTIKTL EENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLKSFCT AKETTIRVNRQPTKWENIFATY SSDKGLISRIYNELKQIYKKKTN NPIKKWVKDMNRHFSKEDIYA AKKYMKKCSSSLAIREMQIKTT MRYHLTPVRMAIIKKSGNNRC WRGCGEIGTL |
| 14257 | 44625 | A | 14340 | 519 | 1286 | LNLEERAFRHSSEHLPHLKVH FRHSSCGIKTKSLLHVSPPTTLIF PYPPLWGNPSN*ARPPCSVHSG PYPQGLASIIAHGSPGNVRGVH V*INDSEGGISRPSTASHKETPR PPTPARHADLAATRPRSLTTSPS \GAGPRA/PSRAGPSVGGGLLRP SGRAPRAEVALPAGLSPAGLAG PPPSGRSTGALPPAAAPTTS GP/P ASTPPNAPAPGHTLSSRSPHRA ARPPPHCGAEWTGFTMRPSW RISQSFIVKDS |
| 14258 | 44626 | A | 14341 | 482 | 700 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14259 | 44627 | A | 14342 | 1368 | 2416 | SSMTQSSCPMTSYLKSKFGEPL MPSYTNPTETGVSKLVNKTQVF TYAHKGVPVSIYFDACQAAHLSK LNNIWTSVKI*DKKESASRATK AITEESKKECPDCDNQWTTHEF NQHLYTGRAALFASQEEKIGYT TGTCYPLNLTILKPNMTFWTKG HKGLLTFDQAGALLGLGIPLVI TKKTQRTQVQLSPIQQFRFYKS FNEHFNSEVSKIQIPPISTENLFV QLAKSIANNLGVTSYVCGGA NMRDQWPWEARELMLQDNFT LPEFVTKFNANPSVWLLRNPIIG KYCIACWGKSFQNQIGETTCLG QQYFEESNRTQWRSFIDDSSIG HFNPFLLQFPTLNQSWYQLE |
| 14260 | 44628 | B | 14343 | 1 | 1071 | |
| 14261 | 44629 | C | 14344 | 89 | 283 | |
| 14262 | 44630 | A | 14345 | 244 | 315 | NPKGQKDREAPLSRSVFVLKIKI KRAFALLHGRF*PSTPAASASP ASKSPRGSGKALASALFYIVQL TK |
| 14263 | 44631 | A | 14346 | 1228 | 1656 | QVYRPSQTPHLALSPERVAPGR RAAGRLAPEARAPRGSP/LPPHR VSEKTIRVVVFHFGARRAGGTP PRAPRGDTGGAPGA\PTYSTPL MSLHRARLESSPTGSSFPADSA KPVPLAVVSLDSR*GQWESRSS IHA\VTN*MTRH |
| 14264 | 44632 | A | 14347 | 2 | 705 | GSWPGLDDGSATRILACPWPGL GDGPAAPKANLPLVRWKPQCF RGEGL*GSSCFSATLLTGDLW ACSSRSTASARLSTYPSAFTSG WCSSLGPTEEAPGSWINCPLAG ILGAATSPKPSAIPQASPEVSLD AEDTGMKP*DSA\GPPGPARGL CGRGCGLSPACMGLRP/PSPPA QSPSTALTSLT\PSPFHPPRKKW SPPSAPAPSAPSPAPASLTSPAP PAPSPAPTAPAP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14265 | 44633 | A | 14348 | 367 | 1174 | WVRGQPSQSQDLACSTPTS* WPPGRAPPPPLP/PPPPLPPPTP ASPPLLHPPRRAPPPPPVP\SFTP ASPPDPVPRPTKALTGLP/LCP LPCMGR/PFVPYLGGLPCLGP DFSSL**SPGGWDRPVRPLGISQ IPE\PPLTMGL*MQ*IPP*PRFQG HYAPLPPQLTLCISVKTPGRNPR GLPMHKILQPQNPSQPPCEL PQ AHCPTTPPPKQCPAAFSILPVT FADKDPGA APEGTVKAPMPTQ *EL*PLRPREHRVLSGPTAGQT |
| 14266 | 44634 | A | 14349 | 332 | 988 | RRAGTPASWGHNGARAKTPSR ACACLGLYPIHQPTARRAPAAR SHGPGPPALPRKGA AHGPRSVS HHPLRPCSRSSCLAWPCLHHPQ PLHCHPHRHWPKWHPHPLAPH PLLGLHPRSRPQTTPWTSCGPSR RLPTPSGSWPAPFDRDWP N*AR PSALCCPFCQEPQLTPCLHLC PH PHPHRHLPGLSCPHRPPRWRSP QSPCPWWLLWWTGQWWQPGE |
| 14267 | 44635 | A | 14350 | 190 | 718 | FVLQLPPAPKSGLG RWGSPPPG QFSSSQRTGTVRGRGRCAEPRG SLPHPT*GNNK*HGNWMGLGS QGL\GRQPGEDKH CYQR/IGVG GAHLLRPPHQIRSLTSTGSGCS HPWSRELGC SWDQGRASAPLA LRQAWGEGLAGRNHTIVPFHG DISIAPRLLPCRETLFSALCGGES |
| 14268 | 44636 | A | 14351 | 1 | 486 | MKGEVSCKQH QDALQQVLWA MLQDADKQVRRAPGPVENENH CDFVKLREMLICTNMEDLREQT HTRHYEL YRRCKLEEMGFTDV GPENKPVRVLLFKSLSDSKRVK YDEEWIRLPVE/MKY/MLERKV TQKQP*VPLVFVSWRSR*ESLR REEENQQCHVLEL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14269 | 44637 | A | 14352 | 1 | 2380 | MMWSVLLQPVVLA AVERQGE ALEFLIGVPESDGENGTKLENT LQDIIQEDFPNLRQAHVQIQEI QRTPQRYSLRRATPRHIIVRFTK VEMKEKMLRAAREKGRVTLK GKPIRLTADLSAETLQARRDRG PIFNILKEKNFQPRISYPAKLSFT SEGEIKYFTDKQMLRDFVTTRP ALKELLKEALNMERNNRNFFG VTFAFFVGGQSLGKALQETSIPF LREEDLEKTSILETGNGDWEAT RGLPEECAGMRERDCQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSPKDADDTSIYMFYQ KVGDN SIDSWKNAGR VFKDSD KFDANDPILKDQTQEWSGSATF TSDGKIRLFYTDYSGKH YGKQS LTTAQVNVSKSDDTLKINGVED HKTIFDGDGKTYQNVQQFIDEG NYTSGDNHTLRDPHYVEDKGH KYLGLIPTYDISSNIYLISK SCLW QANFRLNSALAQSPAITNFQFR GHSLKTLDLLTMKNLDSKVNI PVIAKADTVSKTELHKFKIKFM SELVSNGVQIYQFPTDDDTIAK VNAAMNGQLPFAVVGSMDEIK VGNKMVKARQYPWGVVQVEN ENHCDFVKLREMFICTNMEDL REQTHTRHYEL YRRLQLEEMG FTDVAPKNKPASVQETYEAKR HEFHGERQRKEEEMKQMFVQR |
| 14270 | 44638 | A | 14353 | 105 | 328 | |
| 14271 | 44639 | A | 14354 | 107 | 676 | IRPDSLPSASPAQDFYAASSNTF PA/DRWSALT KIYEDQ TSHNIPL SQ/TLIQSKALT FNSVKA EKDE EAAEEKFEVTRVVHIRGLIDGV VEADIVEALQEFGLISYVMVMS KKRQALVEFEDVLEACNAVNY TADNQIHIAGHPAFVNYSTSQKI SRPGNSDDPEREQCASLYHPEP HLFDHHGCSLHYR |
| 14272 | 44640 | A | 14355 | 221 | 648 | LDWLR RVVGIPSLRWTCATLV GTRRAARHRCVNVWECGGLKE ITY*SVEGLCRA/EKPKPLALLE ETCKLPERQVVNAKEKFLEE\IK SATPVNT*MIRKRNCIITDMEK V*AVWIEDQ TSHNLP LSQSLIES RALTLFNYVMA |
| 14273 | 44641 | A | 14356 | 122 | 317 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14274 | 44642 | A | 14357 | 338 | 489 | WLGQN*RHGKQPGPGVGHVGT TVWS*PHSPACWAPAPQGAPT GEEGCHF |
| 14275 | 44643 | A | 14358 | 1 | 459 | RPVWRNSQPPTAAYRWASGR MWSTSFSRWNKTPSGKACSSS DKGPPMAQVPIQQRNVPPPTK/ QPLVLCHGEAPDFSRPPQHRPS LQKHPSTGG/PSHSPLPTSAPSSR AGLPPLAMTDLTSGWRLWTPI QPFRLPPGSCREGTILLCSVMD |
| 14276 | 44644 | A | 14359 | 609 | 2077 | GLKAQPSSSRGHSRGPACAAA PASRVHLPVTFCEPNSSPCPHC TGGWGGRGQ/PACAGNPTASSP CQIECPALRSCLHALMDLGSPQ\ LRGAPRTGVDPRLHLLPQPAL SSPPVLLRGPLLRGTCPLAARQ GQSPPAPGLLGHGPHRGRLPP AQGGHRLPQPPGPRRHRAPQP DPRRPGLRAAAASGPGLAAWG AVRAAERPSSGGLPGGAGPHH ARAQGPRAAPPAAAAPGVAP AGGGA VPGGHPHRPGGEAALP AHGLPAPAAERTAPR\QPCPAC GLIARSDVHHPPVLP/LSGPAP APGRLVGQLGVRGAPSSPVPHP ALHFPRAQP/PPGKGITTTSTQ PAGSPSPCMPPAATPGARHPP GSA\GHRAGV*GHTGPCDPHGP GHHGHAQLL*/DQAAVGVRGP GPWALSGMSQPPTLPTAGHPA PACGVRAFQDGRPPRAKPAL/ LSDKGPPMAQVPIQQRNVPPPT KHPCPGPQSSTWMRQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14277 | 44645 | A | 14363 | 47 | 1250 | EPRPSRSSGGPQLGQGLPRPMK KIPGSSAKTAGPLATRPEVPRAP *SAGRQPWFQRPWGKRKGRKT *NHGSPGVKP/TPGPLNKDKGE KEERPRQQDPQRKALLHMFSG KPPEKPLPNGKGSTESSDYLR SVTPGPWSFSPQVVASGPMMPVH TTKKPA*APPQVL/EPKERQTGA AADMPQPAVRHQGREPLL VVK PTHSRPEGGCREVPQAA/SQNPR PAPGLQTPGTRQTS\SVTPQPCP PAATHSLGLGSNLSFGPGAKRP AQAPIQACLNFPKKPRLGPFQIP ESAIQGGELGAPENLQPPPAAT ELGPSTSPQMGRRTPAQVPSVD RQPPHSRCLPTAQACTMSHHS AAGHDG/DPASQSALPETGKRT LELQPPGGPLISLS*EAGSLSRSE PSCVREV |
| 14278 | 44646 | A | 14364 | 23 | 714 | EAP EIPRQNRMTMKERP VWL PHK*IHPNVAKWSRVPVQVQK NPQFQE\PTPEFIPVPGTSPEAAG FWH*GAHDSPGTRDRSEVEPGR GHPHLGPRDSAAADPGEHSPCD CP*ACPEVRRWPA\APVQIQYIIP SVDDFSLEFHAQDGDSDMRRE NVPFSPAEEGKAAPLYQQPLMI PQANHMAGISPS/SPTAAEFQHR DVHHRGPGTRDRTH TETGRVC PHPVPTDSPAL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14279 | 44647 | A | 14365 | 3 | 1869 | ITTVAPSRPASSDCESDGS*EQD AGPGSRMGPEK*AGPRPTRRVG RWSQTHSQTDGSGAVVPEYP SDR*YAGGRGPG/PGGPTVHP* KRRS*NPQETKMMARRDPKSW AKRLSPV*PRLAALLTSASPSCP LEPRVLPFRVPPSHGLCEGTSYP NSPGT*RPPCRSSAKTAGPLATR PEVPGAP*SAGRQPFQRPWG KRKG\GKPETMEAPG*SQPGAL EQG*GREGRETKATRAEEGSP PHVFRETSREAAAEWKRIHGVF *SSEHGP*FPFSFPSAGGNRGT PLSCLLGVDRDSTILPGCKRANA GPHNQ*EAARGPCPR*SISAAE MSGRGSVLASLSPLRKASLSSSS SLGPKERQTGAAA/AHPSACSQ APGPRASPRGEADTQPPRG*LP RSSPGCLQNPRPAPGRQTPGTR QTSCGDL/SSPARQPPHTAWA* APISASGQEPDLP\SSDSGLPEL PQETETGSLPDPRKRHPGR*AG GPGKSPTSASRNRTWTKYVAP DGQEDTGPQAQRRAASAQQT LPAYCPGLHHVPSLSGQP*WGP ASQS/GSSGDWKTDA GAPASW RPPHFTLLRSREPSLRALMCQR SLRLPVFVSHRASSMRTFRFPPP QRTAILTWS |
| 14280 | 44648 | B | 14366 | 1 | 1519 | |
| 14281 | 44649 | A | 14367 | 312 | 1326 | TTKTGQDKDRLEEFMQQLSGS KRKMSTQPRTELAPPNRHTTTTS TTPATNTTCTATVPPQPQYSYH DINVYSLAGLAPHITLNPTAHP QLKQCVRQAIERAVQELVHPV VDRSIKIAMTTCEQIVRKDFAL DSEESRMRIAHHMMRNLTAG MAMITCREPLLMSTNLKNSF ASALR/PDGSSAIQL*SND*SCS WRPKLYDAFWDLSSLRV**PSR PEGEGRVSSEGMGESLPFSSSW PRQYQSFLCICWTDAPARNTED R*SHNKVLSSVY*NVC*NQLPC SG*AAQSCCQSHHDPQSQVLSQ PGCLCSTHCTARETLRGGHQHC HKD*SAEQGL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14282 | 44650 | A | 14368 | 2 | 1120 | PEPEPGARGGEQLNEDFEG*VA VPTCLHCPALSRQTQSRAIQALT VRRGEATIRPPPCDDTKGGHRF LNELIKVVSPKVGAPSPSSDLPC RMWGEERGWTVGLPEEVKIAE AYQMLKKQGEAHRGWGATRA CLPLPHHERPKNVIFEDEEKSK VRLQGGTYGDSEPRWGSVGS KEMVQE/DSGRAQSTGRRRDG GIELGH\NVKLLTEMVMSHSQG GAAAGSSEDLMKVHLPPCLPHS LPTQPTRTLRMRPTLFRLASDT EDNDEALGEPRAGAEVRSPPLP PPPAPVRGEEVNGDATAGSIPG EEVAGELGGHPSGWRGTESYP AMPTRPGEQASPEQPSASVSL DDELMSLGEEGARPGGGRAQQ |
| 14283 | 44651 | A | 14369 | 1 | 432 | GTRQEVTAGVEPAREWQRRLM EVQWGLERAPYCIQHAPR*RRS PARPGTQSCGLGACWIQ*GALS SPHCTISIRRHCHSLAGSTPAVTS CLV |
| 14284 | 44652 | A | 14370 | 16 | 471 | |
| 14285 | 44653 | B | 14371 | 66 | 206 | |
| 14286 | 44654 | B | 14372 | 234 | 390 | |
| 14287 | 44655 | B | 14373 | 207 | 427 | |
| 14288 | 44656 | A | 14374 | 2 | 572 | FLLERAPYGVGFSLLPGLWLGS RAGVGRHHDKRVLGRAPTWS LEGAVSSM/TPRPQLCVP/WPC WGPSSPGG*QQLGQLSCSYSLV DR*VALLWFWMLVGSPLVKGH CPTPWSRFVDFSVPLATPPGIVY WGLFAVFLFSHLLPARPGEQMS ACCRHLHAPSSPLLTLDSLIVY SCNSQGKLVRFVPPGD |
| 14289 | 44657 | A | 14375 | 175 | 499 | KQNKSMGRKSQGFVASFGNHL YCTASCGMPASSTSTQTWPRVL PLHSQ/ESSHGGCSWRGRR*GP RPRPHKTPVPMVMDSTARNRA RRELVLAWCKSPLATALLVSW DK |
| 14290 | 44658 | A | 14376 | 408 | 625 | VFGEQEVFGYMNKFSSGDF*DF GAPTTLSSEHCTQC VVFYPSAP SFPFPPVPKVHCVIPHSLVPTYE WEHTM |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 14291 | 44659 | A | 14377 | 1263 | 1812 | AGDAAPEDPAGRGQEDLYDEE LPGWGLCIPHPACLPQCHA*VT KAG/ARVKVILPS*DTQRTKDIL KAGGG/PSSIHFINSAHGKPAVI VRPRGIWVLNTTPLSGQWGPYI GVYTAATVDMKSLGSGSLGLQ LALPLAASWLGVLTEAARVFG EQVVFGYMNSFFSGDFWDFGA PITRAVYTVPNV |
| 14292 | 44660 | A | 14378 | 1 | 693 | |
| 14293 | 44661 | A | 14379 | 2 | 1299 | WDYV/KRPNLRLIGVTESDGEN GTKLENTLQDIILENFPNLARQA NIQIQEIQRTPQRYSSRRATPRHI IVTFAKVEMNEKMLRAAREKG RVTHKGKPIRLTADLSAETLQA RREWGPIFNILKEKNFQPRISYP AKLSFISEGEIKSFTDKQMLRDF VTTRPALKELLKEALNMERKN RQINETENQQGYPGIELGSAPSG PNPLFCRHLQMSVDGRHLQNSP PQINRIYIFLAPHHTYSKIDHILG SKTLLKKCKRTEIITNYLSDHSA IKLELRIKKLTQNCSTTWKLNH LLLNDYWVHNEMKAEMKMFF ETNENKDTTYQNLWDTFKAVY RGKFLALNAHKRKQERSKMDT LTSQLELEKQEQTTHSKASRRQ EITKIKEELKEIETQKTLQEINES KSWFFERINKIDRPLARLTKKK REKNQIDAIGN |
| 14294 | 44662 | A | 14380 | 2 | 383 | |
| 14295 | 44663 | A | 14381 | 1 | 1536 | |
| 14296 | 44664 | A | 14382 | 2 | 1118 | REHLAEGMAVG TASADLNISA CWLRRREQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQRK EQAAIFAVLQPPLVIPRKTGSGV DLEQTPADLQKRGTLVTRKTN KQKAIASSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSPAR EQNWTENEFDELTEVGFRRWV ITNSSKLKEHVLTQCKETKKLD KRLEELLTIITSLEKNINDLMEL KNTAGELRDAYTSINS*IDQAEE RISEIGDQLNEIKCEDKMREK\R MKRNEQSLQEIWDYVKRPNLR LIGVPESDGENGTKLENTLQDI QENFPNLARQANIQIQEIQRTPQ RYSSRRATPRHIIVRFTKV |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14297 | 44665 | A | 14383 | 1 | 1154 | MLPILGSRHPSSLGQARKLDYR PSKSQCLEPGTPRACLVLTYLV AKLIYNDYFIHYFAPRGLPPME KNVVFFVIDISGFMFGTKMKQD HNFSLAREQNWTENEFDKLME VDFRRWVITNSSELKEHVLTOC KEANNLEKRLDELLTRITSVEK NINDLMELKNTAGELREAYTSF NSCNDQAEKISEIEDQLNEIKP NRLIGVPESDGENGTKLENTL QDIIQENFSNLAKQANVQIQEI QRTPQRY\SSR\RATPRTH/IIVRF TKVGNGREKMFKGQPGGKGR\ VTLKGKPITLTADLSAETLQAR REWGPIFNILKEKNFQPRISYPA KLSFISEGEIKYFTDKQMLRDF VTTRPALQELLKEALNMERNN RYQPLQNHAKM |
| 14298 | 44666 | B | 14384 | 1 | 1554 | |
| 14299 | 44667 | A | 14385 | 1 | 909 | |
| 14300 | 44668 | A | 14386 | 2 | 207 | DIMSCILQNYNRPPVMALAIPIA VKFLHRGNKELCRNMSNYLSL AAITKAD\LLADHTEVIVKSILQ |
| 14301 | 44669 | A | 14387 | 496 | 1207 | PLITGTHDSGSVESQLIKLILTM HQLFRLVLGQKDLRAGDLFS *NNSEIEDSLTEALEQIKIISSSD YQTNNNDQAVVEICITRITTAIR ETESIEKHAKALVGLWDSCLEH NLRPFGKDEDTPHAKIASDIMS CILPELQPTPQSMALAIPIAVKF LHRGNKELCRNMSNYLSLAAIT KADLLADHTEVIVKSILQGMVR KLSLGTCFGRYLKVFSSSIYGL WEARPRVLEAN |
| 14302 | 44670 | A | 14388 | 219 | 448 | VSLELCLKTTGPDCGCQTSQTP PAAAYHHL/PGAGLPCGPRLPA LCCSCPMGARPL*HHKR/DPSRF QEKTHLYLPSSH |
| 14303 | 44671 | A | 14389 | 542 | 1365 | GTEGVMANRSQEGNGGGSWR AKQVVVTVPF*EQSLVIMLWR RGNT*QRPSEGTSRSHICSFH MSRHCQ*CKLLKEP/VSAEAR DALDTKTHFPLAMIPSYLLNG NIGELPEGPAGGCAQNPGLWAS /RGPARR*RSQASSSPEVRWPPG QCGLRGRPCKKEIPRHPWSRP CASPYRGAGGQRLRRACSAAG RKTPDRRPLPEPTRGPVSQRAV LGKLRAAAGHRIPIGDLGDGLS LGAPPAGRHLHTVLPRLRREFSP CEDALGIGEQQGKKRVT |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14304 | 44672 | A | 14390 | 3 | 723 | PVLRGGIQEFAYIKALYERKFL VPKPIDYNRHA VDMELINGYPL C*IHHVEDPASVYDEAMELIVE LANHGLIHGDFNEFNILDESD HITMIDFPQMDSTSHPNAEWYF DRDVKCIIDFFMKRFSYESELF TFKDIRREDTLDVEVSASGYTK EMQADDELLHPLGPDDKNIETK EGSEFSFSDGEVAEKAENVYGE NESERNCLEESEG CYSDHLETL NK*RKTVYQKRVL MHGV LK |
| 14305 | 44673 | A | 14391 | 1 | 1889 | MGSKVKEVEDDSQMSDLVRG MNAFSKTGSGGVEQGRTGQGG TNGHIKKAKARDRDRRFFKKT QRKVGNDNLQLPLRWTEQHAE THIMNFCSKNYNRNIPGKPRESI DTLNEAACRGRLSKTARKLWS EAQDQRSFQATEMQAFLFSAK RIAAEKKTIIRRDLC SIWGKLL PRPGSQSVPAQIPENLQE QEERA K WLLNGRSKFFPQTSTLGKVT SNKTGVKEPELESRQPNLLKVE MGMKNHEIVPGSLIASLKH GGCNKVLREL VKHKLI WERT KTVQGYRLTNAGYDYLAKTL SSRQVVESVGNQMVGKESYI YIVANEEGQQFALKLHRLGRS FRNLKNKRDYHKHRHNVSWL YLSRLSAMKEFAYMKFRTLEIR DYFYWVKINVLTGPCSPKRGSS GEFVPCLLQLLLGFGDCWHSFG LWHITPVSVSMLTLLPSLLLVK QKKPTLDSRMGQDFVVELQL YLCVLEREVIREYPPDGQIFGRY FDRDVKCIKDFFMKRFSYESEL FPTFKDIRREDTLDVEVSASGY TKEMQADDELLHPLGPDDKNIE TKEGSEFSFSDGEVPEKAENVY SENESEARNCLEESEG CYSDHLE TLNK*RKTVYQKRVL MHGV LK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14306 | 44674 | A | 14392 | 150 | 1910 | STPPGGPSVLM*STEEPGAGRS QPLCDDLSTRPLSCLGAGCCLW PAKRISAKEEPWYSSRSKDKKE KNYSSPETTTSGGCHSPGDSQY QELAVALESSSVTINQLNENIES LKQKKQVEHQLEEAKKTNNE IHKAQMEQLETINILTLEKADL KTTLYHTKRAARHFEEESKDLA GRLQYSLQRIQELERALCAVST QQQEEDRGHCLSSPDQNFSLFTI QSSSCREAVLHRRLLQQTIKERA LLNAHVTQVTESLKQVQLERD EYAKHIKGERARWQERMWKM SVEARTLKEEKKRDIHQELER SLSELKNQMAEPPSLAPPAVTS VVEQLQDEAKHLRQEVEGLEG KLQSQVENNQALSLSKEQKQ RLQEQEMLREQEAQRVREQE RLCEQNERLREQQKMLQEQGE RLRKQEQLRKQEERLRKEEER L/TKAGKEAVGPGGEAVEEGGE ATKAGGEARALPEPQARQAAG RATVQLRGSEQREKERTAVGA ASKGAAGEARRGEDAVHGH SAADL*EGGAAQAVTAADPVR GPAAGSLGQSGAPRSCQPPE PTARDPAKPRGSPWRRRWRTT |
| 14307 | 44675 | B | 14393 | 463 | 3755 | |
| 14308 | 44676 | B | 14394 | 175 | 1835 | |
| 14309 | 44677 | A | 14395 | 102 | 465 | RAYCWAYIRLSCLTVILIAWCS QESALSEEEEDTTRPLETVTFKD VAVDLTQEEWEQMKPAQRNL YRDVMLENYSNLVTGVCQVTK PDV\SSWSKKRSPG*WRKKCL GGTVQNPEEERTAV |
| 14310 | 44678 | A | 14396 | 1 | 330 | |
| 14311 | 44679 | A | 14397 | 1 | 531 | MLLNIPQHTRQSPRAKNYLAQ NVNSVKAWCSQESALSEEEED TTRPLVRLKHLFVSCIILQCSYV LLPLTPEYQLNKFLYVVITMPN FDDFKLISIMFLQETVTFKDVA VDLTQEEWEQMKPAQRNL YRDVMLENYSNLVTGVCQVTKPD V\SSWSKKRSPG*WRKKCLGG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14312 | 44680 | A | 14398 | 1 | 539 | MPTTTTREMTONSSETIKNKNG KKQRKQRKNSKKNRRKQKDE DKTRRQNKRRHHKKNDINPEEE RTAVRLKDGGAPAPQAVQEHD AGICSASGGAQETYILVEGKGE ASTSPGQSKGSREGGVGANETC SKKLYRDVMLENYSNLVT/VG CQVTKPDVYSSWSKKRSPG*W RKKFWEALSR |
| 14313 | 44681 | A | 14399 | 322 | 1227 | FDLKMSKCRKTPLQQLASPASF SPDILADIFELFAKNFSYWKLPL NNEWQLPDPSEIFTCDHTEFNA FPWI*RTP*NEVKKPTGVIRTW DEWHEHTCFH**SGE/ISFPHGR KSVNAELWTQAWCKFHEILCS FPLIPQEAQNGKLNLSHLCEAP GAFIASLNHYLKSHRFPCHWSW VANTLNPYHEANDDLMMIMD DRLIANTLHWYFGPDNTGDI MTLKFLTGLQNFISSMGTVHLV TANGSFDCQ*NPAGDQRMVKG HCYFPSWNWLHLSKHTQCGNE FIFMTKKKQSLTAKSLPDFTS |
| 14314 | 44682 | A | 14400 | 3 | 183 | KRKEITNSLDAAASRGTVPAAL AGVQYLEPRAGAAGRLGGAG WGRVPRPGSS/SSLVLVGR*GW CPVLRTQGRCCRPPGGCWVGA RPAWELLSLVLVGR |
| 14315 | 44683 | A | 14401 | 21 | 399 | IWNSAPTASRRPWSLAPGSPRS TWCVASTPPCAPGKAREPRDRS EVPPATAPAVLQSHWPCPRSSR SGSAGNCVGPPHSWAPGHSQH LTPGPGHGGPRGP/CWHLLMQT AWPALTPPGAMPGEAEGQ |
| 14316 | 44684 | A | 14402 | 59 | 478 | RCSQPWHCPAALAGVQYLEPR AGAAGRLGGAGWGRVPRPREL LSLVLVGR*GWRPQEQLFPH LRRPVGTRSESTWGNRAGAAT W/RAATPSPWRT*NGTKSKQW TASGLWQKGDGWD*GSGKPPL PLSVPAGQRLVPVC |
| 14317 | 44685 | A | 14403 | 1150 | 1319 | PRRLPTACTP*RS/CSRYWMVP KSPRMTMMMWTKLARMGAQ W*PRKSNACLSRAASS |
| 14318 | 44686 | A | 14404 | 34 | 304 | LPSRGAGLGTCSPPCLSLPPTPW APVRPEPPRRAPPAPRRVPST TQ/EARRSAASLLSPARPAHRD GTNNSRRATLRAVTLTARVRG F |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14319 | 44687 | A | 14405 | 1 | 360 | SSSLSYLPAGQGSGPAARHA*ASHPLHGLLCGPSLPNEHRPLLQGAQSH*PPKG*GVRAHGVGLA GRSTCSP/ECGIH*VKPAGLLSFLGPRCFYEL*QSPRRSAAASLLSPARSRAHRE |
| 14320 | 44688 | B | 14406 | 80 | 1166 | |
| 14321 | 44689 | C | 14407 | 1 | 543 | |
| 14322 | 44690 | B | 14408 | 1 | 930 | |
| 14323 | 44691 | B | 14409 | 1 | 1473 | |
| 14324 | 44692 | A | 14410 | 388 | 606 | |
| 14325 | 44693 | A | 14411 | 1 | 798 | |
| 14326 | 44694 | A | 14412 | 687 | 832 | |
| 14327 | 44695 | B | 14413 | 1 | 1218 | |
| 14328 | 44696 | B | 14414 | 1 | 642 | |
| 14329 | 44697 | B | 14415 | 1 | 807 | |
| 14330 | 44698 | A | 14416 | 554 | 724 | |
| 14331 | 44699 | A | 14417 | 216 | 494 | |
| 14332 | 44700 | A | 14418 | 1 | 3408 | |
| 14333 | 44701 | A | 14419 | 330 | 858 | VPSLDGQRGLELDTECRLVYLQ SLS*T*RFSTSSPEQLDTECRLV HSQTLC*TQGADWCIYKP*VGL QVELPASAPWLAFLSPWVFN GTGRHGAGGGARRGGSGCTGA HGVGGRLRHGRLQVPSAPWE GSCSLPSPIGPPFKRAHSVLQKG SSTLMVGTCASSPKVVPFHLLS |
| 14334 | 44702 | B | 14420 | 182 | 1513 | |
| 14335 | 44703 | B | 14421 | 1 | 1608 | |
| 14336 | 44704 | C | 14422 | 1 | 1830 | |
| 14337 | 44705 | A | 14423 | 167 | 433 | LPSRGAGLGTCSPCLSLPPTPW APVRSEPPRRAPP/GSTVSPIN HPRAEECERMARDWQAAPPAA PVRDPLGEASWAPEFFGSMLPL |
| 14338 | 44706 | B | 14424 | 32 | 352 | |
| 14339 | 44707 | B | 14425 | 103 | 451 | |
| 14340 | 44708 | A | 14426 | 158 | 921 | LPSRWAGLGTCSPCLSLPPTP WAPVRPEPPRRAPPSAPRRPVP RPPKG*GVPAHGAGLAGSSTCS PDICRVCRSEGTPEKPLYHPCVC TGSIKFIHQEC\YSPDMPSRLPIQ DIFAGLVTSIGTAIRYWFHYTLV AFAWLGVVPLTAWHQLLDLGS TLNPGCSHLVILKLTSTKTLP NKATFILVVLSQDKTLMEDPR MEDKWKEDRFSPFNSEALEITL GERHRPQTASVIPWFCSSRHVL NLGKINFEVD |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14341 | 44709 | A | 14427 | 242 | 515 | IQSVHWCIHKP*ARHRVLIGVFT IPELDIKVLHVPTRLRNPAGFTH WILHRDCRCSCMPVLRHAPALL SPWVVNGTGRSRAGDSTHRRG SG |
| 14342 | 44710 | A | 14428 | 759 | 988 | TWPRKPLFPPRPLGL*WEGMLQ RSLTCPGDIFPIILVISIWLLVTY ANFGSWL*FLPRKWVFPFFIPVP NKFLIFI |
| 14343 | 44711 | A | 14429 | 130 | 788 | VLQLIKAVWTPRTQEPSWLPPV NPARELQVELPASPAPCARTPQ LLGGRWDWAPWSRGWRSFGE ARAAQKPMEGVGGSGMAGCR SRALPHGKAAKARRAIEHSTGG LALLGDPVHSPQPLARVLSPLP RASRAGWLLRVRGPPSPRPPGT PAGRQAPHAAPVPARASPSTPP/ CRAERVGSSPGQPRKGLPQCRG EAEGLLKCHQSGSPGRGEELW HSR |
| 14344 | 44712 | A | 14430 | 108 | 1686 | ANRCPLPHPGTGAGRCLGASA GRAEEAGV*GPLHEGLGYRPA GLFLRADTGHRTPGWGGGGGG AGGRGGAAPGPGVGATRRFAG RRGCARHGAAVPAAVR\CCERL VLNVAGLRFETRARTLGRFPDT LLGDPARRGRFYDDARREYFFD RHRPSFDAVLYYYQSGGRLRRP AHVPLDVFLEEVAFYGLGAAA LARLREDEGCPVPPERPLPRRAF ARQLWLLFEFPESQAARVLAV VSVLVILVSIVVFCLETLPDFRD DRDGTGLAAAAAAGPFPAPLN GSSQMPGNPPRLPFNDPFFVVE TLCICWFSFELLVRLVCPSKAI FFKNVMNLIDFVAILPYFVALG TELARQRGVGQQAMSLAILRVI RLVRVFRIFKLSRHSKGLQILGQ TLRASMRELGLLIFFLFIGVVLF SSAVYFAEVDVRVDSHFTSIPESF WWAVVTMTTVGYGDMAVPT VGGKIVGSLCAIAGVLTISLPVP VIVSNFSYFYHRETEGEEAGMF SHVDMQPCGPLEGKANGGLVD |
| 14345 | 44713 | A | 14431 | 1 | 427 | |
| 14346 | 44714 | B | 14432 | 8 | 323 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14347 | 44715 | A | 14433 | 20 | 1050 | FNLVYMSHVSDGALSESASAT AASWPPHGFLLQHFVPGRPQVPI CLYLLGQKTG*HMAPLLRQVT GSPIPPKTTPGRGIRNMKRNEKR RYKTLMDAGWELHQELSLGRT SSLPPYKGPWPSPGFQKVSKG ANPVEIKRGVMLAVDAVIAEL KKQSKPVTKEEIAQVATISAN GDKEIGNIISDAMKKCKGRKGIIT KISSVQSIVTALEIANAYCKPLV IIAGDIDGEALTTLLNRLKVGL QVVAVKAPGFGDNRKNQLKDT VIATGGEVGEVTVIKDYAMLL KGKGNKSQIEKCVQEIIDQSDV TTSEYEKEKLS\EKLSDGVAVL KSHPWFSCTKIYPLT |
| 14348 | 44716 | A | 14434 | 3 | 764 | TTATVLARSIAKEGFEKISKGA NPVEIRRGVMLAVDAVIAELKK QSKPVTTPEEIAQVATISANGD KEIGNIISDAMKKVGRKGVITV KDGKTLNDELEIIEGMMKFDRG\ YISHPFINTSKGQKCGISRDAYV LLSEKKIS\SIQSIVPA\LEIAHAH RKPLVIIAEDVDGEALSTLVLN RLKVGLQVVAVKAIPGFGDNR KNQLKDMAIATGGAVFGEEGL TLNLEDVQPHDLGKVGEVIVTK DDAMLLKGKGDK |
| 14349 | 44717 | A | 14435 | 1 | 3288 | MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGTRLRRAEDVFPPVI GVAAHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNDPQGT SMYHGWVPDLHIHAEDTLLPF YLGEKDDVTYAIPKTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPLMLRLAIETVAHDYDVI VIDSAPNLGIGTINVVC |
| 14350 | 44718 | A | 14436 | 2 | 422 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14351 | 44719 | A | 14437 | 529 | 2484 | WGINIIKKNKKAAPRAFGVRLE ECQPATENQRWQDLNVISSLLK SFFRKLPEPLFTDEELPLAPSFCE EEENGGRGGGSPSPRYRLEPMDT IFVKNVKEDGPAHRAGLRTGD RLVKVNGESVIGKTYSQVIALI QNSDDTLELSIMPKDEDILQLPA ERESGGEASEPPRVVRPEPSTRA LEPPAEDRGDEVVLRQKPPTGR KVQLTPARQMNLGFGDESPEPE ASGRGERLGRKVAPLATTEDSL ASIPFIDICVRPCAWLHALLDW MAQQRVLDMQGGSIGMGVSW DRELEEKGSEKGYDEPTSPSIDL QAKHVPASAVVSSAMNSAPVL GTSPSSPTFTFTLGRHYSQDCST SAHLNIFAGIFDISNDHLQVSTL ESNFTRIHLTHYTGGNFPAWLA WDAVPFSSDLLNLGVHVLETG AGTPFLGSACSSDGIASQMNTA GLPQIRDLPGHYYETLKFLVGH LKTIAHSEKNKMEPRNLALV FGPTLVRTSEDNMTDMVTPHA *PLTRSWETLIQALQTGSSVTKR YKGKENPCGLTRSLRQCPTLST FLPNIWQDSAPWRPGVSGPVG LKDSTTCSSAKSKGSWAPKKEP YAREMLAISFISAVKPQAQEA GDAGAGQQHRRRLGAGGAQS LGRGPQRRGHQERS |
| 14352 | 44720 | B | 14438 | 1 | 1473 | |
| 14353 | 44721 | A | 14439 | 5 | 694 | VPDKWGWCLFMSRYLETAIRT AACAASPRYLNPGRCSAARGPS SQSPRPPWSGHKKRTASPGWG GQSAASPMPPSRSWPASVGGPE FRLSETPSRPFTLSGMK*GWQV HSWAPALFCSVMSFSPDTCCLC K*AHSQPCSPSPSTVILLRETSSN WDWQPEDLGAPKASASPPPSTT RITRLRSSELQLRRLNPSDSCHR GFCFSFRCLLTPEHVLPKTVLRI QPGCKVA |
| 14354 | 44722 | A | 14440 | 303 | 757 | MAWKVSLRGRKVAGRAPSCLR WASPPSSGQSVKSLLLPPARRL CPGPGVPARCHRI*GLGPGRG WRGEWRRDTNPWEPPQPRSPS/ G/PNCAWSDGCPRGAPRRPRAL *AGAARRAAPARI*VPWRGSAG GCSNRRLQVPAHE*TPTPFIRYL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14355 | 44723 | A | 14441 | 1 | 534 | RHEDHSEPTFLISPSLLCFLLP PPLPRLTPIPAALLVPAVQRME PVLFLPAPGAAACRVWHPALPP PRQAAVSSSRPCY\PCVARSA PAGRVRAAGVPPAPPSSSPRLGRV GGRSRSPNVVFRVRGAAPG/PG L*ISPWTP/PLNEAS*RQRGCPAS FAVYGGQEWPPQWPGPPRGP |
| 14356 | 44724 | B | 14442 | 157 | 2143 | |
| 14357 | 44725 | A | 14443 | 258 | 4089 | QLITCLSRPETGGKFEVDTQRP VCPPSRARAARASAAVAAAA TLTPPTMDSFDLALLQEWDL LCVYEPDRNALRRKERERRNQ ETQQDDGTFNSSYSLFSEPYKT NKGDELSNRIQNTLGNDEM KDFLTDRTNQSHLVGVPKPGVPQ TPVKNIDEHFVADSRAQNQPSSI CSTTTSTPAAVPVQQSKRGTMG WQKAGHPPSDGQQRATQOGSL RTLLGDGVGRQQ/HSGQTSVQC GGGPSDPGEATCHGGQ |
| 14358 | 44726 | B | 14444 | 1 | 1326 | |
| 14359 | 44727 | A | 14445 | 453 | 710 | SQHFGKPRQVDHLRPGV*DQP GQHGETPSLLKIQKLTGRGGAC LW/QSQLRRLRQENRLNLGGG GCSEPGSCHCPPAWATERDSVS |
| 14360 | 44728 | B | 14446 | 32 | 290 | |
| 14361 | 44729 | A | 14447 | 244 | 426 | |
| 14362 | 44730 | A | 14448 | 69 | 221 | QWRFCGIERGERWGKD*EIGW LPCLCGKK*IWETFILFCTKKN SSALGSC |
| 14363 | 44731 | A | 14449 | 27 | 220 | AVILTAKICSFTPEPSKTTSPGG TNNSRRATLRAVTLTVKVCST P*GSAASFLKSVRPRTHQ |
| 14364 | 44732 | A | 14450 | 115 | 732 | EPETRIDPLSWNSSQLPVAALH LPGMSSVGAGQAICNLCCGLDL VSPSSLPALERTGPPWNRGPK GRGRLPSL/TVSQPSLVIPPGTG KSEVNADRSRPPAYCSNLGRYS GPGPPSLVIPPGTGKSEVNADRS GPPAYCSNHFPSALP**RSSMRS LSLQQTSAWTCRHFHTSLKSR WRFPNLNSCLLCTCRPNTTWKP CLGACTL |
| 14365 | 44733 | A | 14451 | 528 | 875 | EHGYFQGTGQKGCCKSGKPPG GTLKTLLVTLREPGRQLQSP*TS LWVSRLP*YP*GDTGENCPKLS FHLRNLGPS*AG*RERPPQGG LYLPPQAYRLMQGSFAWPLFGY APSPQR |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14366 | 44734 | A | 14452 | 2788 | 3414 | ACFSYIAFWRINTTSTANLSKES LTSTTSRSWVINVNIVIFCTDWL FYKWLLKNFPIYFYMIFFPNQIT FHSMGSCAARASPTSTTPCSTA PSPIDHPRAEE\SSTRRV TGRQL HLQPAKICSFTPEPSKTTSPPGG TNNS\SALP*EL*HSPR RSAASL QFRTR*YPYRYQSQGP GSHF*L PLPLPSSIHDHF*LFHLQHTFQS HALLP |
| 14367 | 44735 | A | 14453 | 662 | 1338 | VLQLIKAVWTQRPLGGRWDW APWSRRWCSSGRLRPHRNQWS GWEAQAWGLQVPEPCPAGRQL RPGKSSSTAPVCTSCCRTRSTA GPTGCPSTRRDPTLSASPS*TST TSLATATASASMWAGSCTSIST RGSASLVHQALTWP GSGPASPR KRVTGSH PVA*AGVRWRAHRS LPQT PGLK*SSHFS LPSGWN YR HSNHPISQSFP HLSPLSIPQNH CHHGPF SM |
| 14368 | 44736 | A | 14454 | 3 | 415 | DFLLFSEILPASQSASAILPALPA SHRCPCLDVPLPPEVPGPARLP VAAASVWRPVQHLSLLGRWA GPT*DRTESRETNAEVEADLPP LYAHGRLEPTAGPSGASAVLST SSEYCPGPHPKMGHRRVTSCLS TCQS |
| 14369 | 44737 | A | 14455 | 659 | 818 | |
| 14370 | 44738 | A | 14456 | 2 | 710 | |
| 14371 | 44739 | A | 14457 | 349 | 493 | SS*VRWVSGR*HPQ*STLSAPLG ETSGCHQGGLHDLKIVVL |
| 14372 | 44740 | B | 14458 | 1 | 1338 | |
| 14373 | 44741 | A | 14459 | 83 | 426 | |
| 14374 | 44742 | A | 14460 | 93 | 345 | APALCLQILLDCKSVRNRTSRF RPREVGIIQQYKKGGAAGKGG TGNAPGFLLSKDS*KDPTPLPP PLLL*GQRDH*IQLHQE |
| 14375 | 44743 | A | 14461 | 1 | 1302 | |
| 14376 | 44744 | A | 14462 | 1 | 1174 | |
| 14377 | 44745 | A | 14463 | 274 | 1428 | |
| 14378 | 44746 | A | 14464 | 411 | 627 | HCLSHFQNTGPRGDVDFQQEL FPVLMADIRKEERSHLCRSSRR TWTILDKS*IQGSRLSSKEQGW GWGTSRK |
| 14379 | 44747 | B | 14465 | 1 | 1553 | |
| 14380 | 44748 | A | 14466 | 226 | 449 | SLQPD I*CSGLRGSLLLV*PKSD |
| 14381 | 44749 | B | 14467 | 1 | 2061 | |
| 14382 | 44750 | B | 14468 | 10 | 1099 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14383 | 44751 | A | 14469 | 34 | 406 | GGGFISLDTGSHHKSHPGGS*H ALGWVRPHTLNSP\PSQQPGNC GNPAWEC*GPHG/APSRWSCST PCRPSHPKVPAVRVAGPAGGCT PYRT/PTRRTPR*RPGPCAACDR P\LHPHCGRPGPAYPR |
| 14384 | 44752 | A | 14470 | 623 | 1671 | VLRSVSSWLPTSMAMTVLAPM LRAMSAGRLLM*PPSMSRCPSL GSHSGGR*PDS/GHAGAHVPPQ GAIFVDSHG*GGDICGHVEVRQ P/QGPQSAYPGRPDGCCG*RQT Q*TWR*LGT*GPTQVPAPKSCS WPTPGPAASCGRWRCAPRRTTLR *KSQWTCRPPGPRGPPPLMPL VLRCASSPWPRPRLAQQQWCS P*APSPSGRSRCAGPRAWRKPS RRAHAAWQCGAKRGGADSA GAGAPSTSCAYLATPRCAWGP HPPLGGAGLAA*GRAQPCSPAS APAGRG*APGPPGPQ*GCSRVP AGSARSASARRPSGRVRYGV HPPAGPATLTAGTLGCYPVRRP PGVPG |
| 14385 | 44753 | A | 14471 | 32 | 972 | QSGTFSTKNEGRTRDVEDGR GPRVGRCGTCVYVRYVHDRPH APPHERRNDGNTQRTGNAR PGTAMPTATTDQPKGRSTRHK ETKRGRRTARNKGQNNPRK/RP RKDKRKQGSAGEGERGAGGKE KGQPRDTEAKGDRRTDFPPPNG P*GQSKRGANIGGWFPPLGT PNPPLPGPQSAQVSGP*TPQMW MPTGTGCCGGSQSGSPPWCV SP*PVAEALFHSST/PAPRHPSPP SSSPKHSHQPSTPPP*ISLGQGPC RPPKRRPAPDQPQVPRCPEPSC AYLATPRPTMRMQSACRGSAR SRASARRPSG |
| 14386 | 44754 | A | 14472 | 1 | 3128 | |
| 14387 | 44755 | B | 14473 | 239 | 5474 | |
| 14388 | 44756 | A | 14474 | 542 | 781 | PASII MTGSISHITILTRVNRLN ASIKRHLTDWQIR/IKSQDLSV CYIQETHFTCKDPHKLKIGWR KIYQVN*KQKKK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14389 | 44757 | A | 14475 | 724 | 1340 | QLTLQGRRVAPR*PSRVALEQE/ CGYNALLRYEGFENDSGLDFW CNICGSDIHPVWGCAASGKPLV PPRTIQHKYTNWKAFLVKRLTG AKTLPPDFSQKVSESMQYPFKP CMRVEVVDKRHLCTRVAVVE SVIGGRLRLVYEESEDRTDDFW CHMHSPLIHHIGWSRSIGHRFK RSDITKKQDGHFDTPPHLFAKV RSFYKNPHL |
| 14390 | 44758 | A | 14476 | 1822 | 2226 | KRLFTNRTRITPFVAINSHHHHH HHITIINTIITTTSTINSHHHHHY YHHHHHHHHHHQHNTTTTNTTT TNTTTTNNNTTTTITTTTNTT TTSTINSHHHHHNQCHHHHH HHHH/HHHHHQYHHHHH*HYQ \\HHHHHHYHHHHHHHHHHQ/ HHHHHQHHNQHHHHQQQH DHHHHYHHQH HHQH YQH HHHHHNQHCHHHHHHHHHQH HHDPPHHQH*HSHQH |
| 14391 | 44759 | A | 14477 | 232 | 625 | EGCCCIAMVQKYQSPVRVYK YPFELIMALRKRYPRCCVTC* TGGAQQVGFRLDLPLSLCTP* CLWRTSSSNF*RKAAGCSGSRL QSHHFGLIPQTPAPKPWSSPLHI TKPQTLGQRDPGPRTRKRSK |
| 14392 | 44760 | A | 14478 | 1 | 808 | MPKTTACNVHTVTWASCENAD SDSTGLRHHDSCEDPASPGRS LCLVPHPTRPAVRGGRPAGGRC PAVPAEGPWRHLQQAQEG LKR LAGGLERLLENPVRRALPQGA QGHRAEPTEARPHPAPEHRRAG AAAERAERLESQPVGASAAAA SAASARIPYLVAVPAAGPPRHR CRRHRRGPGTSSGPRTALIRPAT ARARAGIVSEPRTPAGATRAP WRQGSHNPVAPSAP*LLRGPSIP WQIRPMPCTSHQTCSERRPSG RWQMPGSACRRSLETSSAGAG RAQEAGGRLGETSGESG/RAGL YLKELRAIVLNQQLVVRTQRQS IDELERRLNELSA*NRSLWEHP QLPQAQPPPGFLT*PSPLPALL GTAAAATAGAQEHLQDHGQRS SARPLPAPELASFQNEQLLAQ PEPDPGGRAHTTQSPHQHPGTL GVKANKEKKGPPGCCAAPGTP LQQESPAPSARES |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14393 | 44761 | A | 14479 | 1 | 831 | MIRYFGDYWTQALLTLIPGDPK HPRGPPVKVGVYGGQGYINSL ALCHNFIWRELNRFSLQDVPL VRYIDNIMLIGSIKFLGVQWCG ACRDIPSKDPADPMVLEVSAD RDAVWSIWQALIDESQQRPLGF WSKSLPSSADNYSPPERQLLAY YWALVETERSTMGHQVTMLPE LPVMNWVLSDPSSHK/ANGLA GWSGTGKKHDKWIGDKEIWRR GMWMDLSEWSK/D/VKIFVSHV SAHQRVTSAAEEFNQVDRMT RSMDDTTQPLYPTTPVIAQWAHE |
| 14394 | 44762 | B | 14480 | 56 | 3476 | |
| 14395 | 44763 | A | 14481 | 3 | 591 | DPADPMVLEVSEADRDA\VPIS ESQQRPLGFWSKALPSSANNYS FFKRQLLACYWVLVEIEHLM GHQVTMRPELPIINCVLSDPCSH KVGHAQQHSIIKWRWYIHDWA EGTSKLHEEVAQIPMVSTPSLP QPAPMASWEVPYDQLTEEEKT RAWFTDGSARHAGATQK WTA VALQPLSGTSLQDSSEEKSSQW |
| 14396 | 44764 | A | 14482 | 1 | 1275 | MEKNDIDQSRRRKVVMENNV QLVRYGEQASDLKTATKFKSPS EVKHIRFIQAFIGSKLLMRPW TTVTQILSLKSAKIALSESLIPC RKRAEFVEKQTQAFIMQVSDL QQKVHAQPSQVSTVKVKALIG KEWDPATWNGDVWEGPDEAG DTEFVNSDEAFLPEATAFPSPEV GNDQTVWGLLDTGSEMLIPG DPKYRGPPVKVGAYGGQVIN RGLAQIQLSMDPVGHRTRPVVS SPLPECIIGTDILSSRNPHIGSLT DITLVHYIDDIMLIGSSEQEVTIT LDLLVQAVAQAALPVGPYPDA DPMELKVSVAARDVWVSLWQ APIVTMRPERPIMNWVLSDPSS HKVGCAQQHSIIKWKWYIRDW ARSGPEGTNHSRRVCS/LPQVQ APSAR*ATARRGGQAASGCCLF WSCTCFNFDV |
| 14397 | 44765 | A | 14483 | 604 | 1760 | NSWCRWFNFRY*YPTFYWES* NT*IPLREWFG*NHDASCP*TLD SKSFSFETRGTGSPCSSLQTAYC GTLWIVQGV |
| 14398 | 44766 | A | 14484 | 2710 | 3060 | |
| 14399 | 44767 | A | 14485 | 3 | 227 | |
| 14400 | 44768 | A | 14486 | 3 | 266 | |
| 14401 | 44769 | A | 14487 | 2 | 564 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14402 | 44770 | A | 14488 | 2 | 503 | FFFLLPIGFWRQHIPRLSVLLQHI Y*VT*NAASFEWGPEQEKA*Q VQAVVQVALPLGPYDPADPML LEVSADKDAGCTRLQAPIGE SQWRS LGFRSKALRSSAENYSS FERQLLACYWALVETECLTLG HQVTI*PELPIMNWVLSDPSSHK VGHEQQHSIIKWK |
| 14403 | 44771 | A | 14489 | 2 | 469 | |
| 14404 | 44772 | A | 14490 | 1 | 633 | MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFSIPVHEAHQKQFAFLPQ GYINFPALCHNLIRRELDFFLLL QDITLVHYIDDILLIGSSEQEVV NTDLLIHKRSKEAHTAASRIR VSCLPEQKSHEQTLPEQVPSS GDIKEYFPNAFVLLTTASLQGG DNTSQLQLTWKAPEDIKMSKT DADADEEIEALRG |
| 14405 | 44773 | A | 14491 | 1 | 518 | MTVDYCKLNQVVIPIAAVSD VVSLLLEQINTSPGTWYAAIDLA NAFSIPVHKAQQKQFAFSWQG QQYTFTVLPQWYINSPALCHNL IRRDLDCFSPLDITLVHYIDDI MLIGSTIKWVVHSS/DSIIKWKW YVHDWARAGPEGTTNGLAG*S GTCKKHEWKTGDKGIRGRG |
| 14406 | 44774 | C | 14492 | 33 | 932 | |
| 14407 | 44775 | B | 14493 | 27 | 2457 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14408 | 44776 | A | 14494 | 332 | 2158 | RGYVFCSWKKTDGS/WRMTVD YCKLNQVVIPIAAA VSDVVSLL EQINTSPGTWYAAIDLANAFFSI PVHKAQQKQFAFSWQQQYTF TVLPQWYINSPALCHNLIRDL DCFSLPLDITLVHYIDDIMLIGP RQLLACY/WALVETEHLTISHQ VTMRPELPIMNWVLFDPSSHKV GCAQQHSIIKWKWYVHDWAR AGPEGTTTPVISQWPHEQCGHG GRDGGYAWAQQCRLPLTKAD LNTATAKRPIQQQRPTLSPQY GTIPQGDQPATWWWVDYMGs LPSWKGQRFVLTGIDTYSYGf AYPACNASAKTAICGLTECLIH HHDIPHSIASDQGFHMAKEVR QWAHDHGIHWSYHVSHHPEA AGLIEWWNGLLKSQQLQCQLGD NTWQGWGKVLQKV VYALNQH PIYGTVSPIAKIHRSRNQGLEVA PLTITPRDPLAKFLLPFPATLQS AGLEVLVPEEGLPPGDTMIPL NWKLRLP RHFGLLLPLNQQA KKGVTVLAGVTDLDYKDEITL LLHNGGKEEYAWNTGDPLGLL LILPCPMIKVNGKLQQLKPEAL VPKGVVFPFGDTTMLSLSWKL RLPSGHVGLLMPLSQVQKGV |
| 14409 | 44777 | A | 14495 | 1 | 3187 | MAEGKEEQVLSYTDGSRQREN EEDAKAETPDKTIRSHETYSLPR EWEYEGNRPHDSITSQWVPPTTR GNYGSTIQDEIWVGDHSGYVRP VPVPRSLNSDISYFGVGGKQAV FFVGQSARMISKPADSQDVHEL VLSKEDFEKKEKNKEAIYSGYI RNRKDDYDNHTGIDLVGTHIATI KGSNEEDTDTPLFIGKVRTLFP FVNGSAEIMLMPSNQHKTE KGRANLGVFSVFAPRGEHTLQ VKAIYNKSIIEGP |
| 14410 | 44778 | A | 14496 | 266 | 467 | |
| 14411 | 44779 | B | 14497 | 152 | 1245 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14412 | 44780 | A | 14498 | 1 | 1445 | MLRAAAGGQGLAAAGMGLCA RPAGGSQ LPRERMKG NRACLP LPPAVALTKGREKPDAGHQGR STQMMRESERGPCTHWTEERP GRQLKILLQKQMRQNTLMAFQ VSWDGRNKEIGRTFPHATAPHT QQLIFAMKIKRTGVTVEPWGLF ETGQRIRPIQAAGL*LSSSSTTC VALAPLLTMHVKSLALLSAP/Q MGALSTITSITTTTRRQTPAESHF PAARFHLLAPHSP LPPCCPGEP SESAVTVLCFAKGKTAQDAAV PTTSLTAAGHLAPRS*SSWSRM PVKVRRAPDSL PETS AHALPLT H*SWLPSASWGPASRALPGSEW VLKPVWQ/AITGPV SQITSSPGIP KPGPLQA*GSAHPQALGFSVL QIPLSNSPTSPMTPLPRPKISNS SLPSQ/PPQALFPNRW TNSSSPV HVITSAAQ\PRTPREWPAVSFYR TTATTASLIPHLWAPPQEN*QTS PAQNGSTLPCMSQATFHFPSP |
| 14413 | 44781 | A | 14499 | 44 | 455 | HLRNRTR/PSQITPHIYNHLIFDK /PLFNIWWWENWLAICRKLKLD PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/TGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP |
| 14414 | 44782 | A | 14500 | 1 | 346 | |
| 14415 | 44783 | A | 14501 | 1926 | 2448 | DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKHKMKKCS SLAIREMQIKTTMRYHLTPVRM AIIKKS GNNRCRRGCGEIGTLLH CWWDCKL VQPLCKSMWRFLR DLDP AIPLLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14416 | 44784 | A | 14502 | 1 | 2142 | MIILIDAEKAFDKIQPFMLKTL NKLIGDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIRQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFFKKYKPLLNIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHSRWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELKQIYRKK\TNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM |
| 14417 | 44785 | A | 14503 | 209 | 3816 | QGRPTFRFRKYREHHKDTFREE QLQDT*SSDSPKLK*RKKC*GQ PERKVKLPTKGSPSD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITDPTEIQITIREYYKHLANK LENLEEMDKFLDTYTLPRLNQE EVESVNRPIGSEIEAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQPIEKEGILPNSFYEASH LIPKPGRDTTKGNFRPISLMNI DAKIL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14418 | 44786 | A | 14504 | 1 | 2877 | MENDFDELREEGFRQSNYSELR EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLRSRCDQLEERV SAME DEM NEMKGEGKFREKRIKRNE QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQT TISEYYKHLYTN KLENLEEMDKFLDTYTLPTLNQ EEVESLNR PITGAE |
| 14419 | 44787 | A | 14505 | 1 | 2347 | MELKTKARELHDECTSLSSRFD QLEERVSVMEDEM NEMNLPTK KSPGPDGFTAIFYQRYKEELVP FLLKLFQSIEKEGILPNSFYEPSII LIAKPGRD TTKENFRPISLMNI NAKJLNKMLANQIQHIKKLIH HDQVGFIPGMQGWFNIRKSINV IQHINRTKDKNHMIISIDAEKAF DKIQQHFMKLTNLKLVLEVLA RAIRQEKEIKGIQLGKEEVKVS L FADDMIVYLENPTVSAQNLLKL IGNFSKVSGYKINVQKSQAFLY TNNRQTERQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENNKPL LKEVKEDTNEWKNIPCSWVGRI NIVKMAILPKVIYRFNAIPIKLP MTFFTELEKTTLKFIWNQKRAC IAKSIFSQKNKAGGITLPDFKLY YKATVTKTAWYQNRDIAQ WNRTEPSEIMLHIYNYLIFDKPE KNKQWKGDSL FNKWCWENWL AICRKVKLDPFLTPYTKMNSR WIKDLNVRPKTIKTLEENLGITI QDIGVGKDFMSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRV NRQPTTWEKIFATYSSDKGLISR IYNELKQIYKKKTNNPIKKWAK DVNRHFSKEDIYAAKKHMKKC SSSLAIREMQIKTTMRYHLTPV RMAIIKKSGNNRKIQ/GGIWCD RIL*R*TTCRVAKEIQLS*RR/W KRLQRTLSIPVLDAV*PPMF*AS |
| 14420 | 44788 | B | 14506 | 1 | 2265 | |
| 14421 | 44789 | A | 14507 | 1 | 2832 | |
| 14422 | 44790 | A | 14508 | 1 | 2109 | |
| 14423 | 44791 | A | 14509 | 1 | 2757 | |
| 14424 | 44792 | A | 14510 | 1 | 2304 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14425 | 44793 | A | 14511 | 1 | 2685 | MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRIKNLTQNRSTTWKLN NLLDDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQKELEKQEQTTHSKASRRQ EITKIRAELEKETQKTVQKINES RSWFFERINKIDRQLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHLYANKLENLEEM DKFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAIFYQRAIRQEKEIKGIQLGK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELKKTTLNFIWNQK \RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLDPFLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD |
| 14426 | 44794 | B | 14512 | 1 | 2337 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14427 | 44795 | A | 14513 | 1 | 1544 | HINRAKDKNHMIISIDAEKAFD KIQQHFMKLTNLKLGIDGTYFR KSiNVIQHINRAKDKNHMIISID AEKAFDKIQQHFMKLTNLKLG DGTYFRKSIN/DNPAYKQSQRQ KPLIISIDAEKAFDKIQQPFMLK TLNKLDNIIVYLENPIVSAPNLL KLISNFSKVSGYKINVQKSQAF LYTNNSQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTKKWKNI PCSWVG RINIVKMAILRKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA PVAKAILSQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDI GQWNRTEPSEITPHVYNYLIFD KPEKTKQWGKDSL FNKWCWE NWLAI CRKLKLD PFLT PYTKIN SRWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTWEKTFATYSSDKG LISRIYNELKLIYKKKTNNPIKK WAKDMNRHFSKEDIYAAKKH MKKCSSSLAIREMQIKTTVRYH LTPVRMAIIKKSGNN |
| 14428 | 44796 | B | 14514 | 110 | 2153 | |
| 14429 | 44797 | A | 14515 | 1 | 3210 | MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNLL LNDYWVHNEMKAEIKMFFETN ENKDDTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQ KELEKQE QTHSKASRRQEITKIR AELKEIETQ |
| 14430 | 44798 | A | 14516 | 3 | 2820 | ENKDDTYQNLWDAFKAVCRG KFIALNAHKRKQERSKIDTLTS QLKELEKQE QTHSKASRRQEIT KIRAELEIETQKSLQKINESRS WFFERINNIDRPLARLIKKKREK NQIDTIKNDKGDITTDPTIQT REYYKHL YANKLNLEEMDKF LDYTLPRLNQEEVESLNRPI TG SEIVTIINSLPTKKSPGPDGFTAE FYQRYKEELVPFLKLFQSIEKE GILPNSFYEASIIIPKGRD TTK KENFR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14431 | 44799 | A | 14517 | 687 | 2274 | LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMFFTELE KTTLKFIWNQKRARMASILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWRTEP SEITPHIYNYLIFDKPDKNKQW GKDSL FNK WG WENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKTLEENLDITI QDIGMGK DFMSKTPKAMATKAKIDK WDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKRCSSSLAIRE IQIKTTMRYHLTPVRMAIHKKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMRKNTK TLI |
| 14432 | 44800 | B | 14518 | 1 | 3192 | |
| 14433 | 44801 | A | 14519 | 1 | 2814 | |
| 14434 | 44802 | A | 14520 | 1 | 3144 | MGDFNTPLSTLDRSSRQKVNK DTQELNSTLHHADLIDIYRTLHP KSTEYTFFSAPHHTYSKIDHV GSKALLSKCKRTEIITNCLSDHS AIKPELRICKLTQNRSTTWKLN NLLLNDYWVHNKMKAEIKMFF ETNENKDTTYQNLWDTFKAVS RGKFIALNAHKRKQKRCKIDTL ASQLKEVEKQEQT HSKASRRQ EITKIRAE LKEIETQKT LQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14435 | 44803 | A | 14521 | 1 | 2616 | TTYQNLWDAFKAVCRGKFIAL NVHKKRKQERSKIDTLTSQKEL EKQEQTTHSKASRRQEITKIRAE KEIETQKTLQKINESRSWFFERI NKIDRPLARLIKKKREKNQIDAI KNDKGDITTNPTEIQTIREYYK HLYANKLENLEEMHKFLDTYT LPRLNQEEVESLNRPIGAEIVA IINSLPTKKSPGPDGFTGEFYQR YKEELVPFL/LKLFQSIEKEGIM NIDAKILNKILANRIQQHIKKLI HHDQVGFIPGRQGWFNICKSIN VIQHINRAKDKNHMIISIDA EKA FDKIQQLFMLKTLNKLIDGTY FKIIRAIYDKPTANIILNGKKLEA FPLKTGTRQGCPSPLLFNIVLE VLARAIRQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLISNFSKVSQYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDANKWKNIPCSW VGRINIVKMAILPKVIYRFNAIPI KLPMTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSEITPHIYNYLIFD KPDKNKQWGKGSFNKWCWE NWLAI CRKLKLDPFLTPYTKIN SRWIKDLNVRPKTTKTLEENLG ITIQDIGMGDMFMSKTPKAMAT KDKIDKWDLIKLSFCTAKETT |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14436 | 44804 | A | 14522 | 782 | 3024 | SKTVPTGNSLEPTQNCWLQQW LPQDIEIEKQEQT/HSKASRRQEI TKIGAELEEIEETQKTLQKINESR SWFFEKINKSDRPLARLIK KKR EKNQIDAIKNDKGDITDPTEIQ TTIREYCKHLYANKLENLEEMN KFLDITYTLPRLNQEEVESLNRPI TGSEIEAIINSLPTKKSPGPDGFT AEFYQRYKEELHINRTKDKNH MIISIDAEKAFDKIQRFMLKTL NKLVLVFLARAIRQEKEIKGVQ LGKEEVKLSLFADDMIVYLENP IVSAQNLLNLISNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNERKEDTNKWK NIPCSWVERINIVKMAILPKVIY RFNAIPIKLPMFTFFTELEKTTLK FIWNQKRARIAKSILSQKNKAG GITLPDFKLYYKATVTKTAWYS YQNRDIDQWNRTEPSEILPRIYN YLIFDKPEKNKQWGKDSL FNK WCWENWLAICRKLKLDPFLKP YTKIKSGWIKDLNVRPKTIKTL EENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKLSFC TAKETTIRVNRQPTEREKIFATY SSDKGLISRIYKELKQIYKKRTN NLIKKWVKDMNRHFSKEDVYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRITI VLLPGSLIVRSFHVTLNAILLHP |
| 14437 | 44805 | A | 14523 | 1 | 1701 | |
| 14438 | 44806 | A | 14524 | 1 | 4434 | |
| 14439 | 44807 | A | 14525 | 1 | 2913 | MGGPAALCIAVVPGLVVALC LEEGLGSGIATWACSPWRISQG THLTFRSSLAVAAIPEGLPIVVM VTLVLGVLRMAKKRVIVKKLP VETLGCCSVLCSDKTGTLTANE MTVTQLVTS DGLRAEVSGVGY DGQGTVCLLPSKEVIKEFSNVS VGKLVEAGCVANNAVIRKNAV MGQPTEGALMALALKDQEDIY FMKGALEEVIRYCTMYNNGGIP LPLTPQQRGAGPGDTALPSAAS AFARMSAAERNDAFQG |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14440 | 44808 | A | 14526 | 1 | 3009 | MGDFNTPLSTLDRSMRQKVKK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEITNYLSDGS AIKLELRIKNLTQNRSTTWKLN NLLLNDYWVPNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTTHSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK |
| 14441 | 44809 | A | 14527 | 1 | 4800 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVNNEMKAEIKMFF ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTTHSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK |
| 14442 | 44810 | B | 14528 | 1 | 2901 | |
| 14443 | 44811 | A | 14529 | 569 | 3443 | RKH*TWKRTSSTSHHKNNMPN* LEKQEQTTHSKASRRQEITKIRAE LKEIETQKTVQKINESRSWFFER SNKIYRPLSRLIKKKREKNQIDT IKNDKGDTTTDPTEIQTIREYY KHLANKLENLEEMDKFLDTY TLPRLNQEEIESLNRPIGTIVT IINSLPTKKSPGPDGFTAIFYQR YKEELVPFLLKLFQSIEKEGILP NSFYEASIIIAKPGRDTTKKEN FRPISLMNIDAKILNKILAKRIQ |
| 14444 | 44812 | A | 14530 | 3591 | 8157 | TGTSQKKTFMQPKKHKMKCST ITGHQSNANQNHNEIPSHTKLE WRSLKRSGNNRDVGNVVEAM YGDLPPIMLIGHSMGGAIAVH TASSNLVPSLLGLCMIDVVEGT AMDALNSMQNFLRGRPKTFKS LENAIEWRNIKDLSWADSIKNV AAASLACISGALPASAVTTSPD NKRMAENVLYKYERLLAESPNH VVAEAVIQRPNIPLQTRDTYPE GLCQTLGSQPTLYQIPSLYCSYE TNSNAYLLLQPIRKEVI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14445 | 44813 | A | 14531 | 172 | 328 | AVKTEPEMKSQATKLSVVHEK KSQEGKPKEHTEPKSLPKQASD TGSNDAHNIKAVSR*SHRQPSC LWFMKRNPKKESRKNTQSQKA YPSRHQIQEVTMLTI |
| 14446 | 44814 | A | 14532 | 3 | 660 | TSPDCWEEGRSVDWPRPGPALS LHNCKLDLGIEGGTLQPPTPSF* PTGTRAV/PTRRRSRQETQLNSE RTVSPGSR**EKRTSRAW/RSPL QGP GPGHAGQVAGGTGPRTGS TRGD/TLQKCGKIQSVPLNCELI PI*/PSILKPKVLPSCSPGIGASS\N CPSD*VFFCTS*PWPYLLSYPLS MNFYRYHDHILKLLVQYTLYL LLQFLQVLLKYLLSHPKQHS |
| 14447 | 44815 | A | 14533 | 1 | 1086 | MVDNDVPWPLVVAQEKGPDP LCLSSKGYRPLALVQLDFHQVS VTSKIFILSGALRSLTGAATAD WTCRVLVIYPHDIMADSECNSL LVPSTTRKIMKHMLASEKIKTQ NFNYNVDECVSLLYHHKANKL EAAEARQECCELLRVASVSRHC W/RDPAHPHSCWPRC*APHCLG PARAPNARPAKPATTWNLRSSR APCAAPVPTQSWAGAPSGTAG AEPS*ECRPPENQARTAGSGVH AEACAPATCPACPGPGPCSGLP SSGRALFLL/CATLAIPCV*V*LC FLATPPPCR*HVTAPSAGKCIW* PDA*VTK/PRDLCGPVQVARDN GPRQVAQKKESSSYVSWFGTFI SRVGDRSPPPRAATL |
| 14448 | 44816 | A | 14534 | 23 | 506 | PDIDNIFSEFGAKSKPYLTVDQ MMDFINLKQRDPRLNEILYPPL KQEQVQVLEIKYEPNNSLARKG QISVDGFMRYLSGEENGVSPE KLDLNEDMSHPLSHYFINSSH TYLTGMNFLVLCYFSQSHQISP TSTFCCSEAEV/WFSSISCEVPLR TLGFHH |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14449 | 44817 | A | 14535 | 341 | 1248 | KNAFTSFLTSFPPGQISVDGFMR YLSGEENGVVVSPEKLDLNE SQPLCFMGIWGLFCWCFIAGQL AGNSSVEMYRQVLLSGCRCVE LDCWKGRТАЕЕЕРVКILAY*ІY MCSHF*EVIEAIAECAFKTSLP TFLLLFLFSLSPKQQAКMAEYC RLIGSSIFKEYAFHFY*LESGVPL PSPMDLМYKILVKNNKKSHKS SEGSgKKKLSEQASNTYC*NGD MMICY*NLТGEADTESDADDS GNV/CLFYSYFQGTAGSEAMAT EEMSNLVNFLTFFVLLLLNSE RNKSFEМSSFVETKGL |
| 14450 | 44818 | A | 14536 | 574 | 647 | C*PGNM/HISGQHLVAGEKEAE SEDEEEEDMKLLGTPEGGSKFT QKKVKLAADEDDD/DDDADDD DDDDDDDDFDDEETEEKAPV |
| 14451 | 44819 | A | 14537 | 3 | 630 | PGATHASAPPGVLRKCGSGPV HIIGQHLVAVEEDAQSQDEEEE DVKLLSISGKRSAPGGGSKVPQ KKVKLAADEDDDDDDEEDDD EDDDDDDDFDDEEAEQAPVKK S\RDTPAKNAQKSNQNGKDSK PSSTPRSKGQESFKKQEKTPTP KGPSSVEDIKAKMQASI/EKKG GSLPKVEAKFINYVKM\CSRMT DQEAI\QDLWRWRRSL |
| 14452 | 44820 | A | 14538 | 1 | 1971 | |
| 14453 | 44821 | A | 14539 | 316 | 1169 | RVGGQSHGTQRISLCRHSVCSP LARQSPSNMK*VRTEEIQMAVS CYLKRWQYVDSG\PLKQGLR LPQTAEELANLTVHRESHCAD IVSAVPICQAEPQQYE\QFGRL RNFLIDSDSPHSHEVMPLLYPLF VCLHLSLVQNSPKSTVESFYSR FHGMFLQKAS\QKGVIEQLQTT QTIQDILSNFKLRAFLDNNYVV HLQEDSYNYLIHYLQSDSYTAL CKMFILLIHLDVQPAKTTD*QL YASGSSSRSENNYLEAPDMPSPI LQNDAALEVLERIKQVKDGC PSLTTVCFYNT*QLLNTAEISPD SKLLAAGFDNSCIKLWSLQSRK LKSESCQVDMSRIHLACDILEE |
| 14454 | 44822 | A | 14540 | 1 | 297 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14455 | 44823 | A | 14541 | 2 | 1089 | APLLGECRSGRGLASSRSTRRT TMTQSVVVQGKLRRAGRDLVA AESSGHVSCLSYSLFLSSGRS RLALREHA AVNQVPARRREPPR LSARSSSPYSFHLQSE*L*KKIH* LYFIFLSQAVLIDMEEGVVNEIL L*IRTNQIKK*MQGIFKIHLIFR AVGHKVFGSLYQDQILEKFQIL HNYILNHL C*FLKTL*SSGTGSG LGTFLK VLEDEFPEVYRFVTSI YPSGEDDVITSPFLVEYHLHPLF LIASLPMFFPQKSLFDIISKIDLM VNSGKV/GGTTVKPKSLVTSSS GALKIELHLKCIHLKLIKFSF*C* LFSSARFEGSLNMDLNEISMNL VPFPSS*EIVSLKYVLYFN |
| 14456 | 44824 | A | 14542 | 129 | 461 | TCISGWHLFRASVTCPIQTSPH NWHISDNSSLPNNIFVCWNLL GMTRNYIIFIEQPLKMNLWKIA TSKIRGKAFSDGIS\GNPQCNT RFHVVEKRTGQLLPGRYYSKPF |
| 14457 | 44825 | A | 14543 | 1 | 522 | |
| 14458 | 44826 | A | 14544 | 1 | 927 | MEDLLTEARSPYWGRARAKIQ DSCWSVTSDPNAGSVDILAPLL LPSPSSYLPNFTCTVSVVTSHLH EAFLDLGFRGTGGSNCKTSRQV QLNNQKRKKKSKSLPFHMSL QIQNYKTQEEPHAKPSSQQHQH SEHESIQTCLVFRSSMTYMHTL KLIREKGSIMLSSTQGECPNSTC RWPAAEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNLWKIATSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQT T*INPDKISIQKHDIHAYIEAD KRKRKHNAVIHTG*M/YQI/GTC RWPAAEHPLGSTHREDQEHVIR VPPEKVDLGETIHGVQVICSIAS TEKGKPSYYHSFGMTRNYIIFIE QPLKMNLWKIATSKIRGKAFSD GISWEPQCNTRFHVVEKRTGQI LNVKTMRMKTFMMIYYHLMN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14459 | 44827 | A | 14545 | 1 | 882 | MAEILTQVPDDMLKKKTTPRVK SVWRSQRGSCTPLIGTTTELTD TSHMSIRNMDRSHINVHTVRKP SADLPYFRTHEWAHTGGKPYD CEECKGSFISRSSIRRHIMHSG DGPYKCNFCGKALMCLSLYLIH KRTHTGEKPYECKQCGKAFSH SGSLRIHERTHTGEKPYECSECG KAFHSSTCLHAHKITHHTGEKPY ECKQCGKAFVSFNSVRYHERT HTGEKPYECKQCGKAFRSASH LRTHGRTHHTGEKPYECKQCGK AF*PRFQMT*RRKLPE*NQCG EVSUGH\HSLNRHHRADTGHKP YEYQEYGGQPKYKCTYCKKAFS\ YLPYFRTHEWAHTGGKPYDCE ECKGSFISRSSIRRHIMHSGDG PYKCNFCGKALMCLSLYLIHKR THTGEKPYECKQCGKAFSHSGS LRIHERTHTGEKPYECSECGKA FHSSTCLHAHKITHHTGEKPYEC KQCGKAFVSFNSVRYHERTHT GEKPYECKQCGKAFRSASHLRT HGRTHHTGEKPYECKQCGKAFG CASSVKIHERTHTGEKPCSSNTS |
| 14460 | 44828 | A | 14546 | 3 | 395 | SAEVGAAETTLTELRTVQSLEI DLDSMRNLKASLENSLAGILLHL ESELAQTRAEGQRQAQEYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH |
| 14461 | 44829 | A | 14547 | 2 | 1044 | AKTSSQMPSPQEGMCGKACTP ALSQADSLCPLLRLASEVEGYS LPACAEPYVQSECLSHLSVWSL QHALSSLASMSFTTCSAFTNYW SPGSVQVPSYGTQPVSHAASVY AGLGGSGSRISVSHTNG\GGLA GMGGIQNEKETMQSLRDRLAS YLDRVRGLETENWKLESKIQEH LNVTRL*LETEIEALKKELLFM KKNNEEEAKGLQAQIASSGLTV EVDAPKS/QDLAKNMADSRAQ YDKLARKNREELDKYWSQQIE ESTRVVTTQSAKVGAEMTLT ELRHRVQSLEIDLSTRNLKAS LENSLREVEARYALQMEPSLLF SKIIFGRVWEISYLHVFEKGQV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14462 | 44830 | A | 14548 | 1 | 1212 | GPGTGIAGGLAGMGGIQNEKET MQLNDRLASYLDRVRSLETE NRRLESKIREHLEKKGPQVRD WSHYFKIIEDLRAQIFANTVDN ARIVLQIDNARLAADDFRVKYE TELAMRQSVENDIHGLRKVIDD TNITRLQLETEIEALK*ELLFMK KTPEEEVKGLQAQIASSG\LTVE V\DA PKSQDLAKIMADIR\AQY DELARK\NREELDKYWSQQIEE STTVVTTQSAEVGAAET\TLTEL RRTVQVFGDSTWTSMRNLKA\ NLENSLAGEVEARYAL\QMEQL\ NGILLHLESQLGQTPRTEAQRQ AQE\YEALL\NIKVKL\EA EICHL TRPPSWKIGEDFNL\GDS\LDER NSMQTIQKTTTTRRISWIGQSGV LRPIDTKVLEALSQQEASGTL GKQEANKKFQSFK |
| 14463 | 44831 | A | 14549 | 1 | 2382 | |
| 14464 | 44832 | A | 14550 | 2 | 173 | |
| 14465 | 44833 | C | 14551 | 1 | 732 | |
| 14466 | 44834 | A | 14552 | 455 | 682 | AWKRAVALGKSRPMGAVAFK RRMQPVAGPRAMQEKFPFSSSS SLSIPPAF*YRLALSLAEPSSRW RARTGALMQL |
| 14467 | 44835 | A | 14553 | 158 | 368 | |
| 14468 | 44836 | A | 14554 | 87 | 251 | |
| 14469 | 44837 | A | 14555 | 1 | 1026 | |
| 14470 | 44838 | A | 14556 | 201 | 578 | |
| 14471 | 44839 | A | 14557 | 336 | 767 | AFVRAGSRFGGTPGARPDPA TRAPNPVGQSRHLRAASSRGRL FLRRTRDRKFRRPRLSRLLG AI/GCRWNQPRAAEKSFSAGAV LDFSPGLSCLPAVQGS GPAARH A*ASHPLHGLLCCPSIPDEHHPL LHGAQSHRPPKG |
| 14472 | 44840 | A | 14558 | 6 | 535 | ARHRVLIGVFTIPELDILSTSPD SGAQLASPSDPAPGLQVELPAS PARCARIPQPLGGRWDWAQTQ EPSWLHLVEPAPGLQVELPAS TPCACIPQPLGDRWDWAPWSR GWCSLGRLGPHRSPWSGWEAE AWRAAGPEPCPTGRQLRLGEK SSAAPVGWHCWGTQYTLRSH WPGC |
| 14473 | 44841 | A | 14559 | 375 | 638 | |
| 14474 | 44842 | A | 14560 | 92 | 514 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14475 | 44843 | A | 14561 | 54 | 380 | SCHHYCRIHRRCARFLAGP*LPS RGARLGTCSPPCVSLPPAPWAP VRPEPPRRAPPPAPQRPVPSTTQ GLRSAGARRGTGRQLHLQLRG SAASFLKSVRPRTHQFRTH |
| 14476 | 44844 | A | 14562 | 531 | 773 | |
| 14477 | 44845 | B | 14563 | 92 | 1774 | |
| 14478 | 44846 | A | 14564 | 1 | 390 | LHDLQLSKPLSDDTALTDDGG/Q PLPARWWAQPGRLQRCARFLA GP*LPSR/WGRARDLQAMPEP PTPSVGSCAAQASPTSAAPCSM APSPIDHPRAWPVLCSCFCLLS LFVASISSCSQHQPQMVGTMVC L |
| 14479 | 44847 | A | 14565 | 165 | 545 | SLHSLCWWLQQLWVTDTCPR CSVQDCRQRWASAGNQS*RLL VDPAPGLQVELPANPVPCARIP QPLGGRWD*APWSRGWCSSGR LGLHRSPWSGWEAQAWRAAG PEPRPAGRQLGAMSKVETGT |
| 14480 | 44848 | A | 14566 | 1 | 309 | SACLAGRPIRGEGRPRDLQAM PEPPTPSMGSCAARASPTSATPC STAPSPIHHSRAEECGHTALG/H GRQLHLQPRNLPQTINWRTTYS SFPATLNRLDGGG |
| 14481 | 44849 | B | 14567 | 1 | 843 | |
| 14482 | 44850 | A | 14568 | 143 | 535 | |
| 14483 | 44851 | A | 14569 | 375 | 571 | |
| 14484 | 44852 | B | 14570 | 289 | 972 | |
| 14485 | 44853 | A | 14571 | 27 | 363 | |
| 14486 | 44854 | A | 14572 | 2 | 490 | |
| 14487 | 44855 | A | 14573 | 574 | 961 | RLTLPDRLGSPPDTHQAQQITW ALLPQGFADSPHYFSQAQISSSS ITYLGILHENTRALPADHV*LIS QTPISSTKQQLLSFLGMVRYFC LWIPSFTILTKPLY*FTKANLAD PTDPKSFPHSSFRSL |
| 14488 | 44856 | B | 14574 | 182 | 1513 | |
| 14489 | 44857 | A | 14575 | 894 | 1305 | QTQEPSWLHLVDPALGLQVELP ASPVPCARIPQPLGG*WDWAP WSRGWCSSGRLGPHRSPWSGW EAQAWRAAGPEPCAGRQLRP GQHPL/RHMNKSQALSLLIAQP LGINLLSWPPKYNRPVPLIGL SGLLIPATF |
| 14490 | 44858 | A | 14576 | 531 | 801 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14491 | 44859 | A | 14577 | 441 | 783 | RAPPPAPWRPVPSTTQGLRSAG EQRGTGRQLHLAAPVRDPRG EAIWAPESGRSAASILKPARPPA HREERTTPDAPP*EL*HSPRRSA ASLREDPWLHS*SQ*DQEP TNS GHTVSQDQSYYS*LEVSETKNP PIPDTL |
| 14492 | 44860 | A | 14578 | 344 | 1632 | FLAGPYLPSHGAGLGTCSLPCL SLPPTPWAPVRPEP/PPMSTTPCS TAPSPIDHPRAEECERTAQDWQ AAPPAAPVWDPLGEASWAPES GTNISITPGNATFVTRVQGQAW FASCITGHDMSSLKTSSVVVLR RQSEALLPANLTCNWQDSSAL ATLESALSQVRHKRFTFTLMVF TGSAIDIMATVSI VVSITESVQ TTAFVDNLAKNICDELLQDM DEAGNQHSQQNNTRTENQTPH VLTHKWELNNENIRIQGGEHYI LGPVGGRDEKTLLLR TYCLKSQ EGADTKCRNKH NKETQKQSKS LVYSSTLNPEKLLVCKRLSLEL TRPENTLRCTNIGKLKAVAGG MSAASGIYLETDTQPYPLKQEL KEIKECVGKNSVVVFLVRKK LSVSQYAFARCLDAKHSTSENV EIAGKLRIQSFEVVGKQL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14493 | 44861 | A | 14579 | 3 | 2233 | NWLPSVSRQCETHKIAANQSLT QRQMPLTSLYCDVVLVPSVGL ESLQSPYYRTSPCDPVSQFCLIK ISASSLPVLSLWTKLNAQSYQ RDYRHDNKAHYFQKLVTMQE NLYVLLCDEELDAVSLEAVHQ QKMKNRQAHSSSGCCQKVAN APRNEESSGQFRVIGNEKFEKG PCGVRQQIFEKVLLPNRTCEFV TPRFNRNFEDLIKDLKAAETLID FLVYEPKNQRRLVNRFRLPCKL LHNLGHPLKTDAAQSPRKPPGP SWMPSPFGSKPPSHPLVSPHLNP QVWDTSSPSLATEHASLTISLKP NHPYPAQSQYSIPQHALKGSKP VITRLLEHGLLKPINSPYNPILP VQKLDKSYRLVQHLCLIQIVL PIHPMVPNPYTLSSIPFTTHYS VLDLKHAFFTIPLYSSQPLFAF TWTDPDTHQAQQITLAVLPQCF IDSPHYFSQAQISSSSVTYLGIL MKTHIGLGAVEQGVVLVGEAR AAQEPMEWVGSGM/CGLQVP SPAPWEGS*GPARNRAQ\PVTIV PVLDFNPAPHIIPDTPDHDCI SLIHLTFTFPFHISFFPVPHLEHT WFIDGSSTRPNCHSPAKAGYAI VSSTSIIEATALPRSTTSQAKLI AYTDSKCAFHILHHHAVIWEER NFLTMQGASINAFLIKTLKDI LLPKEAGVIHCKGHQKASDPIT QDNAYADKVAKKQLAFQLLSL |
| 14494 | 44862 | A | 14580 | 1 | 642 | SGTVPPTFVRTVIQAQGARTVI QQSLIGSLYIFRHCVRQCQIESV FVIIIWSRVGYDEKGFCLFTSVL GVWGHVVRTKPCLLITWRTLKS RSGLE*PAGFSSSPGTSPQIRKQ KRGVPQHPVCDLPGRFRPRAGT PLAAQIQVPGLPPCGHQE*NRR WAGSSALCPPYLCARAGTGAV CRACEPAGV/AGWAWAWWAP HSEHAASPAGPRQWGT |
| 14495 | 44863 | B | 14581 | 393 | 549 | |
| 14496 | 44864 | B | 14582 | 1 | 591 | |
| 14497 | 44865 | C | 14583 | 226 | 828 | |
| 14498 | 44866 | A | 14584 | 1 | 1362 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14499 | 44867 | A | 14585 | 1 | 585 | MANVHQTMPMRLRKLPSDFKP PEPKSNSQRVSTEAGTAGALTP QHVRHSSPASLQLGAVSPGTL TPTGVVSGPAATPTAQHFQQSS FEIPDDVPLPAAREMAKTSSGQ RYFLNHIDQKTTQQDPARKTML SQMNVIANPPVQQNMMS\PQS PQGGV/MGGSNSNQQRQMRPQ QLQMEERLQLKQQ*LLQQELALR |
| 14500 | 44868 | A | 14586 | 345 | 1053 | RWRLQNLSFCSSCSGSGSEGAT CFARGRQQSNLQSKIKFPSNTD SRSTGYNSFDRQPNICFYKRQE TPHTGPHVPEGRPYMPG*CG A*SPGPFASRN*SEKN*SYKCSL HTAFNVIFSSVI**RYCTRQWHI VKCLDSFCDFLISDELRRASTD AGTAGALTPQHVRHSSPASLQ LGAVSPGTLTPTGVVSGPAATP TAQHLRQSSFEIPDDVPLPTSW GEAKTSSGSKIPF |
| 14501 | 44869 | B | 14587 | 607 | 1185 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14502 | 44870 | A | 14588 | 1 | 2142 | MIILIDAEKAFDKIQPFMLKTL NKLIGIDGTYLKITRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVLEVLAQAIQEKEI KGIQLGKEEVKLSLFADDMILY LENPIVSAQKLLKLISNVSKVSG YKINVQKSQAFLYTNNRQTESQ IMSEFPFTIATKRIKYLGIQLTRD VKDLFKKYKPLLNKIKEDTNK WKNIACSWIGRINIMKMAFPR WELNNENTWTQEGEHTLGPV VGWGKRGGIALVDIPNVNDKL MVLEVLARAIRQKKEIKGIQLG KEEVKLSLFADDMIVYLENSIV SAQNLKLISNFSKVSGYKINVQ KSQAFLYTNNRQTESQIMSEFP FTIATKRIKYLGIQLTRDVKDLF KENYKPLLKEIREDTNKWKNIP CSRIGRINIMKMAILPKVIYRFN DIPKLPMTFFTELEKTTLKFIW NQKRACIAKTILSKKNIAGGITL PDFKLYYKATVTKTAWYWYQ NRDIDQWNRTEASEVTSHIYNH LIFYKPDKNKKWGNDSLFNKW CWENWLAICRKLKLDPFLTPYT KIHRSWIKDLNVRPKTIKTLEEN LGNTIQDIGMGKDFMTKTPKA MATKAKVDKWDVIKLSFCTA KETTIRVSRQPTWEKIFAIYPS DKGLISRIYKELKQIYRKKVTNN PIKKWAKNMNRHFSKEDIYAA NRQMKKCSSSLVIREMQIKTTM |
| 14503 | 44871 | B | 14589 | 1 | 1647 | |
| 14504 | 44872 | B | 14590 | 1 | 2025 | |
| 14505 | 44873 | B | 14591 | 4 | 2121 | |
| 14506 | 44874 | A | 14592 | 2 | 1879 | |
| 14507 | 44875 | A | 14593 | 1 | 2130 | |
| 14508 | 44876 | A | 14594 | 1 | 3018 | |
| 14509 | 44877 | B | 14595 | 1 | 3171 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14510 | 44878 | A | 14596 | 1 | 2700 | MEKKQSRKTGNSKNQSASPPP KECSSLQATEHSWMENDFDEL REQGFRRSNYSELKEEVRTHGK EVKNLEKRLDEWLTRITNAEKS LKDLMEKTMARELLDECINLS SQFDQLEERVSVMENQMNMENK PNLRLIGVPESDGENGTKLENT LQDIIQENFPNLARQANIQIQEIQ RMSQRYSSRAIPRHIIVRFTKV EMKEKMLRAAREKGRVTLKG KPIRLKADLSVETLQARREWGP IFNILKEKNFQPRTSYPGKLSFIS EGEMKSFTDKQKLRYFVTTRP ALKELLKEALNMERNNRYQPL EKQIQTTIREYYKHLANELEN LEEMDKFFDTYTLPRLNQEEVE SLNRPITGFEIEAIIINSLP/TKKSP EPGGFTAIFYQRIEKEGILPNSF YEASIIIMLKPGRDTTKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHQDQVGFIPGMQGWFNIR KSINIIQHINRTNDKNHKKIISIDA EKAFYKIQQPFMLKTLNKLIGID GSYLKIIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NLVLEVLARAIRQEKEIKGIQLG KEEVKLSLFADDMIVYLENPIA SAQNLLKLKGNFSKVSQYKINV QKSQAFLYTKNRQTESQIMSEL PFTIASKRIKYLGIQLTRDMKDL FKENYKPLLNEIKEDTNKWKNI PCSWEGRISILQMAILPEVIYRF |
| 14511 | 44879 | A | 14597 | 1 | 2310 | |
| 14512 | 44880 | A | 14598 | 1 | 1305 | |
| 14513 | 44881 | A | 14599 | 1 | 2148 | |
| 14514 | 44882 | B | 14600 | 1 | 777 | |
| 14515 | 44883 | A | 14601 | 2 | 2971 | |
| 14516 | 44884 | A | 14602 | 1 | 3810 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14517 | 44885 | A | 14603 | 1 | 1773 | MNIGAKIINKILANQIQQHIRKLI HHDQVGFIPGMQGWFNICKSIN VIQHINRTKDKNHMIISIDAEKA CDKIQQRFMLKTLNKLIDGKY LKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFNIVL EVLARAIRQEKEIKDIQLGKEEV KLSLCADKMIVYLENPIVSAQN LLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLQIHQTRDVKDLFKEN YKPLLKEIKEDTNKINIPCSCVG RINIVKMAILP/KELEKTTLKFIW NQKRARITKSILSQKNKAGSIM LPDFNLYYKATVSKTAWYWY QNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSL FNK WCWENWLAICRKLKLDPLLTL YTKINSRWIKDLNVSPKTIKTLE ENLDITIQDIGMGKDFMSKTAK AMAAKAMSTKAKFGKWDLIK LKSFCTAKETTIRVNRISYASS STSLQAFSRKILNCSKRFFKIAQ MCKLVELRPQDMHTSRGSGNC SEARTLLCDFSAGRTSVNHGRI WRQIREAGAADPEIGLEV CNKN PTSFTLFYFLSYTTG |
| 14518 | 44886 | B | 14604 | 1 | 2070 | |
| 14519 | 44887 | B | 14605 | 1 | 3190 | |
| 14520 | 44888 | A | 14606 | 1 | 3370 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 14521 | 44889 | A | 14607 | 569 | 3030 | RKH*TWKRTSSTSHHKNMPN* LEKQEQTH/SKPSRRREITKIRA ELKEIETPKTAQKINESRSWFSE RINKIDRPLARLRKKKREKNQI DTIKNDEGDITTHPTEIHTIIREY YKHL YANKLENLEEMDKFLDT YTLPRPNQEEVESLNGPIAGSEI QAIINSLPTKKSPGPDGFYQRYK EELVPFRLKLFQSIEKEGILPNSF YEASIIIPKPGRDTTKKENFRPI SLLNINAKILNKILANRIQQHIK KLMHHDQVGFIPGMQGWFNIR KSINVIQHINRTKDKNHMIIISID AEKAFDKIQPFMLKTLNKLGI DGTYHKIIRANYDKPTANIILNG QKLEAFPLKTGTRQGCP LSPL FNIVLEVLARAIRQEKETEGIQ LKKEEVKLSLFADDIMIVYLENPI VSAQNLLKLISNFSKVSGYKIN VQKSQVFLYTDNRQTESQIISEL PFTIASKRIKYLGIQLTRYVKDL FKER/YNEIKEDTNKWKNI PCS WVGRINIVKMAILPKVIYRFNAI SIQLPMTFFTELEKTTLKFIWNQ KRAHIAKSILSKKNKAGGIMLP DFKLYYKATVTKTAWHWYQN RDIDQRNRTEPSEIMPHVYNHLI FGKPDKNKQWGNDSLFNKWC WENWLAICKKLKLDPFLTPYT KINSRWIKDLNVRPKTIKTLEEN LGNNIQDIGMGKDFTSKTPKA MATKDKIDKWDLMKLKSFCTA |
| 14522 | 44890 | A | 14608 | 1 | 2742 | |
| 14523 | 44891 | A | 14609 | 1 | 3828 | |
| 14524 | 44892 | A | 14610 | 1 | 2667 | |
| 14525 | 44893 | A | 14611 | 1 | 2325 | |
| 14526 | 44894 | A | 14612 | 1 | 3057 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14527 | 44895 | A | 14613 | 603 | 2973 | DNTARGETIRQQHLLFTNIRCSA ASAADTQANRVWSGPPANSNR PAAIRVLTVRRKTNKQKGHPH QNPICTSPPSSKTKETQTTIREYY KHLNANRLENLEEMDKFLDTY TLPRLNQEEVESLNRRITESDIE AIINSLPTKKSPGPDGFTAIFYQ RYKEELVPFLLKLFQSIEKEGIL PNSFYEASHILIPKLGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKKHIHGQVGFIPGMQGW FNIRKSINVQHINRTNDKNHMI VSIDAEKAFDKIQPFMLKTLN KLGIDGPYLKIRAIYDKLTANII LNGQKLEAFPLKTGTRQGCLLS PLLFNIVLEVLRARIRQEKEIKGI QLGKEEVKLCLFADDMIVYLE NPIVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTGDV KDFFKENYKPLLNEIKEDTDKW KNIPCSRVRGRINIMKMAILPKVI YRFNAIPIKLPMFTFFTELEKTTL KFIWNQKRARIASILSQKNKA GGITLPDFKLYYKATVTKTACH RVGRAQQHSISKWKWYIHDWS QVGPEGTNSARYPDTTQKWT AAALQPLSRTSLKDSHEGKSSQ WAE LRAVHLVLRFAWKEKWP DVQLYTDSWAVASGLAGWSG TWKKHDWKIGDKEIWGRATPV IAQWAHEQRGHGGRDGDYAW |
| 14528 | 44896 | B | 14614 | 1 | 3105 | |
| 14529 | 44897 | A | 14615 | 1 | 3654 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14530 | 44898 | A | 14616 | 735 | 2839 | RSFPRS RPS PFLLSRYLRIH MV FSVLPFGLQNP KYLLSGSLQEK FRTPGINSHKTLDPNRVIIK VRR RLEKEKALRAYVGKSEVRNMH LRERCKL*KKREKNQIDTIKND KGDITTDAT EIQTTIREYYKHLY ANKLENLEEMDKFLDTYILPRL NQEEVESLNR PITGSEIEAIINSL PTKRSPGPDGFTA E FYQTYKEE LVPFPLKLFQSTEKEGILPNSFY EASIIIPKPGRDTTKENFRPIS LMNIDAKILNKILANRIQQHIKK LIHYDQVGFI PGMQGWFNKRK SINVIQHINRTNDKNHMIISIDAE KAFDKIQPFMLKTLNKL GIDG TYLKVIRAIYDKPTANIILNGQK LEAFPLKTDTRQGCPLSPLLFNI VLEVLARAVRQEKEIEGIQLGK EEVKLSLFADD MIVYLENPIVS AQNLLKLISNFSKVSGYKINI QK SQAFLYTNNRQTESQIMSELPFT TASKKIKYLG IQLTRDVKDLFK ENYKPLLNEIKEDTNKWK NIPC SWVGRINIMKMAILPKVICRFN AIPKLPMPFFTELETTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITPHIYNYLI FDKPEKMSIIDTGGWYEAPVSS FFKEGLCRTGTENQVNRQPPAA SPFKVYV SCTGSLHPRPHYFLE |
| 14531 | 44899 | A | 14617 | 1 | 2250 | |
| 14532 | 44900 | A | 14618 | 1 | 2870 | MKA EIKVFFETNENKDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITKIRAE LKEIQTQ KTLQKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITTDPT EIQTTIREYYKHLYAN KLENLEEMDKFLDTYTL PRLNQ EEVESLNR PITGA EIVAIINSLPT KKSPGPDGFTA E FYQSWAETQP KKENFRPISLMNIDAKILNKILA KRIQQHIK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14533 | 44901 | A | 14619 | 248 | 2623 | RQWAGVVGRCSHLASWVSSNT SETGAIRSSSTEVDAPDDSMMLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAIFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASII PKRGRDTTKKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIPGMQGWFNICKSINVI QHINRTKDKNHMIISIDAEKAF DKIQQPFMLKTLNKLIGDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTRQGCPSPLLFNIVLEV LARAIQKEKEIKGIQLGKEEVKL SLFADDMIVYLENPIVSAQNLL KLISNFSKVSAYKINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKKWKNIPCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFKL HYKITVTKTAWYWYQNRDIDQ WNRTEPSEITPHIYNLIFDKPE KNKQWKGKDSL FNKWCWENWL AICRKLKLDPLTPYTKIHPRWI KDLNVRPKTIKTLEENLGNTIQ DIGMGKDFMSKTPKAMAACA KIDKWDLIQLKSFCTAKETTIRV NRQPTKWEKIFATYSSDKGLIS RIYKELKQIYKKKVTNNPIKKW AKDMNRHFSKEDIYAANKHM KKCSPSLAIREMQIKTTMRYHL |
| 14534 | 44902 | A | 14620 | 1 | 3253 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEITNYLSDH SAIKLELRINKLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRQKERSKIDTL TSQLELEKQEQT HSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKRE KNQIDTIKNDK |
| 14535 | 44903 | B | 14621 | 1 | 2758 | |
| 14536 | 44904 | A | 14622 | 1 | 5178 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14537 | 44905 | A | 14623 | 1 | 3382 | MGDFNTPLSTLDRSTRQKVNK DTQEFNSALYQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCERTEIITNYLSDHS AMKLELRIKNLTQNCSTTWKL NNLLLNDYWVHNEMKAEIKM FFETNENKDTTNQNLWDAFKA VCRGKFIALNAHKRKQERSKID TLTSQLEKEKQEQTHSKASRR QEITKIRAELEIETQKTLQKIN ESRSWFFERINKIDRPLARLIKK KREKNQIDTIKNDK |
| 14538 | 44906 | A | 14624 | 965 | 4091 | TWKGTTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLLNDYWVHNEMKAE IKMFFETNENKDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKEKQEQTHSKA SRRQEITKIRAELEIETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID |
| 14539 | 44907 | A | 14625 | 3 | 3229 | |
| 14540 | 44908 | B | 14626 | 1 | 2791 | |
| 14541 | 44909 | A | 14627 | 1 | 3158 | MVKGSIQQEELTILNIYAPNTG APRFIKQLLSDLQRDLDSHTLIM GDFNTPLSTLDRSTRQKVNKDT QELNSALHQADLIDIYRTLHPK STEYTLFSAPHHTYSKIDHILGS KALLSKCKRTEIITNYLSDHSAI KLELRIKNLTQSRSTTWKLNNL LLNDYWWRKQERSKTDTLTSQLE KELEKQEQTHSKASRRQEITKIR AELEIETQKTLQKINESRSWFF ERINKIDRPLARLIKKKEKNQID TIKNDKGD |
| 14542 | 44910 | B | 14628 | 1 | 7849 | |
| 14543 | 44911 | A | 14629 | 1 | 3985 | MENDFDELREEGFRRSNYSEL WEDIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE LHEECRSLRSRCDQLEERVSAM EDEMNMKGEGKFREKRIKRN EQSLQEIWDYVKRPNLHLIGVP ESDGENGTKLENTLQDIIQENFP NLARQANVQIQEIQRMPQRYSS RRATPRHIIVRFTKVEMKEKILK AAREKDRSTRQKVNKDTQELN SALHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKID |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14544 | 44912 | B | 14630 | 64 | 5735 | |
| 14545 | 44913 | B | 14631 | 891 | 6894 | |
| 14546 | 44914 | A | 14632 | 33 | 476 | |
| 14547 | 44915 | A | 14633 | 1 | 360 | GQGEPKQLGRHPGVLRPHVVS AKTGDAC/IWTQVRNLFPERPK VQWKEGCALQSGNSQESVTEQ GSKVSAYSLSPLTLKADYEK HKLYACEVTHQGLSSPVTKSFN RGEIIEGEVPPCI |
| 14548 | 44916 | A | 14634 | 40 | 508 | LPGECHRAGQQGQRLQPQLLG LLMLWVPGSGGEIVMTQTPLSS SVTLGQPASISCRSSQSLVHSDG NTYLTWLQQRPGQPPRPLIYHV FKRFSGVPDRFSGSGAGTDFTL E/ISGRVEA* ^Δ DVG VYYCMQG\T QFPCSFQGGTKLETKRTVAAPS |
| 14549 | 44917 | A | 14635 | 3 | 652 | AWWNSETPAQLLFLLLWLPHY TSGEIVLTQAPGTLSPGERAT LSCRASQTIGSTYLAWYQQRPG QAPRFLIYGASSRATGIPDSSSSS SSSSSSSSSSSSSSSSSSSSSQQ YNNWPPGGTFGP\GTKVEIKRT VGCTHLFFIFPAHLMSQLKIWE LPSACVPVCNNFYPREVQSYSG KVDN/VPSNRVTPRESVTEQD\S KDSTLQPSAATLDA |
| 14550 | 44918 | A | 14636 | 3 | 440 | |
| 14551 | 44919 | A | 14637 | 457 | 1270 | SRRVSFPPSA*QAVSDPSRQQLP SLRLRWGPGRSFPANLGRGV RWVGGRDPLAA\LP*SSGPLNA GRLFARPQESGAPRIGNVRDVP RAREDVGTQAGRREREFRLFG PAAVVGGERHLSFPRAAGAG GRAGAAGRRSAPPGGLGSCRSC RISAGPHGNDVPTLGGRGW/PL *NSGAEKL*EQ*G*/TGTGSWSL AAILGGVPREP\GFRGAGRET LG PRGWLVMLSRAVLLHVSLLCT CHSSWVLLHSDLACHADNNPD IQSCLFPMSKY |
| 14552 | 44920 | C | 14638 | 90 | 465 | |
| 14553 | 44921 | A | 14639 | 116 | 439 | |
| 14554 | 44922 | C | 14640 | 278 | 364 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14555 | 44923 | A | 14641 | 116 | 687 | EIKDAALQLPLWRAQDRERAM KERREKREREREKERDREKKRK EKMFCRKSCHTIMEPTPELSCV LPCLAPIVLAPPPLPLPVLPYPY ATR*LPQQNRQSTLTEAHGLVTR GPITLATNRCMPSTTRDRRLT PPSTLPNTTNLSWGVREGPNQD PEPSLSPCVPHDPFDYNAESLFS YWLVSVTPTMTAHTP |
| 14556 | 44924 | A | 14642 | 474 | 1166 | HPNRQGLRAPATAPGHPGREQ ALCEAPQGPQGKCGPPRAQEA Q/GTEPRRASRAAGACRHHWP QVA\RPGAGAPAGAARLGGV*E PGRAA/APRLPLPSQCCHR*GTS PAHLSASRSSSATCPWRRTAGR SGPSPCMTL\KQRQGHPRDGWI RAPSCDVTNRGLSSLNLGGS QQLLLASRPLGSGSGALEALEH GKSRA PWEPWLHGTHNPVHGK DPAGSTSHWPRPPAPRT |
| 14557 | 44925 | A | 14643 | 283 | 806 | PRGSFSSTGRTRNAAGSTSNCSL RSLSARIEERKVS RVCGVPNHR HLRLGALTTRPSWNGAIPTLA KLPAKRC*RRSGRRSKTWSFPG ST*LGNFAEEMICAASARPAGV PGPALPTPLRAPLPGVPTSSR GRMCARLSCC/HAGRPVPARPG AARARRAAAGERHRPPALRV |
| 14558 | 44926 | A | 14644 | 1 | 338 | |
| 14559 | 44927 | A | 14645 | 1 | 1091 | MSNDGRSRNRDRRYDEVPSDL PYQDTTIRTHPTLHDSEAVSA DPLPPPPLPLQPPFGPDFYSSDT EIPAIPDLKPVRRFVPDSWKN FFRGKKKDPEWDPKPVSDIRYIS DGVECSPPASPARPNHRSPLNS CKDPYGGSEGTFSSRKEADAVF PRDPYGS LDRHTQTVRTYSEKV EEYNLRYSYMKSWAGLLRILG VVELLLGAGVFACVTAYIHKDS EWYNLFGYSQPYGMGGVGGL GSMYGGYYTGPKTFVLVVA GLAWITTIHILVLGMSMYRTIL LDSNWWPLTEFGINVALFILYM AAAISLM*MIPTRGGGLCYYP LF NTPVNA\GSAG*KEDR*LQ*SSC LSP**FISLV LWFA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14560 | 44928 | A | 14646 | 398 | 1107 | SPGLVCGLLIFCKVTVPICAGPY RCPFGGLRH*SAR*QPPSGLREN GARPPGGEWLCPC*FPP*PLNSR WKLPPRLVT*GEPWAAGEKFP RLGAGTGPAAGEGLPRARDWE PGRAGPERWAPGRGPAGTPAK TAAVKRSAPLPGS\GDYANGER KPPPSFPCQVKSGNL*VLCG*RL SLPAA*KPKKA*RRGRRQSPGK TGYQVQQTRPKNDPKSSIGPSP KNRQSLCLQPLWSFLIQ |
| 14561 | 44929 | A | 14647 | 1 | 540 | MGVRDPLEEAVCALAELQHCA GRFAALFRASRQERLSLLKLCP QLPLPPRALSQGYKPLIGLLAF FQRCTAQRGGI*RGSLATVTLAS CGGLCPV*TSQRRCLPVRGKLP TQASVMANAPPRTLQHLRSTS DCCAGSENFKPVDSLGLSGVG GSTELDHLAPWLQPAFQGSEW FYLTF |
| 14562 | 44930 | A | 14648 | 169 | 487 | EVCYYPSETYFCQFVKLILCPV LFPCWQGVVIQPKLSCMRCLST LLRGVSQ*GYMGVRDPLEEAV CPLAELEHCAGRSAALFRAGRQ ERLSLLKLRLPQLPLSPSA |
| 14563 | 44931 | A | 14649 | 1 | 210 | |
| 14564 | 44932 | B | 14650 | 1 | 1683 | |
| 14565 | 44933 | A | 14651 | 1 | 529 | MDSEVQADDEVSDENGELIGN WGKGGMGVSDPLEEAVCPLAE LERSAGRSAALFRASRQECLSL LKLT/LTAAPSPRGTAFRSPFKS PAQRRSIIC*Q/LYSCKTFRSTVA PMPRLCLPQASGKVQ*EN*SWA IPA*QGTSPMCSLCSGAPHQPG APLVLPLPPPVRNRLRRELQCWL |
| 14566 | 44934 | C | 14652 | 295 | 430 | |
| 14567 | 44935 | A | 14653 | 452 | 637 | |
| 14568 | 44936 | A | 14654 | 151 | 446 | MVLSHWHSRCHWGMKKNYLQ LARCLPKWLPSFVFETQGPCDV STQGTLLVYGLQRPWEKHSI*A R*HHP SQHGPSQLPLARGGSSP TPCASRM RQHPT |
| 14569 | 44937 | A | 14655 | 2 | 335 | EDRSAFRPRQPHTLHPLHARSL APRSPTPPSPSPDTQLGLSGPTS GPESAPTA/PGNPSWRSSRWGSS SPCAASST*KSPYP*/CSPT/CAFP SPRLPFCRSAYQPAAGAGR GK |
| 14570 | 44938 | B | 14656 | 373 | 502 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14571 | 44939 | A | 14657 | 1 | 400 | GSPAPAAMDEERALYIVRAGE AGAIERVLRDYSKVKSPGPGR AVSHPRAAALRACTSHSPPPPSFR GCAL\PPPKTFPAWACVFVPPAF SIHAS/SHPTTPTVAPTPLIPGPA A*PPVLLSSVQVTPPESVDVHL |
| 14572 | 44940 | A | 14658 | 659 | 1177 | ARKGSALLRLYLSNAWCVCVK VLRIFSTASAYITRRDSSLGPVW TFLNFSFGSPGEIPTFFFFPVFP LPLVAWFCPASFCPLQCPLVPS EPSPPPHSGDAHCSPPKTFPAW ACVFVPPAFSIHAS/SHPTTPTV APTPLIPGPAA*PPVLLSSVQVT PPESVDVHLCPVPHS |
| 14573 | 44941 | B | 14659 | 1 | 318 | |
| 14574 | 44942 | A | 14660 | 2 | 131 | |
| 14575 | 44943 | A | 14661 | 354 | 762 | CPEIRPPS*THGTK/SHFPPTASG THSVLEAL/PDTQRQSPRVHQ DPSPAI/PALLPSPHEHGPQHLL QLPSHRCHPDTAPFNCDVAKAC PGHATAALEHPYLSGRQSPSP THLPKLPAGRGYTVCALPKGPG ERSAV |
| 14576 | 44944 | A | 14662 | 157 | 413 | ALVCS/SSLAIEMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL |
| 14577 | 44945 | A | 14663 | 1926 | 2448 | DFIAVITTRKQLKTKYNAHHSK QAITKHFSPKISDLILCLKKKIM NRHFSKEDIYAAKKHMKKCS SLAIEMQIKTTMRYHLTPVRM AIIKKSGNNRCRRGCGEIGTLLH CWWDCCKLVQPLCKSMWRFLR DL\DPAPILLGIYPKDYKSCCYK DTCTRMFIAALFTIAKTWNQP |
| 14578 | 44946 | A | 14664 | 1 | 1584 | |
| 14579 | 44947 | A | 14665 | 1 | 4729 | |
| 14580 | 44948 | A | 14666 | 1 | 1566 | |
| 14581 | 44949 | A | 14667 | 1 | 1424 | |
| 14582 | 44950 | A | 14668 | 1 | 576 | |
| 14583 | 44951 | A | 14669 | 1 | 3325 | |
| 14584 | 44952 | A | 14670 | 1 | 2195 | |
| 14585 | 44953 | A | 14671 | 1 | 3162 | |
| 14586 | 44954 | B | 14672 | 287 | 2018 | |
| 14587 | 44955 | A | 14673 | 1 | 1073 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, =possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14588 | 44956 | A | 14674 | 1 | 3335 | MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLS DHS AIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNVYKRKQERSKIDTL TSQLKELEKQEQT HSKASRRQE ITKIRAE LKEIETQ |
| 14589 | 44957 | A | 14675 | 1 | 1838 | MIIPIDAEKAFDKIQPFMLKTL NKLGIHGMYLKIIRAIYDKPTA NIILNGQKLEAFPLKTGTRQGCP LPPLLFNIVLEILARAIRQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPIVSAQNLLKLISNFSKVSGYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGKDSLF NKWCWENWLAICGKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNLIELKSFC TAKETTISVNRQPTWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPIKKWAKDMNRHFSKEDIY AANRHMKKCSSLAIREMPIKT TMRYHLTPVRMAIHKKSGNNRC WRGCGEIGTLSHCWDCNLVQ PLWKAVWRFLKDLELEIPFDPA ISLLG/TYPKDYKSCCYKDTCTQ STFTCRQHLPL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14590 | 44958 | A | 14676 | 1 | 2354 | MGDFNTLLSALDRSTRQKVNK DIQELNSALHQADLIDIYRTLHP KSTEYTTFFSAPHRTYSKIDHLV GSKALLRKCKRTEIITNCLSDHS AIKLELRIKKLTQNHSTTWQLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWYVKDTRI SGMLWYVKAVCRGKFIALNAH KRKQERSKIDTLTSQLELEKQ EQTHSKTSRRQEITKIRAELEI ETQKTLQKINECRSWFFEKINKI DRPLARLIKKKREKNQIDAIGN DKGDIITDPTEIQTITREYYKHL YGNKLENLEEMDKFLDTYTLF RLNQEEVESLNRPTGSEIEAIGN SLPTKKSPGPDGFTAIFYQRYK EELRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNIPCS WVGRINIMKMAILPKVIYRFNA IPIKLPMFTFFTELEKTTLKFIWN QKRARIAKSILSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMLHIYNHL IFDKPDKNQWKGKDSLFNKWC WENWLAICRKLKLDPLIPYTK INSRWIKDLNVRPKTIKSLEEDL GNTIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWEKFFAIYSSDK GLISRRYNELKQIYKKKTNSPIK KWTKDMNRHFSKEDIYAAKRH MKKCSSSLAIREMQIKTTMRYH |
| 14591 | 44959 | A | 14677 | 1 | 3144 | |
| 14592 | 44960 | A | 14678 | 1 | 2745 | |
| 14593 | 44961 | A | 14679 | 1 | 2742 | |
| 14594 | 44962 | A | 14680 | 1 | 3264 | |
| 14595 | 44963 | A | 14681 | 1 | 2982 | |
| 14596 | 44964 | A | 14682 | 1 | 3102 | |
| 14597 | 44965 | A | 14683 | 1 | 1443 | |
| 14598 | 44966 | A | 14684 | 1 | 3723 | |
| 14599 | 44967 | A | 14685 | 2 | 1841 | |
| 14600 | 44968 | A | 14686 | 572 | 744 | DLLTTIRMPTDVKKCSSSLAIRE MQIKTTM*YHLTPVRMPIIKKS GNNRCWRGCGEI |
| 14601 | 44969 | A | 14687 | 1 | 3588 | |
| 14602 | 44970 | A | 14688 | 1 | 5569 | |
| 14603 | 44971 | A | 14689 | 1 | 3992 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14604 | 44972 | A | 14690 | 755 | 2415 | QELRVSGWSPASAPANT*CPPA QPCPTRRSGGQRAPARTSRPG SRPRTASALPRPAAQKAASRSA RASRTNPYTAPKPLPSVESALQ EAAIGEHAHQQRVSTCAAPA APPSPAWPWSAARSAAPPPRT* ASAPA*SPL/PVRLKKSPGSSNC EARGEWKT/PALPVQLGAHGP PQPAAVPCASPGSGAGPRWSRS ARRTPRGPLQRGRTWVSPDPGR EATPSGTQWPQKTRGSLPGS*C APETPCSAA*SSGTSPRGAGGC CPGTVPPALEGHN*PQRWGSHS AGRVENTRAEGPQCQAGAPAGC SLGVGGQRGPPGLPPIPVGLC* TCRSS*MEAATGSVEKCKRMA SLMQASRWSFLRVAPVSGQVK YTPGTARWAEPSSLGSDTTLVP GAS/RAPADGGFGLKFLSHLVS DGVLRGCGPRPGTASAPAGLR AAAAIPSVPSLVGPWRGGLGAG WLGFSLWAFSPTDSLFS*PGPA LLNLMSALNS*KNFFMVAARS CGGGTRGRGGTGPSRGRGRRR PATGRK*KKKKKKKKFTSPPEV PPSPGLPRDNRL |
| 14605 | 44973 | B | 14691 | 1 | 822 | |
| 14606 | 44974 | A | 14692 | 1 | 2789 | MAAVRKQLPRGVLYGGSGAL LSTAAADTSLLLGSLQERKSAS AGPGYLRSSVAAWSGLWLTGA SEAHSVVLACFSRKDVEASLSV GLPVHPDASCARRLDAADGVA GGSPRLPQSTDGWRLTAHSLPQ STDGWRLTAHSLPPPTDGWRL TAHSLPQSTDGWRLTAHSLPPP TDGWRLTTHSLPQSTDGWRLT AHSLPQSTDGWRLTAHSLPQST DGWRLTIHSLPQSTDAWRLTA HSLPQPMDGWSCRSAQWCV |
| 14607 | 44975 | A | 14693 | 176 | 440 | |
| 14608 | 44976 | A | 14694 | 114 | 253 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14609 | 44977 | A | 14695 | 124 | 890 | GSRAWDRPRLEVA AATTLFY GYGFVSAELKKASKRMTCHKR YKIQK\KAPEHHRKIRGEAKKR GHNKPRKDPGVPNSAP\FKEAL L\REAELRKQRLEELKQQQKLD RQKELEKRRKLET*SWIFKPSN V\DPMEK\EFGLCKTE\NKA\RSG KQNSKKLYCQELKKVIEASDV VLEVLDARDPLGCRCPQV\EEAI V\QSGQKKLV\IYLNKSDL\VP KEDL\ESWLKLF*RKDLPSNGCF RASTKTQRVKGKITKVSFIS |
| 14610 | 44978 | A | 14696 | 553 | 997 | EVTACWQSSQPSLT LGASSAW APTLAAL EEPFSPPLHCGSPFLG WPRLEPAPSAPPWAPVRPEPPQ QGPPSAPGRPIPTTQGLRSADA GRRTGTQLHRQPAKVCSF/IS*S QRDHEPTRRNEQLQTRRLKSCN THREDLQLHSRRKKL |
| 14611 | 44979 | A | 14697 | 1410 | 2036 | |
| 14612 | 44980 | A | 14698 | 3 | 630 | RYKGSPPRHQTQEPSWLHLVDP APGLQVELPASPAPCARIQPL GGRWDWAPWSRGWCSSGRLG QHRSPWSGWEAQAWRAAGPK PCPAGRQLRPGEKSSTAPVGRH CWGIQYTLRSHWPGC*VPHSSG PAGLAGCSGTPAGPQAPHAAP V\PARA/CSLHTSLQAEGVGSSL GQPRKGLPQCRWGLKGSSNAA KVGAQAGEVQARALRTAS |
| 14613 | 44981 | A | 14699 | 190 | 383 | ASHPLRGLRSGRSLPDERHRL HSAQSHRPPKG*GVRAQGAGL T/WQLHL*PQCGIHWVKPAGLL |
| 14614 | 44982 | A | 14700 | 1 | 1095 | |
| 14615 | 44983 | A | 14701 | 1 | 777 | |
| 14616 | 44984 | A | 14702 | 1 | 933 | |
| 14617 | 44985 | B | 14703 | 1 | 996 | |
| 14618 | 44986 | A | 14704 | 978 | 1207 | ASLPLRGLLCCPSLPEERRPLLH GAQSHRPPKG*GVRAHGAGLA/ WQLHLRPRCGIHWVKPAGLLS LGPHQQSSKSA |
| 14619 | 44987 | A | 14705 | 111 | 558 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14620 | 44988 | A | 14706 | 1 | 1103 | MKPWALKVSVTALKVARLEFV PPDVRCSEFLPCGVKLQTFV SVTALKAAARLELFVSPGGLVVS LASGVKLQTFPVSVTAHKSSVD PRSEQQDQLLQRAKEQTFHTVE GDRSGSPDGAQLASPSGSRT RAAGGAACQSRALRPHSSALG WSMGLGAVEQGAVLIREARAA HEPMERVGGSGMAGCRSRALP REKAAKARRETEGSAAVSGWL SGIAQWPKIDHEGFRAVKMPQ AAWLLKAVTFIDLTTLSGDDTS SNIQRLCYKAKYPIREDLLKAL NMHDKVAAGFPAGQTHLKTRL EEIRLAVEDGATEIDVINRSLV LTGQWEG/LYSPVVYSALPCNI* HSRLFLPSGNALLLWLWCLHS |
| 14621 | 44989 | A | 14707 | 2 | 2300 | |
| 14622 | 44990 | A | 14708 | 2 | 1058 | ARSNIRMVTAFRSLPAGSSGAA RAMSAHNRGTDLDSWISKIQ VNHPAVLARRAEQIARRTVK KDWQAAWLLKAVTFIDLTTLS GDDTSFNI*RLCYKAGYPIREDL LKALNMHDKGITTAACVVP ARVCDAVKGTSRPAG/CVNIPV GISRAAGFPAGQTHLKTRLEE IRLAVEDGSLQKIDVINRSLG A*QAQWEALYDEIRQFRKAC GEAHLKTLATGELGTLTNVY KASMIAMMAGSDFIKTSTGKE TVNATFPVAIVMLRAIRDFFWK TGNKIGFIPAGGIRSAKDSLAW LSLVKEELGDEWLKPELFRIGA STLLSDIERQIYHHVTGRYAAY HDLPMS |
| 14623 | 44991 | A | 14709 | 576 | 998 | VLQFLKAACPEFVPSGVPMCSE YLPSGGFVVSLASGVKLQTFPV SVTALNALRLELFVPPGGLMVS LASGVGSCRSSR*VLQLIKAVWT QRPLGGRWDWAPWSRGRRSFG EARAAQKPMEGVGGSGMAGC RSRSPAPREGS |
| 14624 | 44992 | A | 14710 | 2 | 589 | RHHPRHAVQARFPAGPLAGA QRGSGAE*RGPOGSVPGAGLS GGESL/PGETDRGADKEERGRQ RWQRALGRLSAGADPLPAELR GRRQRRGR*AGQRAAQEAACE APIQSGGARNGRRG*GRRL*GC YQ*V*FPGLTRGWGRGSRPSAV HCGWEPP*AGKPSGQTPRHSG* PAGVDGLPPKVTGPPPGTPQPR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14625 | 44993 | A | 14711 | 1 | 1596 | MRLTRCQAALAAAITLNLLVLF YVSWLQHQPRNSRARGPRRAS AAGPRVSLPPHPLTCVWRCSR AMDRPPAASRPETTVATEFVAL VLDGARAEAHALLERMVEALR AVSARLVAAPVATANPARCLA LNVSLREWTRYGAAPAAPRC DALDGDVLLRLRDLFNLSA PLARPVGTSFLQTALRGWAV QLLDLTFAAARQPPLATAHAR WKAEREGRARRSALLRALGIRI VSWEGGRLEWFACNKKNQRC |
| 14626 | 44994 | A | 14712 | 225 | 980 | VPSRTWAEYRTRFVPHSLGQPR SSHIPQSPQTDQTAQGQALAP PAGRSGQ*GRPGRRARLGPGER HS*APPPLSQLLLQTFPHLQALP SAHARPSGQPHADRGHSRSPSG /DLSTSSVLKVVRPQAGGPKQA RCPQAGRVCHCPRGGRRGPE/Q Q/GG*RPEAPQASPEKGSTGLRP SAKDSKNQGTGIFLRCQVAPRP EALCCPPPRGADTPVSPCLWVA GAGIPLQPPEGAEGAVLGLSLCT LCPGSPDSPPTS |
| 14627 | 44995 | B | 14713 | 405 | 893 | |
| 14628 | 44996 | A | 14714 | 178 | 499 | |
| 14629 | 44997 | A | 14715 | 231 | 436 | |
| 14630 | 44998 | A | 14716 | 141 | 393 | |
| 14631 | 44999 | C | 14717 | 97 | 351 | |
| 14632 | 45000 | A | 14718 | 119 | 358 | |
| 14633 | 45001 | A | 14719 | 21 | 614 | PPCTSLRPLHAFSGKMTLNRG TSLLDSQLHNLIALQMTCFKD VEIPNFFWEPSVTPSHRNINMYF PAAVFGFLPISGTLFSYCKIVSSI LRVSSSGGKYK/AFTTCGSHLS VVC*FYGTGFGGYLSSDVSSSP RKAASVSMYTVITSM LNPFY SLRNRDIKGVLRQPHGSTVQFQ YLLICSIPFVWVKKGSKVK |
| 14634 | 45002 | B | 14720 | 162 | 1263 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 14635 | 45003 | A | 14721 | 696 | 1791 | VWIALKSENITCELLLFKMQTQ CQVLVYLFPIFQPSFLGKRCPI TDPQNLTDVSI FL LLEVSGDPEL QPSPCWA VPC PCAWVTVLGNL LIILAISPD SH LHTPMYFFLSNLS LA\DIGFTSTTVPK\MI VD IQSHS RVISYAGCLTQMSLFAIFGGME EDMLLSVMA YD WFVAICHPL YHSAIMNLC SV GFLVLLSFFFF\ LSLSDSQLHNLIALQ MT CFKDV EIPNFFWEPSQLSHLACCDTFTN NIIMYFPTAIFGFLPISGTLFSYY KIVSSILRVSSSGGKYKAFSTCG SHLSVVC*FYGRGVGGYLSSDD VSSSPRKGAVASVMYTVVTPM LNPFIYSLRNRDIKSVLRRPTEH CLISKK |
| 14636 | 45004 | A | 14722 | 1 | 1971 | MTRKVTLLLR TW RGGCGRLA MGMEATPQGS LH PLFQEHWIR AEDFGVLS PM H PN SVQGVDDM IRLGD LN EAGMVH NLL IRYQQ HKIYVSLPSPVSTGEPLTGANLL DREKKMMHRGHCPIALTEGVS GPDNPEGRARAKAKAKARAEL PLPGAEGTDHLLPSQTYTGSILV AVNPFQVLPLYTLEQVQLYYSR HMGELPPHVFAIANN CY FSMK RNKRDQCC I SPQNRVGAQTD VLKVFOHLLISLICKTTLQACCI PSHPYLSSAPGPPPLTTQCRSYS DSLLGPQLFGDVCYNCSHVIEG DGEALCSLPHPTCSPGAWVLQL VSPLNKA WC VSCFSCSTCNSKL TLKNKFVEFDMKPVCKRCYEK FPLELKKRLKKLSELTSRKAQP KATDLNSAEGPLAQLGAVGA/V TGITHEPHIPQVENG SQ QLDDV PALGV\ENWRIFMAERMEAQG GQRLLLSTMHEEYEFVSPSSVAI AELVALFLEGLKERSIFAMALQ DRKATEGGPVGLTKKQGLLAS ENWTLGQNDRTGKTGLVPWH CLYTIHTVTKHSDSCCTAVPTL LEASSGCIFMSYKKHITLTPKSA DSNKR P STLGSQFKQSLDQLMK ILTNCQPYFIRC IK PNEYKKPLG FSDSFMLIKLIRIDKVQYDSFSYI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14637 | 45005 | A | 14723 | 1 | 1197 | MNMNIKKIVKQATVLTFTTALL AGGATQAFAKENNQKAYKET GVSHITRHDMLQIPKQQQNEKY QVPQFDQSTIKNIESAKGLDVW DSWPLQNADGTVAEYNGYHV VFALAGSRKTLMTHQSTCPKH RASRVGPSNSLQNKQTVKKGD QTSVRRKRNDLKVEERHKNHH LARELTSSAAAASPTGHAAATA QAPQRHVEVGRAAAPAGDLGE GIVGEQVLGAERLVGPDASRAR ALCVLGDRREAGHTAEMTAAP PAQVPGPGGPTALRRPSSYLGL GVDEQNPMMSVDGDEDDVRVQ HQELRDCLIKHTILIRGEFVTRS LNIAQAADRRDAFVKGIYGALF LWIVKKINAAIFTPPAQDPKNV RRAI/GLLDIFGFENFENNRIIRT LCWRYREARC |
| 14638 | 45006 | C | 14724 | 1 | 1032 | |
| 14639 | 45007 | A | 14725 | 1 | 4960 | MSTTSIFQQLNLLSHSHKQKQ QIQLPNGRSRYSCMAAFRMQ YFLSLPMKSLILVGFERLQAIAR SQPLARQYQAMRQRTVQLQAL CRGYLVRQQVQAKRRVVIQ AHGQGMAARRNFQQRKANAP LVIPAEGQKSQGALPAKKRSI YDTVTDTEMVEKVFGFLPAMI GGQEGQASPHFEDLESKTQKLL EVDLDTVPMAEPEEDVDGLA EYTFPKFAVTYFQKSASHTHIR RPLRYPLLYHEDDTCCLAA |
| 14640 | 45008 | A | 14726 | 86 | 370 | RTWMTHVWRRRRVQAAPTAY SSFRPGTSPCPAQPRAGARA*TR SGTSIMPTGFSSHTSCLTVPPFT ASSAGQHRQRHRKTTAAGHPT TTGAASF |
| 14641 | 45009 | A | 14727 | 3 | 455 | MQSVLPAHGVSSSTRASSRVTL SSPSTSTNCRGRKSSRVTS SGPGGGGGGPGSGRFGIDPPRK FAAAGSFSTGAPSSVMVVRVSG MPSLSW*QYP*SCSTLGCRSRSS STISLSSLWA/VQPIAAPYPPELA TQLPISCR*SPSPCAPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14642 | 45010 | A | 14728 | 338 | 1782 | NQLSK*KAHSIRT*TALQQSSGR SQICIVQSSADALPSSRCTNPSSST FTPTPLPPRPHPRCTSTLGCRSR SSSTISLSSLWAASR*QPLRTPN SRTQLPRSWPLKSTALSPPPPGQ ATRLCWWMVSSK*RTWMTHV WRRRRVQAAPTAYSSFRPGTSP CPAQPRAGARA*TRSGTSIMPT GFSSHTSCLTVPRLHCVLCWTA SSTPQESSPGGWTRPWPSWRRRC CTCTGAGRYLQNSTAS/T/PVPS TSVSQTAPSPKEDYRCWPSYHH GSLPPFSVQPG*GCGMSVRAMP SVGPLWSPTRPPGQIKRQNYLL NYWSCWKMTLLAGIIPSSST/GS RPADLDYFLGSSQCPRDERTLK GHVSCDPTSSISITGEKLKQKLE S/SSTLADTKSAFLQDSWT/SSLP TLGASAI\RTTSAS*TDQCPPAP GPLHVSV/SLNSTYPSRLCSSTCS TVDSFQIIPMPN*MPFSTCGAFC WCLWFSAITALYFVM |
| 14643 | 45011 | A | 14729 | 148 | 1040 | WCTGSQFSKGTWEILLRKKPSL GNVGALPCVATACLTTVEKRA PRGHPLAPVLGDICPKVGSMS STSEL/CTWGNFEFWGRNKYNH WF*WGWALLHQFKMGKAQG LQEASFYRKDTY*A\TMP*NPIG ISEFGTLALPGCKNVFERFMS RFELPGKAAAMTDNTNVNYVR YKGDYYLCTETNFMNKVDIET LEKTEKMWKPRFRGICPQLQG CSVTEQGFESDDAKSWALQH PKRPAQQDWAMSRGNQGWAN LGLKIIRGEAVTTTRAKEVS VVLKVLEVTDGKVVAREKKLRDSR |
| 14644 | 45012 | A | 14730 | 189 | 507 | AAGADTSQGGPGGPPPSQSQR\ PKSPSAGRKGSQSPQPQKKGL PSPQGTRKSAPSSKATPQASEPV TTQLLGQPPTQEEGSKAQGMR* PPQRLGASTQQQTNQEAA |
| 14645 | 45013 | A | 14731 | 2 | 356 | DGVSLCHPGWSA VARSQLTAT SASWAVCWQGCGETGILLPCW WECEKVQPLWKQYGRLSCEDH LNS*VQVILTTQPPILFPKWHL FTFPPTGQKDSFSSTLLPTHCPG GRGCSELRSRHCTPAWVTE |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14646 | 45014 | A | 14732 | 1 | 408 | FFFFFYTTFFLFFYFYFFEMESH SVTQAGVQWYNLSSLQPPPPRF RRFSCLSLPSS*DYRCPPPHPAN FLCF**RQGFTLLAKMVSIS*PH DPPTSASQSAGHVLTSKWELNI EYTWVIKMGTA DTGEHKNGEG WE |
| 14647 | 45015 | C | 14733 | 262 | 536 | |
| 14648 | 45016 | A | 14734 | 179 | 745 | TDCLHNRCHRSRSPPPGPPG*R SRADWWRRGRCWGSWCASSR RVC*RCPAPSASFCCRSRGRQ GRTFPPSPCPAPD*TQPVSPGDS TRPCPPPSPPAHRAT/GCCGRR RLPGNASYLASPGKEAGEFPAS QGDS*PGQYGYIGDSSS/RPTRG TWMKASTPRHPIAPQICGA*G FGEHQEVPVREK |
| 14649 | 45017 | B | 14735 | 1 | 1164 | |
| 14650 | 45018 | A | 14736 | 35 | 542 | VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGAL PLDVTTFY/KDYGDKLNMESE KYKLDKESYPVFYLF RDGDFEN PVPYTGAVKVGAIQRWLKGQG VYLGMPGCLPVYDALPGEFIR ASGVEARQALLKQGQDN |
| 14651 | 45019 | A | 14737 | 11 | 908 | VRPPSHVTADSGRSPLSLTYLPL QEPGDMAAAVPRAAFLSPLLPL LLGFLLLSAPHGGSGLHTKGA LPLDVTTFYKVIPKSKFVLVKF DTQYPYGEKQDEFKRLAENSA SS\DDLL\VAEVGISDYGDKLN M\ELSEKYKLADKESYPVFYLF R\EGDFEPPSSHYTGG*RLGAIQ RWLKGKGKVYLGDLGLVCT V*LTPWSGEFIRAISGVKARQAL LKQGQDNLSSVKETQKKWAEQ YLKIMGKILDQGEDFPASEMTR IARLIEKNKMSDGKKEELQKSL NILTAFAQKKGAEKEEL |
| 14652 | 45020 | A | 14738 | 3 | 227 | |
| 14653 | 45021 | A | 14739 | 1 | 424 | |
| 14654 | 45022 | A | 14740 | 1 | 207 | |
| 14655 | 45023 | A | 14741 | 2 | 352 | |
| 14656 | 45024 | A | 14742 | 1 | 441 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14657 | 45025 | A | 14743 | 1 | 461 | MTVDYRKFNQVVTPMAA/AVP DAVSLLEQINTFPGTWYAAIDL ANAFFSIPVHEAHQKQFAFLPQ GYINFPALCHNLIRRELDFFLL QDITLVHYIDDILLIGSSEQEVV NTLDLLIHKRSKEAHTAASRIR VSCLPEQKSHEQTLPEQVP |
| 14658 | 45026 | A | 14744 | 1 | 928 | |
| 14659 | 45027 | A | 14745 | 283 | 1074 | |
| 14660 | 45028 | A | 14746 | 450 | 1970 | VRVLSPEKELKLWKNTHKLL SYPTVGAAVTQLQNLAMGVI GSHGARGQVVALNRQRQDDL QPFTRVTVHWGKGYDRTFWGL LDTGSELTLTPGDPKHHCGPPV KVGAYGGQVINGVLAQVQITV GPQTHPVVISPVPECIIGIDILSS WQNPHIGSLTGIMVGKAKWKQ LELPLPRKIVNQKPYCIPGGTVE ISATIKDLKDAGVVIFTTSLFNS PIWPVQKTDGSRMTVGYRRL NQVVTTPATAAAPDV/VVSLLE QINTSPGTWYAAIDLANAFFSIP VHKPHQKQFAFSWQGGQYAFT VLPQGYINNPALCHNLIQRNLD HFPLLQDITLVHYLNDIVLIGSA IKWVMHSS/DSIIKWKWHVHDR AQADPEGTS*PGYGHFWCPIC QQQRPTLSSQYDTIPWAISQLPG DRLIIGPLPLWKGQKFVFTGIDT YSGYGFAYPACNASAKTTIMES QNTLSTLMVFHTALPLTKALTS WLKKCSSGLMLMEFTGLTMFSI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14661 | 45029 | A | 14747 | 1 | 2589 | MGPPYKPPTTWPQTLSYHSTT PVKLQSLSLPPTAARGATEPCH LQAPASSVQQMTTPAPGLKHL GGKSQMCLEQDGRSGSVRGSP CHAGHWVAGAGFGKGTTRTW GHVNLIVPPNCPTASSSAARDS APNQPLLGVVTAQIVPPTCPPA MTVQELIAPLTLPPAAGCRRGV RPFQTRVWLLAQLLRARLGGP GEGVVTCHSWRLERVAPRLAS LWWALAAETAARLDWAAKRP SAWGSIKAAEFSSKATPRLEGA SSRTLWVSYIQAKETTTGKNGP VEPSHLWEAYCRATAPHPAVH SPSAEVITYTCGIVNLLLQGLVP KSHLEHTGCHVVVELIICSVV LPLISRLSDPDWIHLVLMVIFSK ARDPTPCPASGPEQPSVPTSLPL IAEVQQLPEGRAPSPVAAPGFLS KQIQDALCALEGSQALEPKGGE GSEGVEAEGPTETETVLPVST LNFCEIQIDIADKEIEQGEVTT VTALLEGLEKTCSSRPSCLEKD LTNDVTYLDPTIFSFEPLSSPDG PVVIQNLHITGTITAQELSGTGL QPCTRYTVKCETSLDGENSSLQ QLAYHTVNHRYWEFLNLQ/SH QEKKPD*KFIKNIEKMVVS VDNLKTAFPCSESQGPTEELSE AETESKSQTEGKKARKSRLRFS SSKISPALSVTEAQDTILYCLQE GNVESKTLMSGMESFIEKQTK |
| 14662 | 45030 | A | 14748 | 478 | 3507 | SKILRAVIWGSHLVRSAMKTET VPPFQETPAGSSCHLNNLLSSR KLMAVGVLGWLVIHLLVNV WLLCLLSALLVVLGGWLGSLL AGVASGRHLHLERFIPLATCPPCP EAERQLEREINRTIQMIIRDFVL SWYRSVSQEPAFEEEMEAMK GLVQELRRRMSVMDSHAVAQS VLTLCGCHLQSYIQAKEATAGK NGPVEPSHLWEAYCRATAPHP AVHSPSAEVITYTRGVNLLLQ GLVPKPHLETRTGRHV |
| 14663 | 45031 | A | 14749 | 1 | 417 | |
| 14664 | 45032 | A | 14750 | 34 | 350 | RERGQEGGVAGRVEMDVSVVE RGAYADQIWGRPKGGESRGEK RKGRWVQVRALRARVTPAGL GECKWGRGRGD*VRRVKPRAL RERWGDGSTVSDSTPMKPGLE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14665 | 45033 | A | 14751 | 1 | 1604 | MASKRCIRDFRSRGGKLSFQL YATFRKEGCGPVLANGNPGGG RGQEVSATQDLRRGWGIASSAS RFPWRQSWPGRPRLGNYDSGA PGEAKMPKSGKDKKKGKSKGK DTKKLIKTDSEVVDRAKANASL WEARLEVTELSRIKYRDTSRIL AKSNEDLKKKQCKMEKDIMSV LSYLKKQDQEKDNMIEKLKQQ LNETKEKAQEEKDKLEQKYTR QINELEGQFHQKAKEIGMIHTE LKAVRQFQKRKIQVERELDDEI NDLLVKEKIMQLVQQRSQIQTL QKKVVNLETALSYMTEKEFESE VLKLQQHAMIENQAGQVEIDK LQHLLQMKDREMNRVKKLAK NILDERTEVERFFLDALHQVKQ QILISRKHYKQIAQAANLKMRL EHVQEEQNIPKSEHLMAESTAPI V*IRIFWRPKNGHILKEMWILEI *PGSRRKKYCDCLQK*MAVLL GNTTQSSRPSSSRTMLFLDSGET KEFGDESKLQDKIFITQQIAISD VFW*SGATHYSKRTSGV*HSGK SESLQPRGQRLI |
| 14666 | 45034 | A | 14752 | 95 | 473 | |
| 14667 | 45035 | A | 14753 | 168 | 449 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14668 | 45036 | A | 14754 | 1 | 2000 | MAFEQAKQVVKLALDLWPIGD GPVELQVTVLDQHANWSLRQE QHGKRGPLQFTDVAIEFSLEEW HCLDTAQRNLYRNVMLENYRH LVFLGIVLSKPELITCLEQGKKP LTVKRHEMIAKPPGQKNWEKQ ALPLTGCLTKYPSWAKNIDIIVT CSHFARDLWPEQSIKDSFQKVT LRRYENYGHDLNLFQKKGCEV DECKVHKRGYNGLNQYLTTTQ SKIFQCDKYVKVIHKFSNSNRH KIRHTGKKPFKCIIECGKAFNQS STLTTHKKIHTGEKPFKCEECG KAFNWSSHLTTHKRIHTGEKRY KCEDCGKAFSRFSYLAHKIIHS GEKPYKCEECGKAFKRSSNLT HKIIHTGEKPYKCEECGKAFKR SSILTAHKIIHSGEKPYKCEECG KAFKHPSVLTTHKRIHTGEKPY KCEECGRAFKYFSSLTTHKIIHS GEKPYKCEECGKAFNWSSHLT THKRIHTGEKPYKCEECGKGF KYSSSLTTHKIIHTGQQPFKCEE CGKAFKCFSSILTTHKRIHTGEK YKCEECGKAFNSSSHLTAHKRI HTGEKPYKCERCCKAFKRFSIL TRHKRIHTGEKPYKCEECGKGF KCPSTLTTHKTLAEIHAGKKPNK *E/ECSKAFKDTALTRHKIIRTG EKPCEFDECRKAFNQLSTFTKY |
| 14669 | 45037 | B | 14755 | 269 | 1131 | |
| 14670 | 45038 | A | 14756 | 2 | 149 | ALFRAGRQECLSLKLCPQPPL SPTCFVPGR*GFYLHFFQRCAA QRGGI |
| 14671 | 45039 | A | 14757 | 2 | 175 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14672 | 45040 | A | 14758 | 1523 | 2667 | PLLVIHRQTGSGEDLQQTPADL QQRDLLERKLTNRNE*HQHQQ KRHPLKNP'IQMSP/CIKDQRYIN PRSTIKLELGIKKL TENCTTTWK LNNLLLND CW EKQERSKTDTL TSQLELEKPEKTNSKASRRQEI TKIRAELEKEIGTRKTLQKINKCG SWFFEKINKIDRSLARLIKKKRE KNQIDTIKNDEADITDPMEIQT TNREYYKHL YANKLENLEEMD KFLDTYTL PRLNQEEVESLNRPI TSSEIEAVINSLPT/KKRSPGSDR FTAEFYQRYKEEL\VPFLLKLFQ TIEKEGLLPNSFYEDSIILIPKG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHNNQIDFIP GMQG\WFNIHKSINVIRHLNR |
| 14673 | 45041 | A | 14759 | 640 | 1771 | APVARMTA/PLFYTALLVFSAL GNILALCLTCQKRRKINCTGIY LVHLAVSDLLFTVALPGRVVC YVLGSSWPFKGGLCRLTAFVL YTDYGGVYLMACVSVDHYP VVC AHWGPCLRTAGRARLVC VAIWTLVLLQTMPLLLMPMTK PLVGKLACMEYSSMESVLGLPL MVLVAF AIGFCGPVGII LSCYM KITWKLCSTAGRTQ*PAGKDTT GGASPGGSDQPEKTPPAGAAQ EDPVTPRERTPPAGQPERTQ*PA GKDATGGTAREDPVTSRKGRH WRGCLLTLLMLVAVVVCFSFY HLNIKQFMARGMLHLPSCAER RAFLLSLQATVALMNMNCGI/D PIIYFFASTHYRKWLLGILKLKG SSSSSSSSSTLY |
| 14674 | 45042 | A | 14760 | 1 | 401 | MVLVQWLTAITS AFWETQNK SLQFEDK WDFMRPIVLKLLRQE SVTKQQWFDL FSLGATLQDSSG PLL TGKLKKKRKVSGTKY/IEAS SATSLKATTDTHLLLYNPFWI PLTLI*HLCWLQRFA*SCDTPH P |
| 14675 | 45043 | A | 14761 | 184 | 2720 | |
| 14676 | 45044 | A | 14762 | 34 | 251 | |
| 14677 | 45045 | A | 14763 | 2 | 452 | LQIEII*ALEELAAKEKANEDAV PVCLAADFPSAGMGSSCDGQE DELDIKSRAAYNV TLL/NFMDP PKIPHLKEKPYFGMRKMAVRW HHAENLVDRPQVEESED SHLE GRDLDTWHVGVKISWDVKTPG LATPQGDCYFMLGNLWRTKIIL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14678 | 45046 | A | 14764 | 1 | 1701 | MPFKCKKQHTFNKTSPKEGAI FTHGCLCTSPFNSESEHLGNL KLSSWEHLHHRSSQQTLSVRLH VPTQPVEHEFIQLIYIHTGAKL QASKVIIATKDGKRRKSPLWQL KYPKLILREASSVSEELHKEVQ EAFLTLHKHGCLFRDLVRIQ GK DLLTPVSRILIGNPGCTYKYLNT QLFTGPFVPKGSNIKHTEA*IA AVCETFLKLDYLIQETIQALEE LAAKEKANEDAVPLCMSADFP RVGMGSSYNQDEVDIKSRAA YNVTLLNFM DPQKMPYLKEEP YFGMGKMAVS\WHHDENLVD RIQLQLWDPVDGTTASSAVPKQ GRDKRREVPNTLSQPNSEGLI SAFHSRCVHAVFYKLTSAPKTT SLPDVPSDLLAEGLAASRAGQA LWRCDKKSLLTLVRKINLQ GK RDGGRSATNQSQPHLDNTGL ERQLEQKVGRCSR PWRLGHL EGNAQKGHLLHGVNKNQHL LRRHGV SIRAGRAPHLAAADT APGRISCLGHSEALKPRIQAGGL GAESIWQVLWEGGSNSSVFCR HDEEPAAELPLPGKQASGGHM |
| 14679 | 45047 | B | 14765 | 16 | 1462 | |
| 14680 | 45048 | A | 14766 | 89 | 566 | MEQGSITQAWREDALVLTQK GLVSK\SSPKRPHVCHILKAPFC CSCTQHVGQSSSPR*ANPHIRRE STPIAMSDQLQRLQYQFYQIPG TCLLPEVTEKNQGRICMVTDL ETLVHSSFKPISNADCLVPVELE GTMHQIHVLMRPYMDEFLT*M EEMF |
| 14681 | 45049 | A | 14767 | 1 | 305 | LSGLEMFQAGAGAPSSPGY*GS CWAISWSGPPDKHSNRGASCG LETWAGAAATDTAGHPAAGR C*A*AGSGGDQGTGSTAPLPAT P*PLQSLV*AAALPA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14682 | 45050 | A | 14768 | 1070 | 2653 | SLKPCMACL*HS*EKTLSOSSG RSWICAVSFGSPGPAAPLPEL SFPLRPGYTKLLPHATEEVSPFG SGAGRKLGPMLPSTAELCPGTR ARWSEGYRDLGRQAQDLQAG RKS VVTWALEGHPREEERAAA KVQQCQRMWEGCSDPQELIPR PGRNPDPVPDSAVALLPWGPSR VPDLGPDSEHR/PAHSRVQYWL HKAPAPPSPPQLAEPATPPTRP SSPGSRSPSSWHRLRSWSLNAD PWRPRPADLPPGNPAPPSRGA HGTWKG D VRPLGRGSR LFSV CGRREVQRAARRVGTTPGWR APGREREASR*QPPGTG/PASP MGRASSSGSRVSPGPIRRTAPW EGCSCSRHHWGKGLGPPDGE PG\PGSS*VAQPTVGRRSLGPG GAAPARDAAAATPPGDAAARE GSGRHLRAPASRPQHQPSPRS HPPASATTASLQKFRSASSEPPS EDRPFDFSPTAPPQCPRVAPSAG AR*R/AGGRLPE/PR/RPGPWGG GSRTNLTIPTSLHGTPAAARTS PHRKS R |
| 14683 | 45051 | A | 14769 | 748 | 1073 | SQHFGPRWVDRLRSGVRDQP GQHDKTPS LLEMQKVIAGRAGG CL*SQLRLRLRQENPLNPGGGG CSELRSG LCTSVWATGRDSI*K KKKKKKKKRKPWSLLSLIVLVQF |
| 14684 | 45052 | B | 14770 | 59 | 466 | |
| 14685 | 45053 | A | 14771 | 2 | 3184 | HRTGIPGSTISSPGGETVPE\MTA AMRERFDRFLHEKNCMSDLLA KLEAKTGVNRSFIAL\GVIGLVA LVLV\GYGASLPLQPLLGFY PA\YISIKAIGE/SPNKEDDTQW/ V*TYWV\YGVFS\IAE\FFSD\IF LSW\FPF*LHG*KCGFLVGWCN GPEAPSKWGLKLL*QAASSGPF LSLEATKSQIGQVLVKD\LKDQ GPKETADAIH*KPKKSLP*ILL G*KKKKK |
| 14686 | 45054 | A | 14772 | 14 | 455 | PQFPCCRFRALSEEELDNEDYY SLLNVRREASSEELKAAYRRLC MLYHPDKHRVPELKSQAERLF NLVHQAYE\VERRRTPAEIRE EFERLQREEREERLQQRTPNKG TISVGVDATDLFDYDEEYEDV SGSSFPQIEINKMHISQ |
| 14687 | 45055 | A | 14773 | 328 | 479 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14688 | 45056 | A | 14774 | 15 | 1095 | KVAKMATALSEEELDNEDYYS LLNVRREASSEELKAAAYRRLC MLYHPDKHRDPELKSQAERLF NLVHQA YEVLSDPQTRAIYDIY GKRGLEMEGWEVVERRRTPA EIREEFERLLREREERRLQQRN PKGTISVGVDATDLFDRYDEEY EDVSGSSFPQIEINKMHISQSIEA PLTATDTAILSGSLSTQNGNGG GSINFALRRVTSAGKWGELEFG AGDLQGPLFGLKLFRLNLTPTRCF VTTCALQFSSRGIRPGLTTVL ARNLDKNTVGYLQWHCSSPLL QVQRPHRNTRACAPEPSFRPFL HVPTWDAECSGARTPSTAWTS AAVKLREACLSGPGSGSHQLLL LTPRSKRRTGGG |
| 14689 | 45057 | B | 14775 | 508 | 1765 | |
| 14690 | 45058 | A | 14776 | 2 | 639 | GRRRHRRRHRCRSGDCYLPT GTNTQQPLPPPREPLPELPTP DLSMQNSEGGADSPASVALRPS AAAPPVPASPQRVLVQAASSNP KGAQMQPISLPRVQQVPQQVQ PVQHVYPAQVQYVEGGDAVY TNGAIRTAYTYNPEPQMYAPSS TASYFEAPGGAQVTVAAS/SPP AVPFHSMVGITMDVGGSPIVFS AGAYLIHGGMDRPELLANL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14691 | 45059 | A | 14777 | 1 | 2091 | MKPDDNSTQNEGGQSFEERHE TLQRVKFRGGPKTAPGRKLIAF LGQMNSGTSGGQRPVPEEELM AGGATCLPNTAEHQPIRMKNL HTPAFRLCPLTLQDNEADAFW HQAQVDWGMPTGKKPQTLGLT YKTTHDLMSQNS/EGGADSPAS VALRPSAA/APPVPASPQMLPLE LVILGVV/PLDKCIPAQWSKEG QTNSYTYNPEPQMYAPSST/AS YFEAPGGAQ\MVGITMDV/GGS PIVSSAGAYLIHGG/MDSTRHSL AHTSRSSPARSFRSNSKAPSSRK FCC*LPTLSSKTL/SLFSKNLLRK LPLGKHSPDSVQWPWIYGLLV AGSESLASLLFPKASSSGETLGF ATGQLAGESRLPSLLAFILVPID VAVGKEQLVTQTTVYRVQGS GQHLNKAWQEPALVNICGMGE KVDVQVGLCQHRAHLDGWNS SRAASVWPGETLTHHQDQCQA NLPPGIETSILGTKGARYPSQE QGGGRVWLERLDPRG/AVSGT DL*CLPQSDVPPGRA*SGGTGD KSISTHDKSGRGNISKYHY/YGIR LKPDSPLNRLQED/TQYMAMR QQPMHQKPRWCRAELGGAGSP LGMEDVSHVFPEFPAPD/LGSF LLQDGVTLHDVKAL/QLVYRR HC/EDVV/MNLQFHYIEKLWLS FWN/SKASSSDGPTSLPASDEDP EGAVLP/KDKLISLCQCDPILRW |
| 14692 | 45060 | A | 14778 | 94 | 3006 | RTRSLTRKAMAEHAPRRCCLG WDFSTQQVKVVAVDAELNVFY EESVHFDRDLPEFGHVLVDVHG VHVHKDGLTVTSPVLMWVQA LDIILEKMKASGFESQVLALSG AGQQHGSYWKAGAQQALTS SPDLRLHQQLQDCFSISDCPVW MDSSTTAQCRQLEAAVGGQA LSCLTGSRA YEFNLVCDRKHLK DTTQSVFMAGLLVGTLMFGPL CDRIGRKATILAQLLLFTLIGLA TAFVPSFELYMALRFA\GL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14693 | 45061 | A | 14779 | 1 | 710 | MGPAAGAPTSRASRGPRAPALR AAVGRRCPRPEMPCQCHPLAR CGLDPAWTQLPQETAGAPRQD PRCTNQLICEHLPLEGLGFGYL GNKDSLRLHVKVVAVDALNVF YEESVHFDRDLPEFGGLASSAV TQSSS/DDLQQVP*SLQSLHAA* SLQTNASPFTFEHSFLGKRHPK GAGQKRAESPTRPPLRLQEAP GELQRPLPYGTQVPAGLCPSVS GLRLRARALLPYRTHSLSV |
| 14694 | 45062 | B | 14780 | 1 | 252 | |
| 14695 | 45063 | A | 14781 | 73 | 198 | |
| 14696 | 45064 | A | 14782 | 762 | 1080 | AGRAEMQQERESHEEAKDPSP LSPREGSQKQQQNVNTSTPSHC PR/PPLRMPPPAPRRVP/CDHPR AEECERKAQHWQAAPPAAPVR DPLGEASWAPESGGDVESLYI |
| 14697 | 45065 | A | 14783 | 1 | 309 | MTKTEREQNEQLDGGGYGERL GEYSLFLLCVPSELNQGKCERV SSYFGMNLSGVLKKLPFPPTRE SWPPPHFTGTPHNHHGGVSNG ALGCAQRCSLHHATNAGGWER GGVSNRLFFLLSASFSDAKIK PAPSPIDHLRAEEC*/PPLSQPP ALVAWCREHLWAHPKAPLLTP |
| 14698 | 45066 | B | 14784 | 1 | 471 | |
| 14699 | 45067 | B | 14785 | 1 | 1143 | |
| 14700 | 45068 | A | 14786 | 1992 | 2205 | WRSMSGLRKRQLASQISYCPC WS\CP*EESHCRRVSPAPLA*LL SPCPAPQQRSHTDPPFPFKHFP LPFSG |
| 14701 | 45069 | B | 14787 | 389 | 973 | |
| 14702 | 45070 | A | 14788 | 287 | 525 | TNPFNLLQH*KKP*CYTYISITD PTDACHKNKAFSSPAVSQLT/CI FSSTAGSFFVLSGHSCGHLAVFS LWPRSPQLPGTR |
| 14703 | 45071 | A | 14789 | 475 | 616 | |
| 14704 | 45072 | A | 14790 | 1 | 704 | MTKWKSNPQIHMEQLRTLSNP NNLEKSNVKTYKAKIFDDNLI QLTFQQHRQDRDTEQEKKEE EREKRKQQQEPLRKAKMQTV RPGFDLTQGPNCCLTPHGKTWSR LPPKNHRRPYTSRPEGPRVKA* NHGPEGRRGTRLPPAAKRAQ AEEAAQ*WPTRSTLRLEVTPRA MPP\SPSEDPRVAGVHPAPPRGP RSDS/APLRPQLRPPRSLFSLASE PAAAGNARGRHSVLALY |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14705 | 45073 | A | 14791 | 200 | 408 | SPHLMSINLITFANFLFPCE*RNS QFLKS/SIFVMWMIHNGMKCRQ LDTCHCRHGTCCKDSICPLEES PLP |
| 14706 | 45074 | A | 14792 | 240 | 771 | GRGMQSPAQVDPAAKRGNIAG HTAHLWPKGGTLPCLF/YHLLI MQIREQP*SSLEYPTF/RILSLVS GTKLNKILANRIRQHKKLIHHN QVGFIPGMQGGGLPTPGSEQGHL RVSPSSPSTVTLKLFNFMEPFE NLNLSKGKASVHTITQENTDSL KVQGSQFSQGHEKRTLCLKVS |
| 14707 | 45075 | B | 14793 | 1 | 1557 | |
| 14708 | 45076 | A | 14794 | 150 | 1668 | ESDARQGPFPLENTTRPHPSCMQ NHGICRSLHPGLCGCPPTARDA APATAGGVPAY/GPLTGAPPG* LPGAGIGSKQSSTMGPSGAGSC LGL*APSQPAD/PGSIQGVLVIA DTE*PLVGGDGGLEAEHQWQ* EAGP/GGLIPKHMNPQSRQQSLF GRRGYRDSSLSVLGRTGQQT* HAELGAGVMGPGGNGR*GH/G PRGLPCLVQRRGPGVA AVAA GVSVA VPSGMLSENGPGCSK/P HSGDAGQRRGLRENL*GVRALI WGAASSFLLTEQDLQELADCL HSGRKTCFFYFQGRGDVAPGPV APAHHRLAGISTV VPEGPLCV GEDRQLPG/GNQRAEPPP*L VRS VSSLTGLPALGPRQMPNAGAG NGSGK*RGVRGSGPDWDCTGT HGGAGTGKLLWAGLSLFPLSG KSEAHQQR AAGHGYGRGLGSP GRPPRSRKGRVLGSESAPA*GSP QPLRSARQKPESSCPRQGQPVG RGPGAPLEAGHCSFPRPLGP ARSLHPDFPQGLQA |
| 14709 | 45077 | A | 14795 | 3 | 374 | RRPPSWG*RGCSQLPECAADGS LEDHGPLPPMVSCFSRHPAGRF LRVFPPSPLLAVDCCWHNNSYV VAVDCCSATSCSLLLYPSQEFPP HKFLVYLVLSWHQLLGGLELIC TQQPVNPVVS DG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14710 | 45078 | A | 14796 | 73 | 890 | MSLVRTDGKVSFPHSRAASSPP PRFAGSLPWTPKGHGFTSFPRL EGYCPS/REGPSDWGRNSFRVSS WAWRPSQGVSHHTPGQGP/PSP GNRDK*VATRKSPGQPGSSPEP GWSLQSTSSPGATRTKGNLNTL KG*KQVVD*WVGVTGWEGS GAPQSPQPSREWRLSPRGVGVV KETWPSPWSGR*APPCGQPQG QQTHMERGGR*G*QVGACGLG P*GQWSSVTNGKDTRAPWSPPP RQRNGRWPAPPPFTFHYYYYY YYYYYYYYYFFFE |
| 14711 | 45079 | A | 14797 | 273 | 678 | TEESTSVLSVPNQTGAGAARIGI VSLRLCGLYVTSPRAARMHIR PHGPWPGGSHHENGEPES/E GAPASASGRGAPEGQAWPPRD AVLSSLMLALFRTKSARHLVLG TRQTAASPFPPFSQPSWYCSLG VDGG |
| 14712 | 45080 | A | 14798 | 551 | 743 | PTRITRSAGSSSWGSCRPRAPAP FSWSRPCLQGPRG*CRGLHSRF YAAP*VQGHVPVHILPYSKFRRG RAALRPRGQWGLDSVLGTAVC GCGP/RSESDICSGR*GPE/WYIS PPVPPHVHRGFQQL\NCARQVG KGGGGPGCPMLGNHSSQVGL GLGGQDQDSLESPGRVSSPSGP SAASDPGG*GFQGNPDVHPAP APPDW |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14713 | 45081 | A | 14799 | 705 | 2299 | KREWRPRHHPLGPPPRCAGRSA PLSGPASPF*WLPPGHGPCGR MCSRAARGGDVTRYTHNTRAP SCPSLHWVGERG*DAHTRTPSC PSLHWVGERG*DAHTRTPSCPS LHWVGERG*/GCPHSGLQLSFP PRSAGCCKALFEAEKSKGDTGL GKRGWAGGGAGGAARPCICNP TVPCPQSTQSPPV/PPGTR*QLG SSASHSRAASSPPPRFAGSLPWT PKGFGFTSFPR/RGGVLPFPEGP SDWGRNSFR/GPAGPSMW*PAP PSDAQVGHGPGRAGLQRCRGR GGHTPFVLA AAAIDSAYFS*/D P*VFSGSNFPHLSCFPG/GCGEGN Q*ARRRPLAGAAALPGPNLES WVCELSVAGPAVWDPVPSP/GD PTTGPESP/RNSAGACGAQGSM R*T*GTPATWSL/GPPPELPGSR HQRQCECGPAHVQERMPGW ACMLKSVAQRGFQRR*QLSKA QAAAWRV\PGGR\GAGKD*GW RRWGVSRGGGGLCCARGGGGS SVRRGEVEGS/GCARGGGGCAG WRALSPSSLPISGAQELGS |
| 14714 | 45082 | A | 14800 | 1 | 267 | CSAGGPWRAPQPRRFHRRRRP AQLPPPLPLPLPASPRIHNRTF PRPSQRTPPPAALGCPEPGS/RS QGRGHARPPGSGEGDPTVSSPG |
| 14715 | 45083 | A | 14801 | 218 | 430 | |
| 14716 | 45084 | A | 14802 | 9 | 201 | |
| 14717 | 45085 | A | 14803 | 1453 | 1936 | EVEKHL CQG*ELLRAQHN*AA ACRRPRPPAPGPQCSAGGPMAR APAPQVPPPPPCSA\PPPLPLPP LPAS/HAHPQPHFRHGRRSALLP RPPWAVRSRGALAGPRTRAAA GLRGGAGAAPAPADARFPASSP AE*PKFPQNSARALTGFPRCTD PTVSSPGY |
| 14718 | 45086 | A | 14804 | 1 | 580 | TSGCSHSLHKPAGVSTRPPTVA SICAPRPTSPLRRGSLTLWFPF GGHLTLETPGFDSCPEEVEGP RFSTFKTS*ARGRRQRCAPRG RREVGPPSAAESGRARGEPPRC RLLCRGGK/DPQPRAGEGEEAAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR CVWGEPPGRRTRLFPDE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14719 | 45087 | A | 14805 | 279 | 1148 | ALHEFAMSRSLHASLH*S**STC P*QQPAPAPAGEPRARFP GKSSS ASSGPG/WPRNHGKQLHLPAQP Q/QQGRISSPRVAGSGCTGRA LLLAAGLQNSTRSLNPRDPPTIL SHRPLQGM/PDAP/RGCSHSLHK P/SRS/TPLSGQL*PPSAPHAPAQ APSVAGPLPCGLSPGDT*RYWR LLRFDSCPEEVEGPRFSTFKTS* ARGGWRQSRVWASARGASTL QASVQGR*NPQPRAGEGEAAA GTPEGSRAGASGSEGALPSAAS PGNSSGRSRPEAGANPKGAPRR FLGGCLL |
| 14720 | 45088 | A | 14806 | 765 | 4270 | SQDTPGDLQCHGDL*DGAVLS EAPGGERVPRDD*GGVCPEGVP HVSLLRDSVAEALQPRGEAGG DQVPEAHARPPSAQR*PAGAGL RLHPPAAGGVPGQSGGHLPKIQ DDLTSKS*INSITKTLFPNKVTL SDSGRA*ILEGHRSTQGS LGLEA DPGTVSHHQHPCPPNAATHHF HRTARPGVQQGPGPASVQQPES DGDGALLRSPCSLLPQGADEVL LQPDGDKQGGPRGRDSESD*G YSERR*AQDEYQGH |
| 14721 | 45089 | B | 14807 | 133 | 2943 | |
| 14722 | 45090 | A | 14808 | 1 | 814 | MEEELLRELLYSENWWSIPYND TIQELCCWAVLKRTFINGNTSR KPGMKMVTGLKKQERRSKQW GCEKEAKFVPDMWIVLEVGRP EERGIDGKRWGKSCSVEQSVW AFQNPISKAQTLNLSMK/AYE KGKEGVEEKFEARRSWFMRKK AISHLHNMEMQGEAASADVEA AVSYPEDLAKIIDESDYTKQWIS NVDKTVFYWKKMPSRFTIATE EKSM PGFKASKDSLTPLLGTNA AGGF*LKPLLYHSQTSRALKN YAKLTLLMLYKWNK |
| 14723 | 45091 | A | 14809 | 123 | 515 | PKQSAKTIWTSTARPEDVVTCS FKEEFLPGNTHHDFSINKRSDPE LEVSRPLARPENFPANRSHSLE L/RPCRGRWAAHWTGCSSLLD ASSAPRTDQPSLWRNLPTASLG GPWSHNQPGIVFQNTYLMKWP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14724 | 45092 | A | 14810 | 279 | 1136 | VDVDLACVRGLLCSCDEFLSW LALNRTVLATPALPSCLSQMAS SLPGLCARTRRGERADSQRGTC AFFSPARTASQAPLVASSVRKQ RVWAPNPLNCHTLPPSRGSQRG GYIGEEGVFGSRVVGIVVPGPN GSPWPLGVQR/PECVLLGVGSG S/SSHELFSEADFISRL LAPSPSP APAS/MGNAIEEEAPELGPLGRV FVDDFHVDYNFIHLHEDLCYGP LEGPDLDLAGTGDRTPLHSRP RASLSPSALRCP*ALGF/WSTLA WGSPNSSSRVPEAQPPAPSLAE |
| 14725 | 45093 | A | 14811 | 1 | 1597 | GGRKAAVGVETRPQGS AQPTW LPVHGDTCTLLLP CRAWWR GGLPWAASVVGAKCVWTPPER GLLMLHKPMPGWSSGYRVVLP AVAFFRLRAQVTKLGEVSLRF LKREAKLCGFLQKSFLALEKR MKASESSRLKLEGLRGELES WEKLRGLMEERLRALQGGHEE SHLLEQCQGLDAAVAQLTKFV QQNQASLNRVLLAEEKA WDA KGRLEESRAGELAAVYQENLE AAQLAGELARQEMHGELVLLR |
| 14726 | 45094 | A | 14812 | 150 | 1625 | CLGKAFSCREL NAYLR LPTFFIV FSLRQPSLRMHSRAWVKTCGA MPCSCCRIRHCSSVTDM AVRSL ALLQLVNRTPLRRRQISAACQR MSTFLFFRACTF*PRNRSSGRH /DLTARPRQAILRQNFLK/RAQS RNL TAPNSPR**LLVKTYRQTS RPVSAAH*CPR*RGRAALAAAC HSGSPGARRQTAGPAEGPAR*T RRDFL**RAACLRRRWK WPE*L *RSRSSSP*SQGSCPPALPAPRR CSAGSRTGPAARWCRA GAGSR RHAGSSSA***SRR*GRSASGRR PRHGGTAGSGRWLWWARCPA *AGIPWPSWPCHSSWP/PQSVRV VSSG*RASLHSPGLDSSGGGLQ SFLLVQLPAQGKTSSQP RHAA APSAAACPHAE*CTLGSCPRSA TLPSTPPRASPPAG\RSAVSPCPP GHEGVLVISKHLLLLLSRSGRG LGGNVVRPCSVQPM DGVGQEL AVADRDQLPCLVCQDGECPLK ASGRPVLGCP |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14727 | 45095 | A | 14813 | 921 | 1446 | ACCISHGNLWHHLDQKHGLQS *GEKSRLFSRPNLQVPVHTGLD HRARYLTGPRKQGHLPWTPGPS SVFDNENFCKLSVGM*TGRASA RQQIQSPFAESGKAFCSDICSVSL RLCVLPHPWNSRLRSPALRNSL KYSVTSSAAARRKLLPLASGPL RLGPRSLPTRLQVLRWEKVASA |
| 14728 | 45096 | A | 14814 | 1 | 675 | |
| 14729 | 45097 | A | 14815 | 1 | 2341 | MASDLVNRCEACDLPQGPISVH QFPRLSNEVTTTTVGRNSES PNQ RSVSGPWTPREVRRGVAAAAH GFSGQNAKWAAHIPATAMSFA LPYSVLHSPHALTTHPLNPGDA VTMPSTSTVSAANASKGRSFS QCFQSTEEGQERRRPRTSQAKV QQGSTAGKVNELITLAGHIKSQ APHGKRKPPPRDSHVICSMLRK RKPDETPSPSSDAQFSGMLAVA VSSLLCPRSSPSQQWHCHSPSTT ILGSSDVSDTSFQPSTKLGPVHG FPPQSRDCILDFELIRKVTGAWS SLTAGSWETKIQEFSEEDILAPH RITPGPHSSKSPVHFLASLWGR KTKLYHHTIQDKEPRSVPEAGS SGRRDGGGAAHSMCLMAPEPD HPGSPNCRSPATLHADADGN LQREAAKCQGDGTQVSTHVDH TSAPRQAETGPATGENEKMESH GRSKRGLVGADQCPAETLDSY TLLVGHKKRDKDRQTPGPAPQ VNSFVPENYLLRGPLAPLGS AIS MKTAGAVHIRPSGDLGRAPAP AVRPRPRPPRRRRLPGPAHLP GAPRPPAPAPLSRRAARQSPAA AAAPPPGCE/RRG/PAGPASGAG PPAPAHGARPGGKPAANPPRAP QP*P/RRRRSRRAQPRPGPAPL SRMRAEGPARALRPPPHYQPEL GPPSETVGPVTELLAPIPTARFP TRSHYPVTASPARSS*TSGLD* |
| 14730 | 45098 | A | 14816 | 44 | 455 | HLNRNRTR/PSQITPHIYNHLIFDK /PLFNIWWWENWLAICRKLKLD PFLTPYTKINSRWIKD*NIRPKSI KNLEENLGNTIQHLG/IGKDFM TKTPKAMATKAKIDIWDLIKLK SFCTAKETIIRVNRLPT*WEKIF AIYP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14731 | 45099 | A | 14817 | 1 | 279 | IQDIGMGKDFMTKTPKAMATK AEIDKWDLIQLKSFCTLKEITIR VNRQTTEHYPSDKGLISRMLP NF*RLFPAS*KKPPLFDIGKTEK TNYS |
| 14732 | 45100 | B | 14818 | 1 | 2025 | |
| 14733 | 45101 | B | 14819 | 1 | 3570 | |
| 14734 | 45102 | B | 14820 | 1 | 1380 | |
| 14735 | 45103 | A | 14821 | 1391 | 2742 | KKRESSLTHVMRPASF*YQSQA ETQQKKRILDQYP**TLMQKSSI K/YLAKRIQQHIKKLIHHDQVGF IPGMQGWFNIRKSINVIQHINRA KDKNHMIISIDAEKAFDKIQQPF MLKTLNikleEETTVKFIWNQ KRAHIAKSILSQKNKAGGITLR DFKLYYKATVTKTAWYWYQN RDIDQWNRTEPSEITLHIYNYLI FDKPEKNKQWGTDLSFNKWC WENWLAICRKLKLDPFLTPYTK INSRWIKDLNVRPKTIKTLEENL GITIQDIGMGKDFMSKTPKAMA TKAKIDKWDLIKLSFCTAKET TIRVNRQPTKWEKIFTTYSSDK GLISRIYNELKQIYKKKTNNPIK KWAKDMNRHFSEEDIYAAKKH MKKCSSSLAIREMQIKTTMRYH LTPVRMAIHKSGNNRHAPFSIH THIMFGSLYLQIQKDLSILGFW YPRGILEPIY |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14736 | 45104 | A | 14822 | 1 | 1698 | MEDEMNMKQEGKFREKRIKR NEQSLQEIWVYVVRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIIQIEIQRMPPQRYSS RRATPRHIIVRFTKVEMKEKMS RAAREKEIQTTIREYYKHLNAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAIFYQRQSESQI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMFTFFTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLDLP FLTPYTKINSRWIKDLNIRPKTIE TLEENLGITIQDIGMGKDFMSK TSKAMSTKAKIDKWDLIKLSF CTAKETIKVNRQPTKWEKIFA TYSSDKGLISRIYNELKQIYKKK VTNNPIKKWVKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIK TTMRYHLTPV |
| 14737 | 45105 | B | 14823 | 91 | 1596 | |
| 14738 | 45106 | A | 14824 | 1 | 2757 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14739 | 45107 | A | 14825 | 1 | 2677 | MGKKQSGKTGNSKKQSASPPP KEHSSSPAMEQSWMENDFDEI NKIDRLLARLIKKKGEKNQIDT TKNDIGDITTNPTIEIQTIREYY KHLTYTNKLENLEEMDKFLDTY TLPTINQEEIESLNRTITGSEILAI INSLPTKKSPGPDGFTAIFYQRY KEELVPFLKLQFSIEKEGILLN SFYEASIIIPKPGRDTTKKENFR PISLMNIDAKIFNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNIR KSINVIQHVNRTKDKNRMIISID AEKAFDKIQPFMLKTLNKLGI DGTYLKIIIRAIYDKHTANIILNG QKLEAFPLKTGTRQGCPLSPLL FNIVLEVLARAIRQEKEIKGIQL GKEEVKLSLFADDMIIYLENPV SAQNLLKLISNFSKVSRYKISVQ IPQAFLYTNNRQTESQIMSELPF TIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTKKWKNIPC SWAGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKN KAGGITLPDFKLYYKATATKTA WYWYQNRDLQWNRTEPSEIT PHIYNYLIFDKPDKNQWKGDS LFNKWCWENWLAICRKLKLDP FLTPYTKINSRWIKDLNIRPKTI KTLEENLGITIQDIGMGKDFMS KTPKAMATKAKIDKWDLIKQE SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRIYSELKQIYKK |
| 14740 | 45108 | B | 14826 | 1 | 1186 | |
| 14741 | 45109 | A | 14827 | 1 | 2304 | |
| 14742 | 45110 | B | 14828 | 1 | 2995 | |
| 14743 | 45111 | A | 14829 | 1 | 3095 | |
| 14744 | 45112 | A | 14830 | 1 | 3654 | |
| 14745 | 45113 | A | 14831 | 1 | 3189 | |
| 14746 | 45114 | A | 14832 | 1 | 2064 | |
| 14747 | 45115 | B | 14833 | 1 | 3031 | |
| 14748 | 45116 | A | 14834 | 1 | 3192 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14749 | 45117 | A | 14835 | 1 | 3210 | MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRIKNLTQNRSTTWKLNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKA VCRGK FIALNAHKRKQERSKIDTLTSQ KELEKQEQTHSKASRRQEITKIR AELKEIETQ |
| 14750 | 45118 | A | 14836 | 1 | 3144 | |
| 14751 | 45119 | A | 14837 | 113 | 1336 | PTLAGTGNQETSHLGFNAIPIKL RMTFFTEL/EKTTLKFIWNQKR ARITKSILSQKNKAGGITLPDFK LYYKAIVTKTVWYQNRDID QWNRTEPSEIMPHIYNLIFDKP DKNKKWGKDSL FNKWCWEN WLAIRKLLDPFLTSYTKINS RWIKDLNVRPKTIKTLEENLGN TIQDIGMGKDFMSKTPKAMAT KDKIDKWDLIELKSFACTAKETI RVNRQPTWEKIFATYSSDKGL ISRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYAAKRHMK KRSSSLAIREMQIKATMRYHLT PVRMAIIKSGNSSRSNIVHSVT QANALESSWIPLFLIPHIQYISKP QASSFKMYHVTDPILPPSSQHL DQAAIINLCLQWPLLWFECMCP SKIHMLKLTPO |
| 14752 | 45120 | B | 14838 | 1 | 3127 | |
| 14753 | 45121 | A | 14839 | 1 | 2742 | |
| 14754 | 45122 | A | 14840 | 1 | 1998 | |
| 14755 | 45123 | A | 14841 | 1 | 3030 | |
| 14756 | 45124 | B | 14842 | 1 | 2558 | |
| 14757 | 45125 | A | 14843 | 1 | 3828 | |
| 14758 | 45126 | A | 14844 | 1 | 4134 | MRKKQSRKTGNSKKQSTSPPPK ERSSSPAMEQSWTENDFDELRE EGFRRSNYSKLQEEIETKGQEV ENLEKNLDKCITRITNIEKCLKE LMELKAKARELHEECRSLRSRC DQLEERVSVMEDEMNMKQE GKFREKRIKRNEQSLQEIWDYV KRPNLPPIDVPESDRENGTKLE NTLQDVIQENFPNLRQANIQI QEIQRMPQRYSSRRATPRHIVR FTK VEMKEKMLRAAREKAFKQ ASRREDDIAKVTSQ |
| 14759 | 45127 | B | 14845 | 1 | 3555 | |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 14760 | 45128 | A | 14846 | 1 | 3345 | |
| 14761 | 45129 | A | 14847 | 1 | 3451 | HTKNPSVHHHRQRPKVDKTTK MGKKQNRKTGKSKTQSAFPPP KERSSSPAMEQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRN WIKSQDPSLCCIQETHLMCRDT HRLKIKGRRKIYQANGKQKKA GVAILVSDKTDKPTKIKRDKE GHYIMVKGSIQQEELTILKIYAP NTGSPRFMKQVLSDLQRDLDS HTLIMGDFNTPLSTLD |
| 14762 | 45130 | A | 14848 | 1 | 2606 | MVASRSSRVGVFYGGQNSVDG VSRSDGSLNELCLYRPPTGAY LAYDTLDVLP SGQFTVNTPPID VNGKSL LALLWEHTSLLTSMG GGRWAMQPLGQLGQLEHLGD RRDQVLD RSGRSRLDAAQHL RHRPDRRPQGMVGVLTNQKEP RTRWIHSRILPEVQGGTGTVPSE TIPIDRKEGILPNLFDEASIILIPK RGRDTTKKENFRPISLMNIDAKI LNKILANRNQQHIKKLIHHDQV GFIPGMQGWFNICKSINVIQHIN RTKDKNHMIISIDAEKAFDKIQ QPFMLKTLNKL GIDGTYLKIIRA IYDKPTANIILNGQKLEAFPLKT GTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSA YKINVQKSQAFLYTN NRQTESQIMSVFPFTIASKRIKY LGIQLARNAKDLFKENYKPLLN EIKEDTKKWKNI PCSWVGRINI VKMAILPKVIYRFNAIPIKLPM FFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLHY KITVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFDKPEK NKQWGKDSL FNKWCWENWLA ICRKLKLDPFLTPYTKIHPRWIK DLNVRPKTIKTLEENLGNTIQDI GMGKDFMSKTPKAMAAKAKI DKWDLIQLKSFCTAKETTIRVN |
| 14763 | 45131 | A | 14849 | 1 | 2862 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14764 | 45132 | A | 14850 | 1 | 3724 | MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVVSAMEDEMNMKRE GKFREKRIKRNEQSLQEWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLRQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL |
| 14765 | 45133 | A | 14851 | 2 | 2375 | |
| 14766 | 45134 | A | 14852 | 1 | 2376 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKGREITNCLSDHS AIKLELRIKNLTQNRSTTWKLS NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDTFKAVC RGKFIALNAHKRKQERSKIDTL TSQKLELEKQEQTHSKASRRQE ITKIRAELEIETQKTLQKINESR SWFFERINKIDRPLTRLIKKKRE TNQIDAIKNDKGDITADPTDRQ TTIREYYKHLANKLENLEEM DIFLDYTLPRLNQEEFESLNR P ITRSEIVAIINSPLTKKSPGPDGF TAEFYQRYKEELRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMFFTELE KTTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWYRTEP LEITPHIYNYLIFDKPEKNKQW GKDSLFLNLCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKLEENLGITIQDIGMGK DFMSKTPKAMATKDKIDKWDL IKLKSFACTAKETTIRVNRQPTK WEKIFTTYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKHKMKCCSSSLAI REMQIKTTMRYHLTPVRMAIJK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14767 | 45135 | A | 14853 | 1 | 1576 | MDKFLDITYTLPRLNQEEVESLN RPITGAEIVAINSLPTKKSPGPD GFTAIFYQRLISNFSKVSGYRIN VQES\QAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILP/KEL EETTLKFIWNQKRARIAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDRDQWNRTEP SEIMPHIYNYLIFDKPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFLTPYTRINSRWIKDLHV RRKTIKTLEENLGNTIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYNEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAAKKHMKKCSSLA IREMQIKTTMRYHLTPVRMAII KKSGNN/R/CAPGTPERQNHSL WKGS*SQEPSGLAQWIPLPWS AS*DPLA*NSCCQHSLKSTWD AQACARKLRTLKGYRNCQLE |
| 14768 | 45136 | B | 14854 | 328 | 1467 | |
| 14769 | 45137 | A | 14855 | 3 | 3412 | |
| 14770 | 45138 | A | 14856 | 1 | 2907 | MDKFLNTNTLPRLNQEEVDSL NRPITGSEIVAINSLPTKKSPGP DGFTAIFYQRYKEELRIKYLGI QLTKDVKDLFKENYKPLLKEIK EDKNKWKNIPCSWVGRINIMK MAILPKVIYRFNAIPIKLPMTFFI ELEKTTLKFIVNQRALIAKSIL SQMNRAGGIMLPDFKLYYMAT VTKTAWYWYQNRDIDQWNR EPSEITPHIYNYLIFDKPEKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLTPYTKI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14771 | 45139 | A | 14857 | 1402 | 3004 | TEPKTKTT*LSA*MQKGPLTKF NNPSC*KLLIN/IVLEVLARAIQ EKEIKGIQVGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLNEIK EDTNKWKNILCSWVGRINIVK MAILPKVIYRFNAIPIKLPMFFT ELEETTLKFIWNQKRARIAKAIL SQKKKAGGITLPDFKLYYKATV TKTAWYWYQNTDIEQWNRTEP SEIMLHIYNYLIFDQPEKNKQW GKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNV RPKTIKTLEENLGITIQDISMGK DFMSKTPKAKATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELK QIYKIKTNNPIEKWVKDMNRHF SKEDIYAAKKHMKKCSSLAIR EMQIKTTMRYHLTAVRMAIHKK SGNNSLIVGASMDTSLSGPIPY DIQHFD RFGSVTVRRGCAIEFY. |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14772 | 45140 | A | 14858 | 884 | 2925 | GIKYLGIQLTRDVKDLFKERS/Y EPLLNEIKEDTNKWKNI PCSWV GRINIVKMAILPKVIYRFNAIPIK LPM TFFTELEKTTLKFIWNQKR ALIAKSILSQKNKAGGITLPDFK L YYKATVTKTAWYWYQNRDI DQWNRTEPSEITLHIYNYLIFDK PEKNKQWGKDSL FNKWCWEN WLAICRKLKLPFLT PYTKINSR WIKDLNVRPKTIKTLEENLGITI QDIGMGKDYMSKTPKAMATK AKIDKWDLIKLSFCTAKETTIR VNRQPTKWEKIFATYSSDKGLI SRIYNELKQIYKKKTNNPIKKW VKDMNRHFSKEDIYA AKKHM KKCSPSLAIREMQIKTTMRYHL TPVRMAI I KSGNNSPTCVSQD WKL TQAVGLWSAEAEAPKSAQ RRPLAEGHRAAVQRDGSGLQL LCTVKLQVLP CIIAQNGGRKA TSSLEAELTSWRPLCLEDGTGF RGEDTLETVNAEGRENRRKAG HRAAGSSASRRCRNTGRSVQRL RPQKTQAFPTHCHFCLILVVKA TQLNPKSRVRKVFPAPMKHGK ALAGPWANICAGKSSNEIRTC RHGCGQYSAQRSQRPHQGV DI LCSAGSTVYAPFTGMIVGQEK YQNKNAI NNGVRISGRGFCVK MFYIKPIKYKGPIKKGEKLG TLL PLQKVYPGIQSHVHIENCSSDP |
| 14773 | 45141 | A | 14859 | 1 | 2577 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14774 | 45142 | A | 14860 | 3019 | 5574 | RETRGEVKNSKNQSTSAPPKDC SSLADPKKIQTIREYYKHLYPN KLENQEEMDKFLDTYTLPRLN QEEVESLNRPI TGSEIVAIINSLP TKKSPGPDGFTAIFYQRYKEEL VPFLLKLFQSIEKEGILPNSFYE ASIIIPKLGRDTTKKENFRPISV MNIDVKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNHHSI NVIQHINRTKDKNHMIISIHAEK AFDKIQQHFM LKTLNKLIGDGT YLKIIIRAIYDKPTANIILNGQKL EAFPLKIGTRQGCP LSP LFNIV LEVLAIRAIQEKEIKGIQLGKEV VKLSLFADDMIVYLENPIVSAQ NLLKLISNFGKVS GYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNI PCS WVGRJNIVKMAVLPKLPMTFFT ELEK\TTLKFIWNQKRARIAKSI LSQKNKAGGITLPDFKLYYKAT ATKTAWYWYQNRDL DQWNRT EPSEITPHIYNYLIFDKPDKNKQ WGKDSL FNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKDL NIRPKTIKTLEENLGITIQDIGMG KDFMSKTPKAMATKAKIDKW DLIKQESFCTAKETTIRVNRQPT KWEKIFATYSSDKGLISRIYSEL KQIYKKKTNNPIKKWAKDMNR HFSKEDIYAAKKHMKKCPSSLA |
| 14775 | 45143 | A | 14861 | 1895 | 6140 | |
| 14776 | 45144 | A | 14862 | 1 | 2875 | MKAEIKVFFETNENKDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKIDTLTSQLKELEKQEQT HSKASRRQEITKIRAE LKEIQTQ KTLQKINESRSWFFERINKIDRS LARLIKKKREKNQIDTIKNDKG DITDPTEIQTIREYYKHL YAN KLENLEEMDKFLDTYTLPRLNQ EEVESLNRPI TGAEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQP KKENFRPISLMNIDAKILNKILA KRJQQHIK |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14777 | 45145 | A | 14863 | 2843 | 4460 | HQHQQKPHPHRNPIQKSPTS KT KVLEVLARAIRQEQS/GIQIGS QEVKLSLLEDDMIVHLENPIISA KNLLQLISNFTK VSGYKINVQK SQAFPYTNKTQIENQIMSELPFT IATKRIKYLGIKLTRDVKDLFK NNYKPLFKEIREDTNK WKNIPC SWVGRINIVKMAILPKVIYRFN APIKLPMTFFTELEETTLKFIW NQKRARIAKSILSQKNKAGGIT LPDFKLYYKATVTKTAWYWY QNRDRDQWNRTEPSEIMPHIYN YLIFDKPEKNKQWGKDSL FNK WC*ENWLTICKRLKLDPFLTPY TKINSRWIKDLNVRPKTIKTL EE NLGITIQDIGICKDFMCKTPKA MATKAKIDKWDLIKLSFCTA KETTIRVNRQPTKWEKIFATYS SDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSKEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMAIHKSGNNRC WRRCGEIGTLLHCWWDCKPVQ PLWKS VWRFLRDLELEIPFDP AI PLLG IY PKGYKSC |
| 14778 | 45146 | A | 14864 | 1 | 8335 | MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRLRS RCDQLEERVSA MEDEMNMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNKDTQELNSSL HQADLIDIYRTLHPKSIEYTFFS APHHTYSKIDHIVGS |
| 14779 | 45147 | A | 14865 | 1 | 3166 | MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSMRQKVNK DTQELNSALHQADLIDISRTLHP KSTEYTFFSAPHHTYSKIDHIVG SKALLSKCKRTEIITNYLSDHSA IKLELRIKNLTQSRSTTWKLN LLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDAFKAVCR EKFIALNAYKRKQERSKIDTLTS QLKELEKQEQT HSKASRRQEIT KIRAE LKEIETQ |
| 14780 | 45148 | A | 14866 | 1 | 3912 | |
| 14781 | 45149 | B | 14867 | 1 | 2832 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14782 | 45150 | A | 14868 | 1944 | 3531 | LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARMAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQDQWNRTEP SEITPHIYNLYLFDKPDKNKQW GKDSL FNK WGWENWLAICRKL KLDPF LTPYTRINSRWIKDLNV RPKTIKTLEENLDITI QDIGMGK DFMSKTPKAMATKAKIDK WDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKKHMKRCS SSLAIRE IQIKTTMRYHLTPVRMAIHKKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMRKNTK TLI |
| 14783 | 45151 | A | 14869 | 1182 | 3891 | KMIKGISTTDLTEIQT TIREYYK HLYANKLENLEEMDKFLDTYT LPRLNQEEVESLNR PITGAEIVA IINSLPTKRSAGPDGFTA EFYQR YKEELVPFLKL FQSIEKEGILP NSFCEASIILIPKPGRD TTKKENF RPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFN IRKSINVIQHINRAKDKNHMIISI DAEKAFDKIQQHFM LKTLNRL GIDGTYFKIIRAIYDKPTANIILN GQKL |
| 14784 | 45152 | A | 14870 | 997 | 1161 | CTSTVIMSICTKLQNK EHVIEAL RRAKFKFPGHPKIHISKK*DFT KFNADEFED |
| 14785 | 45153 | A | 14871 | 1 | 1458 | |
| 14786 | 45154 | B | 14872 | 53 | 1468 | |
| 14787 | 45155 | A | 14873 | 1819 | 2235 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14788 | 45156 | A | 14874 | 707 | 1613 | VRARAGERARVVRENGKAELP VALVLP SRALSHTFTCTDLKVQ FHQRLRLQEKSGKFIGSNMSQE SDNNKRL VALVPMPSDPPFNTR RAYTSEDEAWKSYLENPLTAA TKAMMSINGDEDSAAA/HRPAL *LLQENQSEPIPREGVGWG*GE ER\ERMTEEEQEGEGGGGGRGG GEGEEEEEEEDVEEEEEEEEEE EKEEEEKGGEKEEENEKEKQR EGRRGKETSNGQMVRPRLPP HQEHSRNYLVFIMDSNMIEICF REASISPKAQAYVLIPDFKNCIY GWEEDSIEILWGLPGSHVL |
| 14789 | 45157 | A | 14875 | 3 | 346 | QRSKCKVPGLGKPLTPPKPE K\PQGQKDRRPTGFKP*N*RRRR SEKSLRFFPPGS/PQAVPIPVGFS FDTNL*HFL*KPLIFIMGGTVSL PHPRSPSAPPGTPQRPMTFCHLK Q |
| 14790 | 45158 | A | 14876 | 1868 | 2666 | GLLLSPFQGLQGVAPRKTRSNL HPGSLAHL SHQPPAPWPPRGLW PPGQETSCHCASGRALGTGSPR PPHAPWLHLEPQRAPHSGAPSP GSSPSAPLHIPVAPENLQSLGHR SPPNPSGPD CYPSGSP/PPSSLD SPGLQTAPGAMFLSPRSGVQSA CPTPRSLDLRNSPASTPDQSVCP TPLSLAWLWPPPSPTSAKSLLFT LTSEVQSFSPPTIPPSSDPPLSK QPASGSCLS SSGHLTSPSVPRHSP WPRSSPQNPHSWTL PSS |
| 14791 | 45159 | A | 14877 | 762 | 1528 | AIPGGAAWPFRAEGAQGPGRK LTFKPLGAQRQSVSGGSEVPPL PLHLKMAPEMPVAL*SPGTGV HPSLLPPT/GPKVPPGRIDRGVPV TLAPQVGTAPIQWHCRGSRCP G/SRPPGGWR/RPCQAPAPPLGQ HLPRLLPPPTGPQGPRPLTPSEP PPWSCWLPASPPAGPSRRVGG GPGTCQGLLR S*GLLLSPFQGL QGVAPRKTRSNLHPGSLAHL SH QPPAPWPPRGLWPPGQETSCHC ASGRAVGTGSRRPRA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14792 | 45160 | A | 14878 | 1 | 963 | MARKDCCSPPGDSSPGRLPLVL PAQCLVLLRLQITAFSSIHVAAN DMMSFFLMAKQDSIAYKYRIF IHSSVDGHHARPLSPSLVVENG GKQVFLLCSDNASPEVSTVALA SCPGTFPRHCGAAESTHICATG LGELTPQGHGHIPNKLACCAT GLEELVPRDHGKLGISWFGFIA GAYLNLARVVGECQGSYGYLS LHHYCYCHYYHYCHYHYHAA TY*NHYYHYHH/HNNSYHHH SYHYHYSYHFYHYHYNCYHHH YHCRHYHHPHDYYHYHA/RHY SLYYCHYLCHYYRYCYHDHSS HQHNHHECLP*VRHSAEHLQY |
| 14793 | 45161 | A | 14879 | 105 | 1448 | CHQPPASPFSSRREPGGSEKPPER GCPAWEPAQAQGPVQPLGEDGP RLCQPPPPSPDHALG/PYGHQRS GRPTLPGPRKPAKKRGR*PSSS TGQ*SHRPTTGTPGGQAGGSG* VTAGGQ*PPQNL*AKISCEMP GPSPGMQQGVKHPSLFSHQTV AKGFTTRWNCRQVCPHRGERK WISSVRPCGGALAPSCA/DGLR GRRTLGSQPLW/PPAAVSAVG QLQPPCHTLTPHPLQNSTQHAE PQRGSVYSL*EGTSPILAAVPFA PHIEKRPFSTFPAGDA*PSEAHA/ PGPACCHSPGGLEGVSRAGPG TSAGRIPGNRERAWPPHSGPS TPPDTSCG/SPGPQLARAGSRA NGSTLPPTRQGFPLGRKDSAGA CGQP*AEGAAAGPSRSPAAER AVLPLPRIGRRKCRGGGPGVET GVSGARRGGDRSGCSAALDA EAPASLAGVSIREG |
| 14794 | 45162 | A | 14880 | 1 | 2421 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14795 | 45163 | A | 14881 | 1080 | 2571 | VHCRFWILALCQMSRLQKSPLL FNIVLEVLA KA I K Q E K I K G I Q L GKEEVKLSLFADDMIVYLENPI V/SAQNLLNLISNFSRVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTKKWK NIPCSWVGGRINIMKMAILPKVI YRFNAIPIKLPLTFFTDLERTTL NFICNQKRAPTL PQVQSLS\QKN KAG\GITL P D F K L Y L Q G L Q * P K TAWYWY\QNRDIDQWNRTEPS EIMPHIYNYLIFDKPWEK/HKQ WGKDSL FNKWCWENWLAICR KLKLDPFLTPYTKINSRWINDL NVR\PKTIK\TLEENLGIT\IQD\IG MGKDFMSNKTPKA\MA\TKAKI DKWDL\KLKSF\CTAKETTIRV NR\QPTKWKKIFTTYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYA AKKHKM KCSTSLAIREMQIKTTMRYHLT PVRMAIIKKSENSRCWR |
| 14796 | 45164 | A | 14882 | 136 | 420 | RESRNL SRGESEDP A EPSRNG *EHPLCYLQ*EFLQVLTMLQAE GTMHHFRSICQVNRNFLERGH/ SPPSPAPPETHGTGSPRPPSGRSR IRAYLH |
| 14797 | 45165 | B | 14883 | 1 | 1197 | |
| 14798 | 45166 | A | 14884 | 3 | 538 | GAGTDGGRTPAPRAFPDPLGEA RTSAPTGPAPGGASAAAPAA VRPAEPA AEETQE QP RAGKRAI HEYRYVYVQQRKTD PQPAVA VFGIPADGD*VSRTAYHAHQPL AWSGR/E*MCLSMAMWNT*ST MKK*ISIRVISRCSGPVHRTN*QI PEPVRAWRF LICRCICFSPGRWI KT |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14799 | 45167 | A | 14885 | 1208 | 2765 | KMAPTWDKMVSSAQMGFNLQ ALLEQLSQDELSKFKYLITFSL AHELQKIPHKEVDKADGKQLV EILTTHCDSYWEMASLQVFEL MHRMDLSERAKDEVREAALKS FNKRKPLSLGITRKEPPLDVDE MLERFKTEAQFTETKGNVICL GKEVFKGKKPKDKNRCRYILK TKFREMWKSWPGDSKEV/RGY G*EIQDADPIQQPQGASRALPY TVVLYGPAAGLGKTTLAQKLML DWAEDNLIHKFYAFYLSCREL SRLGPCSFAELVFRDWPELQDD IPHILAQARKILFVIDGFDELGA APGALIEDICGDWEKKKPVVPL LGSLNLRVPLCIENKLGVGGED WGDQLRVYWWNPSKREGGSG WSHGSEDANQSLKHLRLSANV LLDEGAMLLYKTMTRPKHFLQ MLSPWETTLAQIIMLDWAEETS SDKLKYAFYCSCRELSRLCPCN FEELVFRDWPELQDDIPHILAQ ARKILFVIDGFDPLGGRTLWTL TRGHLRELGNRRKRCPSSWGV |
| 14800 | 45168 | A | 14886 | 213 | 625 | EPGIDTSCLCAGRCRPGKGRA CGGSSPCSWPGQPAPAAAAV PACPSGGRGAGPIQSGTCCSR ADSRCTSWTAW/WPPGLGAAT VQTVMS*TV/WPMHPVPQAGW LALGQGAAAAKHPLTSATTRS WCLGVGPGPWM |
| 14801 | 45169 | A | 14887 | 1 | 375 | MCNAQVLEYMGKSSSLTSDL QLVRDALRSLRNSFSGHDPQHH TIDSLEQGISSLMERLHVMETQ KKQERKPPLVIPRQT/WVWSGP PANSNRPAAGPDC*KEN*RDA LRSLRNSFSGHDPQHHTIDSLEQ GISSLMERLHVMETQKKQERKP PLVIPRQTGSGVDLQQTPTDLQ LRDLTVRRKTNEQKGIASASTK RTSTPKPHL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14802 | 45170 | A | 14888 | 1 | 750 | MGELNQGSWRQGHLPDAAN GIAIRVPRRRKDESRKNPTRKPH SWKPTKNFEDDVÈVMKRSMISI RIEDTHSGPSAAGVLEFAGGPL QTLFAWVSPAEEAQQRLLPVP /CLWKLCPRGAPARC\RQNSPSK LPSGFVYTVRGKLPTQASVVVD APPATKLECPRSTSDCCAGSKN FKPVDLSLLASVGPRVNLQVES SHYGKISVTVAGHCPTHATGRI LGKQALRWSPMCSMFIGRALG LVPVEGGLLQIA |
| 14803 | 45171 | A | 14889 | 81 | 164 | VGKQGLEWTPANSSRPAAEGP DC*KEN |
| 14804 | 45172 | A | 14890 | 1 | 674 | MVVYACSPSYLEAEVGGSLSL VEATNPKNSSKKFLDLISEFCK VSGYKISVHKSVALLYTKNDQ AATQIKNLIPFTTAAKQFKYFGI YLTKEEERLKPSRKKITKKHTK KRTASLILHAMICSQIPKQQQNE KYQVPQFDQSTIKNIESAKGLD VWDSWPLQNADGTPPLVIPRQ T/WVWSGPPANSNRPAAGPDC QKEN*QTERNSINIKKKDIHTKT PLCI |
| 14805 | 45173 | A | 14891 | 619 | 931 | YLLMDFPLLHSLVSLGDKVP HEFWRGCPSCSFGPRFWAGV LVL*APKL*LRQVRSAGKRCGQ KW*IK*/SDRLCVD*NK/WSDSD LKPATSCSLIVTCHSLLGF |
| 14806 | 45174 | B | 14892 | 1 | 658 | |
| 14807 | 45175 | A | 14893 | 48 | 288 | LCSIKKPEKSLLCW*YPGNRVW SGPPAKSNRPAAEGPDC*KEN* QTERNSINIKKKDIHTKTPSEGH QHQRPKTKPGRI |
| 14808 | 45176 | A | 14894 | 801 | 1157 | QSGPSAAGLLDFAGGPLQTLFA RVSPAEEAQQRLLFPSSGKL RPRGAPARCQPELSCMRC\R*SL LGGVSQSGYMGVRDPFEEAAC PLSELECSAGRSAALLRMVRQG HLGLLKLRP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14809 | 45177 | A | 14895 | 1 | 1891 | MPVWVTVVKSWNTQIGRPGH VSALGFELTKNPWPLTYESGDG RSLGKPGAVSRRGGRHGHPHQ QAECDLPAAGRIAGPCERGLERQ EKLPPAPQGGAWHLRLSRERFK SEDAPKIHVALGGSFLNLAF LVNVGSGSKGSDAACWARGA VFHYFLLCAFTWMGLEAFHLY LLAVRVFNTYFGHYFLKLSLVG WGLPALMVIGTGSANSYGLYTI RDRENRTSLELCWFREGTTMY ALYITVHGYYFLITFLFGMVVLA LVVWKIFTLSRATAVKERGKN RKKVLTLGLSSLVGVTWGLAI FTPLGLSTVYIFALFNSLQAHKQ LKDRKVGPHFMQGA VFLEGKF WGVDIASFEPQEQFWWTNLGK EDEDKSFDMPHSWVEQIEISPEE EAMGSAQMVRGVSGPERGSKK RPQLTVSTAFETRCPNGKKVIQ YKRAKLEKWAPYLN SGLVSR LTTYEDLQCTNILEIKEWYQNR EDMLELKHINKTTDLKTDYFKP GHPQALRVHSYKSMQPEMDRV IEFYETARVDGLMKREETPRTM TEYYQGRPDFLSYRHASFG/RPS QEAHSEQCRVKPPAHCAKPAE DDV/RKSACFWSRRSASSCATT AVRTTSRPPSASSCGAPRWTA |
| 14810 | 45178 | A | 14897 | 1 | 425 | HVQQTEISRTVSTGSPHILSCSVP VTLPNGPVLWFKGN/AGPNRKL IYNFKQGNFPRVKEIGDTTKPG NTDFSTRIREISLADAGTY YCV KFIKGRAIKEYQSGRGTQVFVT VSYSSRSQKSEICISGLKSRHQQ NCSFWRF |
| 14811 | 45179 | A | 14898 | 1 | 393 | RQGNFPRAKQIGDTTKPGNTDF STRIREISLADVGTYYCVKFIKG RAIKEYQSGRGTQVFVTEQNP RPPKNRPAGRAGSRAHHDAHT CLSALPERNSTNYFVQPCCCLR LLGLTGFAVKIIQTGKERTSK |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14812 | 45180 | A | 14899 | 1 | 753 | MGSSLSPLVLYVALPVRQPLLRS VVEERSTKMRVSGSPGFQAKFRF YSQGLSWSARGEGLVPAFWL QPYPRPLNFKAEMTEQKENQT YVDGGFRPYIHRRKNLTEGHK AEKEMEPWDGFSDESCRTHCQ VHDYAKGHGEVQRERVDEQK EHLGGRRQDCQQQHLNRRRLHC /TVSGEAPSEASGSVRGHGRAH GLAGSERHGHDDHAPEHQLLQ SVDADHVVPVAWYQFWDDEG RGILSPGDHKKPDRRGAAALY |
| 14813 | 45181 | A | 14900 | 6 | 726 | VEGISRTGIQAEQAPGFTTMP VSVNPGDVLTLACNMSALSPE GPVLWFKSIGPGQQLIFSCNGS HFPRVTPVENTMVDQTDYSIILS CSVPNTLPNGPVLWFKGTGPNR KLIYNFKQGNFPRVKEIGDTTK PGNTDFSTRIREISLADAGTYYC VKFIKGRAIKEYQSGRGTQVFV TGEYVSYPYPLVYNS\PLWDE ASRGRSRQQSLLFCSLHW*YPR KQDLEWTSSKLQQTCCRVA |
| 14814 | 45182 | A | 14901 | 760 | 978 | KKLLLLLLCGIEWHGFSSDSGS GGWVPEG*K*GCEHELLPEDVP SCFGWAECWLVRRTLPLFHYV ELCYSFHG |
| 14815 | 45183 | B | 14902 | 772 | 1165 | |
| 14816 | 45184 | A | 14903 | 1 | 2133 | |
| 14817 | 45185 | A | 14904 | 1 | 1311 | MATTPGRALGSLLPTLLGLTA GQPFISLTGPSHRTSPGDSVPFN CTAVPFNSQDFSDFNVTWLK DSDEHPASAQRLVPDNGGNDFI TSKAWVTLTRQDVSEITCEVT HRLAEPLKTTMNLSQATRNP DGTYSLEHTWQAEATLEEREF ACWVVHDEQPPLKANVTLQAAQ VRRQKGQSVPYKLGGLQR SEPGTRIRLTASSGFSTHQVTV TWLKNKHELNPQTSVQYSGH TYNVTSSVLVPLMDDDVFSHV VCHVEHKLWFFQKTTGLDQY L/QG/DP*QLCGGHLTPSSPRAP PQLPGLQHP/VVFHSQVLLFSC LVAVTCLVQRFYPQNVHLAWLE DCHTLKGTEQPTLKKNNDRSY TLEKLLLVNASVQGPVRLTC MMEHEGQPPKRANLVLSTAAH TAYKPIGSTESIMVTMIITISQM |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14818 | 45186 | A | 14905 | 3 | 341 | RRATRPGN*GGRHNAGRSSARL ETGRPAMAPQGRPRPLGCRTPQ HPGHWPSAPGLLPAPGPVAG MTQAQRWCPEPDAHFLQYTLY FVRHIPQLPKQTPHHYIATRLPC ATQ |
| 14819 | 45187 | A | 14906 | 154 | 679 | GVCCPLLGGVSS*ATWGS GTT* GGNTHLI |
| 14820 | 45188 | B | 14907 | 1 | 2554 | |
| 14821 | 45189 | A | 14908 | 387 | 826 | ARAACLPRGSARGTAGAGEEPP DPAPLHLRGEGPAP/HRPRSPRG MGWPAAPSTRSPST*RRCPLPP RPRWSP*SHPGPRASARLP*LS *RASRSSEAPSPGSLG SVAGQD CSRTGTGFSPPAFSDGQQT PPP APSSVPTLNSLG |
| 14822 | 45190 | A | 14909 | 86 | 2223 | GQEPQVREQKACHHLGSSPPPS WEL*EQRPA GP*N**PSTLTGT GSTTT*QIRMKVN*MGN/DSPQ GKNTPKMYSGEFSPVRVHVPFS LSDLKQIKIDLGKFSDDPDGYID VLQGEDILAKAGAIRHLNIGEG THVCCPLLEEGINPEVWATEGK YGRAKNAHP IQVKLKDSASFPY QRQYPLRPEAQQGLQKIVKDL KAQGLVKPCSSPCNTPI LGVQK PNGQWRLVQDLRI NEAIVPLY PAVPNPYTPLSQILEEAEWFTVL DLRDAFFCIPVHPDSQFLFAFED PLNPMSQLTWTVL PQGFRDSPY LFGQALAQDLSQFSYLDTHVL WYMDDL LLAARSETLCHQATQ ALLNFLATCGYK VSKPKAQLC LQQVKHLRLKLSKGTRALSEER IQPISAYPHPKTLKQLRMFLGIT GFCQIWINRYGKIARPLYTLIKE TQKANTHLVRR TSLQPVAYLS KETGTSLQPVAYLSKEIDV VAK RWP HCLRVVAAIAVLVSKAVK MIQGRALT VWTSHDVNSILTAK GDLWLSDNHNEEKIEHNWQQV IAQTYAAQGD LLEVPLTDPDLN LYTDGSSFVEKGLRKAAYAVFS DNGILES NPLTPGTSTQLAELIA VTQALELEGKREPENPADNASY SCEPLEDLRLLFRRQPIEAVKLQ MVLQMEPQM QSMTKIYRGPLD WPASPCSNVDDIEGTPPKEISTA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14823 | 45191 | A | 14910 | 929 | 1324 | RRYQVQRPSEGTLVYLFWPV*/ PVVGVDPLPTGPDYSLLVPI PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPSPCTPMFHS PCSAMTAVTPSLARP*THGSPP KAQGAPQGVKGPSSGLEAPPW A |
| 14824 | 45192 | A | 14911 | 2 | 286 | |
| 14825 | 45193 | A | 14912 | 220 | 249 | P*N**PSTLTTGTGSTTT*QIRM KVN*MGN/DSPQGGKNTPKMYS GEFSPVRVHVPFSLSDLKQIKID LGKFSDDPDGYIDVLQ |
| 14826 | 45194 | A | 14913 | 1 | 163 | EPENPADNASYSCEPLEDLRL FRRQPIEAVKLQMVLMQEPQM QSMTKIYRGPLDWPASPCS*DF LGRGAFNVINIGAWASRPVQGS AVDLSHGLHLGLHLKNHL |
| 14827 | 45195 | A | 14914 | 1 | 287 | |
| 14828 | 45196 | A | 14915 | 2498 | 2788 | |
| 14829 | 45197 | A | 14916 | 112 | 333 | |
| 14830 | 45198 | A | 14917 | 329 | 1666 | |
| 14831 | 45199 | A | 14918 | 1 | 756 | |
| 14832 | 45200 | A | 14919 | 1256 | 1651 | RRYQVQRPSEGTLVYLFWPV*/ PVVGVDPLPTGPDYSLLVPI PPRARTPRWA*A*MKGCRRSAT A*WCMC*SCRVPSPCTPMFHS PCSAMTAVTPSLARP*THGSPP KAQGAPQGVKGPSSGLEAPPW A |
| 14833 | 45201 | A | 14920 | 1 | 987 | MLVLGYNRKNTTEGTQKQKGT NASDFHFLSQVLEQVVSPKGSK EAQCCVLRHLGCESSESAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLKGKERR QREGERRERKREREREKRESQR KERKREKKGKKREREKDRSDL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLTLWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQA VP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKRTRKKPIN*SMISTI TQGKEENPTAFLERLREALRKH |
| 14834 | 45202 | A | 14921 | 473 | 1015 | |
| 14835 | 45203 | A | 14922 | 3 | 937 | |
| 14836 | 45204 | A | 14923 | 530 | 612 | LQAKVFFLLRWPAIRG*NYGP RGVPH |
| 14837 | 45205 | A | 14924 | 101 | 430 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14838 | 45206 | A | 14925 | 1 | 1587 | MAALTLRGVRELLKRVDLATV PRRHRYKKKWAATEPKFPAVR LALQNFDMTYSVQFGDLWPSIR VSLLEQKYGALVNNFAAWDH PGDIVLDLCAAPGGKTLALLQT GCCLTWSRKCAALSMFSRPA RCLCRARTTAPRAVRRPDQRR ATAAATKQARATPEAPGSAA HSSYCTMIPSACCCLPRQLKPPH AQPARSAKPGLDQPGSHARL RGRGGEARQSLEAIRGGPSGIA PSDIPLPAKPSRRVIAQTYAARG NLLEVPLTDPDLNLYIDGSSFE KRLRKAGIKAVKLQIVLQMEPQ MQPMTKIYCGPLDQPASPRSNV DDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLGKFSDTPDGYIDVLQ GLGQPYYL TWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKRTRKKPIN*SMISTI TQGKEENPTAFLERLREALRKH |
| 14839 | 45207 | B | 14926 | 1 | 939 | |
| 14840 | 45208 | A | 14927 | 1 | 4317 | MQSMTKMYCGPLDQPASPCSN VDDIEVKLEIMLLTERDDGKEV LDVGEERRYIEEYDSK WTRK YNCLAVLRVHSGSQITTMKLIL WYLVVALWCFKDGKIAASRS GGFSYGSSSGDLDRKKPLFSL EFGSPGETEDKSRQRQDAGSPK SEDTAGGFFNSSSSGSDSRTK PFFSLGLGAPGKAEDKSGDSQD AGGKSSEDTPGGFFYGSSSSG DSDKKKPLFSFEFGATGEDEDK SRERWDAGNSRSEDS |
| 14841 | 45209 | B | 14928 | 110 | 269 | |
| 14842 | 45210 | A | 14929 | 1 | 561 | EVFPACSQLVYWGKPITIYPLCE NNVYMLSPNASVCLYSPLAEQ FSHQFPSHDLPSVLAKFSLPVSL SEFRNPLAPAVQETQLIQMVV WMLQRRLLIQLHTYVCLMASP SEEEPRPREDDVPFTARVGGRS LSTPNALSFGSPTSSDDMTLTSP SMDNSSAELLPSGDSPLNQRM ENLLASLSEH |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14843 | 45211 | A | 14930 | 1891 | 2522 | GLSNQNNQPGRCIPDAHPVQDL VQDLVHTWCRVPCTSYVPCV* VPGAYLVHTRCIPGAGPGAYPV HTWCRTWCIPGAGFPAL/RPYH ALLLLSDEKSLLGELPIDCSPAL VRVIKTTSVAVKNLQQLAQDAD LALLQAMGSAVALVMWAWP RATGPLKYCLRVGAGGACGWR PRLVAVSRALLLVWRCGSPWG PALAWQKSPEYSTKVLEKQ |
| 14844 | 45212 | C | 14931 | 113 | 274 | |
| 14845 | 45213 | A | 14932 | 1 | 1634 | MEIPAVILTVAPILHLTSCGFV TGDGLKQAEKGKCAPEEWNPTK FIKLTDNQACFACGLWPLSEIQ RRTSRTVTIISRISALREKNGR KPTSISGSVNEMRQVLVKDQVS MPRVLPTHFVPDEAGFSAGAV WPCAAPLWGSSWTPKVENCS FYIRLSFAISVGGDELKIAKLVS AFPERAYDLVGHQHQRPKVDK TTKMGRNQSRKAENSKNQNM SPPKEHNSSPAREQNWMEF DELREVGFRRSVITNFSELKEH VLTHHKEAKNLEKRLDEWLTR INSVEKSLNDLMELKTTTLREL EAYISFNSQFDQAEERSVIEDQ ISEIKQEVKFKREKRVKRNEQSL QEIWDYVKRP\NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANIQI/QGKLQRTPTKVASSRT ATPRHISVGSPLNMK\EKILR AAQRERSGLPTKGKPFRLTAAD LSAETSTSQKTEWGPIFNILKEK NF\QPRNISYPAK\LSFISEGEIKYF TDQAKCLRDFVTTTAFSCLP*K STRPALKELLKGST |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15459 | 45827 | A | 15549 | 1 | 1214 | MEEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPISVGRPRHQGV MVGMGQKDSYVGDEAQSCKRG ILTLKYPIEHGIVTNWDDMEKI WHHTFYNELRVAPEEHPVLLTE APLNPKANREKMTQIMFETFNT PAMYVAIQAVLSLYASGRRTGI VMDSGDGVTHTVPIYEGYALP HAILRLDLAGRDLTDYLMKILT ERGYSFTTTAEREIVRDIKEKLC YVALDFEQEMATAA\SSSSLEK SYELPDSPRSSTNWQLSGFRLPL RHSFQPSFLG\MESCG\IHETTF NSIMK\CDVDIRKDL\YANTVLS GRTPCTLGIADRMQKEITALA PSTMKIKIIPPERKYSVWIGGF HPWAWLSHLSSKMWVQQARS MTESGPLHSSTANGFLGGLLTL VAFTPFLWTKP |
| 15460 | 45828 | A | 15550 | 1 | 2355 | MKQITFAPRNHLLTNTNTWTPD SQWL VFDMRTSGASFTGETIER VNIPTGYVEKPNKQCRHSVTRY GHGGHSDHTPSLT VATVATQIT PRHSGHGHSCDRNLSLATATA ATLITPHLLWPRWPLGSHSVT WCGHGGHSDHTPSPTTATAVT RITSRHPLRPQQLGSHPVTHYS HGSHTDCIPVTRYAHGGHSDHT PSLAMATAATQMALCHSLWPR QPLGYLVNKIRRKRCTDGVSPS GKAPVFDTGIPWFESRYPSHLL RVSGSPPGYWGIKRHQILNVS NMFGKFKTNLLGYRQAVRHRI LIPAFRGSNPRT PANLFKTLTLIS NMRALENDFFNSPPRKTVQFG GTVTEVLLKYKTAIEKRLEKLA VDPHRDRAQMLKVENVQQAW QQWINKLPPARREDEDVKEIR WMIEELRVSYFAQQLGKNSRA ESMLWSFHKAAIEAARTNIIQA QTRVEAAQATERRIAADIDDSE LKAPRDGRVQYRVAKPGEVLA AGGRVLNMVDLSDVYMTFFLP TEQAGTLKLGGEARLILDAAPD LRIPATISFVASVAQFTPKTVET SDERLKL MFRVKARIPPELLQQ HLEYVKTGLPGVAWSFLYSINQ TICLR LDSIEAKLQALEATCKSL EEKLDLVTNKQHSPIQVPMVA GSPLRTTQMCNKVR/CVNP*AT VVPPPVPQPTTQQYQGLDAGA |

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|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 15454 | 45822 | A | 15544 | 85 | 2249 | SAEAMSGDGATEQAAEYVPEK VKKAEEKLEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEIKAKNYDK GEKLFQRCLMKVLHIDLWKCY LSYVRETKGKLP SYKGKMAQ AYDFALDKIGMEIMSYQIWVD YINFLKGVEAVGSAENQRITA VRRVYQRCVNP MINIEQLWR DYNKYEEGINIHLAKKMIEDRS RDYMNARRVAKEYETVMKGL DRNAPSVPPQNTPEAQQVDM WKKYIQWEKSNPLRTEDQTLIT KRVMFAYEQCLLVLGHPDIW YEEAQYLEQSSKLLAEKGDMN NAKLFSDEAANIYERAISTLLK KNMLLYFAYADYEE SRMKYEK VHSIYNRLLAIEDIDPTLVYIQY MKFARRAEGIKSGRMIFKKARE DTRTRHHVYVTAALMEYYCSK DKSVAFKIFELGLKKYGDPEY VLAYIDYLSHLNEDNTRVLFE RVLTSGSLPPEKSGEIWARFLAF ESNIGDLASILKVEKRRFTAFKE EYEGKETALLVD RYKFMDLYP CSASELKALGYKDVSRAKLAAI IPDPVVAPSIVPVLKDEVDRKPE YPKPDTQQMIPFQPRHLAPPGL HPVPGGVFPVPPAAVVLMLKLLP PPICFQGPFVQVDELMEIFRRCK IPNTVEEAVRIITGGAPELAVEG NGPVESNAVLTKAVKRPNEDS |
| 15455 | 45823 | A | 15545 | 12 | 427 | SAEAMSGDGATEQAAEYVPEK VKKAEEKLEENPYDLDAWSIL IREAQV**YRITFPSLWVQSHYL VLPVNNIFIHLTL*MLFIGFQF*N QPIDKARKTYERLVAQFPSSGR FWKLYIEAEVTILFYFFLYQYCS IHL |
| 15456 | 45824 | A | 15546 | 150 | 469 | SAEAMSGDGATEQAAEYVPEK VKKAEEKLEENPYDLDAWSILI REAQNQPIDKARKTYERLVAQF PSSGRFWKLYIEAEVTILFYFIFS YISIAAFTVVIENKLG T |
| 15457 | 45825 | A | 15547 | 1 | 834 | |
| 15458 | 45826 | A | 15548 | 443 | 732 | SFMRWQKGQLPQLCLHRESHC SPYPQPSFLGMEP/ADIHETTFN SIMKCDVDIHKGLYANAVLSSG TTMYPGIANRMQKEITALAPS MMKIKIIPA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15452 | 45820 | A | 15542 | 254 | 883 | DLRKDSPWEHRQCDKREPGNS APPAPHSWGFAVFNPRAGDVR QLCKRADTRTPSPRAPFGSAGA CRGCGRAGARSLASPKARTCIS SARRRAGGPLQLGAGSGQAKR PDR*TRREGANA*KTLHL/HSSL APSPGGVLAFQEPPGRPQVAC CAATAAGGIRAGERR/PAAAAA AAPWAQKLRLRLQRRGPPGC R**MVSFPRLFSGSTSR |
| 15453 | 45821 | A | 15543 | 1 | 768 | MCDFGKSTSLPASPTSSSANGR DNSTYRLKEQGGFMHSVASRD SCAESARYTDAHYAKSGYGAY TPSSYGANLAASLLEKEKLGFK PVPTSSFLTRPTYGPSSLLDYD RGRPLLRPDITGGGKRAESQTR GTERPLGSGLSGGSGFPYGVN NCLSYLPINAYDQGVTLTQKLD SQSDLARDFSSLRTSDSYRIDPR NLGRSPMLARTRKELCTLQGL YQTASCPEYLV DYLENYGRKG SASQVPSQAPPSRVP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15449 | 45817 | A | 15539 | 1 | 3102 | MYSHVITVCRHVKNGDILLNR QPTLHRPSIQAHRRARILPEEKVL RLHYANCKAYNADFDGDEM AHFPQSELGRAEAYVLACTDQ QYLVPKDGQPLAGLIQDHMVS GASMTTRGCFRTREHYMELVY RGLTDKVGVRVLLSPSILKPFPL WTGKQHINRTKDKNHMIISIDA EKAFDKIQQPFMLKTLNKLID GTYLKIIRAIYDKPTASILNGQK LEAFPLKTGTRQGCPLSPLLFNI VLEVLARAIRQEK |
| 15450 | 45818 | A | 15540 | 1 | 779 | IPMKDHDAIKLFIGQIPRNLDEK DLKPLFEFEGKIYELTVLKDRFT GMHKGCAFLTYCERESALKAQ SALHEQKTLPGMNRPIQVKPAD SESRGEDKKLFVGMNLKQQSE DDVRR\LFEAFGNIEECTILRGP ERQTAKGCAFVKYSSHAEEAAG RPSTRLHGSQTMFGAFVPVWV GQVSADTDKERTMR\RMQQMA GQMGMFNPMAIPFGAYGAYA QALMQQAALMASVAQGGYL NPMAAFAAAQMQQMAALNM NGLAA |
| 15451 | 45819 | A | 15541 | 1 | 1413 | MEYYAAIKKDEFISFVGTWMK LETIILSKLSQMOKTKHRIFSLIV LCDITDILKEFTVAEAGGFALNE IMKEICKSRFSKVSLSLHWMW HSTASLGYHRVNVNTPDPLNLC LGHCWLGLRDTGQKQACGGP GVCPGMFRRACGGNAPCKEAP SVTEASSPDGSLCLGSHVPITP APLSSAQMVCHMVEDRRTVEL ILGATHNLFFSTSPLTWSLRAIP GNCVLFLKDYVTEPVRSSILHI AGPTFKQTPNLPFLKFPEATKA HGPNVYQNDSTCPEPTAQVSH WSSVSSTLIASVPGPEDRKLFV GMLNKQQSEDDVRR\LFEAFGN IEECTILRGPDGNSKARPLASSQ GAPSVKYSSHAEEAQAALNH GSQTMPLMQQAALMASVAQ GGYLNPMMAAFAAAQMQQMAA LN\PNGLAAAPMTPT\QANGQP AAEEN\FANGIHPYPAQSPTAAD PLQQAYAGVQQYAGR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15441 | 45809 | A | 15531 | 5459 | 6324 | LLANVSQLLADISQLLANFTQL FSHFSQLLTYLSKLFTHLPQLLT HFPKLLTHQPELFSNQSQLHPNI TRYSPSPSYSPSPNYTPTSPN YSPTSPSYSPSPSYS/RDLTKLL PFQPTIHTTVSNLYPKLTQLQPQ FAQLQPNLTQV\PTSPSYSPSSP EYTPTSPKYSPTSPKYSPTSPKY SPTSPTYSP\TPKYSPTSPTY\Q PLQSTPQPLPSTHLLAPLTRPLP PSTRPPAPPTRPPPPKAQPTLPLP LVTRPPAPPTVSQARLSARMTV TRRTEGTWGAAAG |
| 15442 | 45810 | A | 15532 | 13 | 941 | SVVLRPLLVAATAATTPVAA AAATNTAKKTATVMVGEMVA GERGVLQMGHDITRFFYSNIQT VINNWLLIEGHTIGIGDSIADSK TYQDIQNTIKKAKQDVIETFEN QVPRILNDARDKTGSSAQKSLS EYNNFKSMVVSGAKGSKINISQ GGGSQGGRGPPISMWLLALC LVGLAGAQRGGGGPGGGAPG\ GPGLGLGSLGEERFPVVNTAYG RVRGVRRELNNEILGPVVQFLG VPYATPPLGARRFQPPEAPASW PGVRNATTLPPACPQNLHGALP AIMLPVWFTDNLEAAATYGGC FRVPKKA |
| 15443 | 45811 | A | 15533 | 207 | 696 | TNLQEKKNQPHQKVGKRYKQT LLKRRHLCSQQAHEKMLIITGH QRNANQNHNEIPSHTS*NGDH* KVRKQQMLERMWRNRNAFTL WVG*TSSTIVEDSMAIPQGSR TRNTI*LSHPITGYIPKGL*IMLL *RHMHTYAYCGSIHNSKDLEPT QRSINDRLD |
| 15444 | 45812 | A | 15534 | 1 | 307 | |
| 15445 | 45813 | A | 15535 | 1 | 381 | LPPPHDRLWCVMFPTLCPSVLI VQFPMSSENMRCLVFCPCNSLL RMMVSSFIHVPTKDMNSGIL*S RPADIELFSINLVNKKIFLKGF GDPLSLQRQLRNIVFSMPCCFPS FLLPWVFSQLSVKPH |
| 15446 | 45814 | A | 15536 | 134 | 278 | DPAFLAPSPV/LMKQAPQATSG LMEPPGPSTPIVQRPRILLVIDD AHTD |
| 15447 | 45815 | B | 15537 | 1 | 840 | |
| 15448 | 45816 | C | 15538 | 1 | 891 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15428 | 45796 | A | 15518 | 3 | 1263 | GRTIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERSAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTQPORYSS RRATPRHIIVRFTKVEMKEKMG LLVPNWTNHSPLFRAILFDYKG FCRFGTTHQTGFSPAGANQGRP LAATLSGPGGEGQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQEIQRTPQR YSSRRATPRHIIVRFTKVEMKE KMLRAAREKGRVTLKGKPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTRPALKELL KEALNMERNNRYQPLQNHAK |
| 15429 | 45797 | A | 15519 | 1 | 1137 | |
| 15430 | 45798 | A | 15520 | 1 | 1578 | |
| 15431 | 45799 | A | 15521 | 1 | 1656 | |
| 15432 | 45800 | A | 15522 | 1 | 1120 | |
| 15433 | 45801 | B | 15523 | 1 | 1541 | |
| 15434 | 45802 | B | 15524 | 1 | 1632 | |
| 15435 | 45803 | C | 15525 | 53 | 352 | |
| 15436 | 45804 | A | 15526 | 1 | 973 | MGKKQNRKTGNSKMQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELQRVSAMDE MNEMKREGKFREKRIKRNEQS LQEIWDYVKRPNLRLIGVPESD GENGTKLENTLQDIIQENFPNL ARQANIQIQEILRIPQRYSSRR ATPRHIIVRFTKVEMKEKMLRA AREKGRVTLKGKPIRLTVDL SAETLQARREWGPIFNILKEKN FQPRISYPAKLSFISEGEIKYFT DKQMLRDFVTTRPALQELLKE ALNMERNNRYQPLQNHAKM |
| 15437 | 45805 | A | 15527 | 1 | 2896 | |
| 15438 | 45806 | B | 15528 | 50 | 658 | |
| 15439 | 45807 | A | 15529 | 1065 | 1260 | RSHALALDSAGSSSPESPH* RASIPHTALGQNAGSWAGTAH SHHGPFLWSDPRHPQVPHRTCC P |
| 15440 | 45808 | A | 15530 | 96 | 219 | EFSTKPRLSGP*SSWEMLILEPL APDTTIDLKLLYSRDF |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15414 | 45782 | A | 15504 | 2 | 991 | RSAGVKAGSRPSPVLQQSASSF NMTDAAVSFAKDFLAGGVA [~] AISKTA VAPIERVKLLQLQVQH ASKQIAADKQYKGIIICVVRIP KEQGVLSFWRGNLANVIRYFPT QALNFAFKDKYKQIFLGGVDK RTQFWRYFARNLASGGAAGA TSLCFVYPLDFARTRLAADV GK AGAEREFRGLGDCLVKIYKSDG IKGLYQGFNVSVQGIIYRAAYF GIYDTAKG\MLPDPK\NTHIVIS W\MI AQTVHCCCPG*LPYPFDT RS/VRNE*MQSGRK\GT\DIMY TGTLADCWRKIARDEGGKAFFK GAWSNVLRGMGGAFVVLVLYE *KSKKYT |
| 15415 | 45783 | A | 15505 | 1 | 613 | |
| 15416 | 45784 | A | 15506 | 1 | 1695 | |
| 15417 | 45785 | A | 15507 | 131 | 723 | LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVSAMEDEINEMKRE EKFREKRVKRNEQSLQEIWDYL KRPNLRLIGVPESDGENGTKLE NTLQDIIQENFPNLARQANIQQ EIQRMPQRYSLRRATPRHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRE WGPIFNILKEKNFQPRISYPAKL |
| 15418 | 45786 | A | 15508 | 1 | 3156 | |
| 15419 | 45787 | A | 15509 | 1 | 879 | |
| 15420 | 45788 | A | 15510 | 1 | 804 | |
| 15421 | 45789 | B | 15511 | 1 | 1230 | |
| 15422 | 45790 | A | 15512 | 2 | 827 | |
| 15423 | 45791 | A | 15513 | 1 | 1011 | |
| 15424 | 45792 | A | 15514 | 1 | 1722 | |
| 15425 | 45793 | B | 15515 | 1 | 780 | |
| 15426 | 45794 | A | 15516 | 1 | 2712 | |
| 15427 | 45795 | B | 15517 | 1 | 855 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15409 | 45777 | A | 15499 | 1 | 645 | |
| 15410 | 45778 | A | 15500 | 3 | 677 | SPPNPRAPYLFPASLQNPNANWS PHFQYLPILSQPRSVLTAFRQQA QPRISMPQAQTPFRPQMERLDQ NIRRSNQPQHSLKPKLIQSKALT LFNSVKAEEKDEEAAEEKFEVTR VVHIRGLIDGVVEADIVEALQE FGLISYVMVMSKKRQALVEFE DVLEACNAVNYTADNQIHIAG HPAFVNYSTSQKISRPGNSDDR SVNSVLLFTILNPIYSITTDVLYT |
| 15411 | 45779 | A | 15501 | 2 | 1712 | DEQRRRSGAMVKMAAAGGGG GGGRYYGGGSEGGAPKRLKT DNAGDQHGGGGGGGGAGAA GGGGGGENYDDPHKTPASPVV HIRGLIDGVVEADLVEALQEF PISYVVVMPKKRQSLV*FEDVL GAGNAVNYAADNQIYIAGHPA VFNYSSTSQKISRPGSDSDSR\SV N\SVLLFTILNPIYSITTDVLYT\I CNPCGPVQRIVIFRKNVQAMV EFDSVQSAQRAKASLNGADIYS GCCTLKIEYAKPTRLNVFKNDQ DTWDYTNPINLSGQGDPGSNPN KRQRQPPLLDGHPAEYGGPHG GYHSHYHDEGYGPPPPHYEGR RMGPPVGGHRRGPSRYGPQYG HPPPPPPPEYGPHADSPVLMV YGLDQSKMNGDRVFNVFCLYG NVEKVKFMKSKPGAAMVEMA DGYAVDRAITHLNNNFMFGQK LNVCVSKQPAIMPGQSYGLED GSCSYKDFSESNNRFSTPEQA AKNRIQHPSNVLHFFNAPLEVT EENFFEICDELGVKRPSSVKVFS GKSERSSSGLLEWESKSDALET LGFLNHYQMKNPNGPYPYTLK |
| 15412 | 45780 | A | 15502 | 1 | 528 | NHQIRNDFTISPGVKADSRTSPI PQQPASSFDITEAAVSFAKDSLA GGVAAAISKMAVAPIERVK/RV PKEHGVLSWCGNLASVIRYFP\ TQALNFTFKDKYKQIFLDGVVDK RSQFWRYFAGNLASGGATGAT SLCFVYPLDFAHTRVAADVKG AGAERELRGFGDCLVKIYKSDG IK |
| 15413 | 45781 | A | 15503 | 1 | 1452 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15407 | 45775 | A | 15497 | 89 | 2490 | PKCCFFCLLSGETAAAQSCLCG KVVLRLRPLRRCRRYSTSGSSGLT TGKIAGAGLLFVGGGIGGTILY AKWDSHFRESVEKTIPYSDKLF EMVLGPAAYNVPLPKKSIQSGP L*ISSVSEVMKESNRPASQ\LQK QK\GDTPASATAPTEAAQIISAA GDTLSVPAPAVQPEESLKTDHP EIGEGKPTPALSEEASSSSIRERP PEEVAARLAQQEKQEQQVKIESL AKSLEDALRQTASVTLQAIAAQ NAAVQAVNAHSNILKAAMDNS EIAGEKKSAQWRTVEGALKER RKAVDEAADALLKAK*LLMDF NKEELEKMKSVIENAKKKEVA GAKPHITAAEGKLHNMIVDLD NVVKKVQAAQSEAKVVSQYH ELVVQARDDFKRELDSTPEVL PGWKGMSVSDLADKLSTDDLN SLIAHAHRRIDQLNRELAEQKA TEKQHITLAL\EKQKL\EEKRAF DSAVAKAFRNIHRKLKYRA*TG QKR*KEVRDAME\NEMRTQLR RQAAAHTDHLRDVLRVQEQL KSEFEQNLSEKLSEQELQFRRLS QEQVDNFTLDINTAYARLRGIE QAVQSHAVAESEEARKAHQLW LSVEALKYSMTSSAETTS\PL GSAV\EA\KANCSDNFTQALT AAIP\PESLTRGVVTVKRPLGAR FYAVQKL\ARRVAMIDETRNSL YQYFLSYLQSLLLFPPQQLKPPP |
| 15408 | 45776 | A | 15498 | 1 | 1212 | MPKKRQALVEFEDVLGACNAV NYAADNQIYIAGHPAFVNYSTS QKISRPGDSDDSRVNSVLLFTI LNPIYSITTPTRLNVFKNDQDT WDYTNPNLSGQGDPGSNPNKR QRQPPLLDGHPAEYGGPHGGY HSHYHDEGYGPPPPHYEGRRM GPPVGEYGPHADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVE KVKISLKKQSPGGRPMGEWL DGYAVDRAITHLNNNFMFGQK LNV/CVGAQAREGSRGTGERK GGEWGPAEEHSEAELVLTHTM GCGSVSKQPAIMPGQSYGLEDG SCSYKDFSESRRNRFSTPEQAA KNRIQHPSNVLHFFNAPLEVTE ENFFEICDELGVKRPSSVKVFSG KSERSSSGLLEWESKSDALET GFLNHYQMKNPSINLVT |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15406 | 45774 | A | 15496 | 2 | 1605 | WQLPHPPAAP SARQIL RACQLS SVTAVAQSCLYGKQLC/GLTTG NIAGAGLLFFGGGIGGTILYAK WASHFRERVEKTIPYSDKLFEV VLGSAPYNVPLPKKSTQSGPLK ISSVSEVTKEFKQPASQLQKQK GDTPASATAGDTVLPVGVQHE ESLKT DHPAIDEGKPTPALSEEA SSSSIRERPCEEIAACLAQEEKQ EQVKTESLAKSFEDALRQTANV TLQAIAAQNTVVQAVNAHSNIL KAAMDNSEIEGKKKS AKWHTV QGALKEHRKAVDEAANALLKA KEEVQAAQFESKLVSQYHELV GQAQDDFKRQLDSITPEVLPGW KGMSVSDPADKLSTDDLNSLIA RAHRHIDQLNRELA EQKATEK QHITLALEKQ TLEEKVQE QELK YEF EQNLSEKLSEQELQFHLS QEQVHNFTLDINTAYARLRGIE HAVQSHAVAE EEAR KAYQLW LSVEALKYS MKTSSAEMPAVPL GSAVEAIKANCS DNEFTKALAT AIPPE SLTHGVYSEETLRVRFYA VQKLARRVAMID |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15398 | 45766 | A | 15488 | 1370 | 2243 | LGKLRLESCGLVAAVRPHSGGL AMPLPNATRPASGRSED/AELK LALEHGHRSESLQGRKHRGVH DNSDIPQAALVGGTTMIIGHVL PDKETSLVDAYEKCRLADPK VCCDYALHVGITWWAPKVKA EMETLVREKGVNSFQMFMTYK DLYMLRDSELYQVLHACKDIG AIARVHAENGELVAEGAKEAL DLGITGPEGIEISRPEELEAEATH RVITIANRTHCPIYLVNVSSISA GDVIAAAKMQKGKVVLAETTTA HATLTGLHYHQQDWSHAAAY VTVPPRLGIPPH |
| 15399 | 45767 | A | 15489 | 307 | 600 | VSRRASSGSPVPLGSLHLQHSA PA/PSAAPKPRSPPARLSRPHLR GESAAPSPSPGPASLAAAAAA RVPAQSPAPSTTPAPRTTLAPR VPHRLAPAP |
| 15400 | 45768 | A | 15490 | 3 | 222 | |
| 15401 | 45769 | B | 15491 | 1 | 1131 | |
| 15402 | 45770 | A | 15492 | 136 | 201 | |
| 15403 | 45771 | A | 15493 | 3 | 556 | ELPRRLVCSKL RADPGR LTPDA CARPGMSRYLLPLSALGTVAG AAVLLKDYVTGGACPSKATIPG KTVIVTGANTGIGKQTALELAR RGGNIILACRDM EKCEAAAK\ D IRGETLNHHVNARHLDLASLKS IREFAAKIIEEEERVDILINNAGV MRCPHWTTEDGFEMQFGVNHL GHFLTTWC |
| 15404 | 45772 | A | 15494 | 11 | 559 | |
| 15405 | 45773 | A | 15495 | 1 | 312 | MAPAADREGYWGPTTSTLDW CEENYSVTWYIAEFSWLMSGF LPTPSSLRDLTASRWVRS LPPSR SPAGRQPGPAEELPKASPCPWG KSLSRPFASF SASSGPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15389 | 45757 | A | 15479 | 1 | 1016 | MERRGPGAATARGRARPGGGP SVGLLATGSSLNPSFHGVARIVP GFIRIARPRDGSFAYESVPWQQS ATQPAGSLSVVTTVWGVGNAT QSQVLGNPMGPAGSPSGSSMM PGVAGGSSALTSPQCLGQQAFA EGGANKGYVQQGVYSRGGYP GAPGFTTGYAGGPGGLGLPSH AARPSTDFTQAAAAA VAAAA ATATATAT/GHRGCSPGEAEPG AEP\DGAMGAGQSFSNQLQHG GPRGPSVPAGMNP TGIGGVMG PSGLSPLAMNPTRAAGMTPLY AGQRLPQHGYPGPPQAQPLPRQ GVKRTYSEVYPGQQYLQGA YP VHSGLSQFPTWQETPRHP |
| 15390 | 45758 | C | 15480 | 1 | 585 | |
| 15391 | 45759 | B | 15481 | 1 | 885 | |
| 15392 | 45760 | A | 15482 | 3 | 440 | GPWPRPVAYLSKQLYRVSKGW PPGLRALAEMALLAQEADKLT LRQNPNI/IGPHAVVTLMTTKG HH*FTNARLTYVKIPT*PLKF/G NTLNPTTLLPVSESPVEHNCVD VLDSVYSSRPNL RDHP*TSVDC ERYVDRSSFTNRCKVTR |
| 15393 | 45761 | A | 15483 | 3 | 368 | |
| 15394 | 45762 | C | 15484 | 109 | 276 | |
| 15395 | 45763 | A | 15485 | 1 | 1710 | |
| 15396 | 45764 | A | 15486 | 221 | 784 | QNSLRSMCQKEKKMAAGVLT HTC\GPWPRPVAYLSKQLDRIS KGWPPGLRALAATALLAQEAD KLTL\GKT*I*RPPHAVVTLMT KGHHWLTNARLTKYQSLLCEN PHITTEVCNTLNPTTLLLVSESL VEHNCVEVLDSVYSSRLNLRD HP*TSVDW*LHVDGSSFTNPCK VTLKKMTSAAPVTPRS |
| 15397 | 45765 | B | 15487 | 509 | 661 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15385 | 45753 | A | 15475 | 1 | 1115 | MKWLLLLGLValsecIMYKVP LIRKKSLRRTLserGLLKDFLK KHNLNPARKYFPQWEAPTLVD EQPLENYLDMEYFGTIGITPA QDFTVVFDTGSSNLWVPSVYCS SLACTNHNRFNPEDSSTYQSTS ETVSITYGTGSMTGILGYDTVQ SGYHHGNHRLNLKGLCSSKRSS TTPPLYDLGQVASPPSGSVSSC DDQSGSVVIFGGIYSSYYTGGL NWVPVTVEGYWQITVDSITMN GEA\IACAEGCQA\IPEPGTFFVT GPTSPIA\NIQSDIEA\SEELDG\D SVLICSAISSLPDI\VFTINGVQY PVPPSA\YILQSEGSCISGFQGM NLPTESEELWILGDVFHPASTLT VF\DRANNQVG\LAPVA |
| 15386 | 45754 | A | 15476 | 1 | 765 | |
| 15387 | 45755 | A | 15477 | 470 | 479 | PRNPSSFLQVQVQHRFLQLFVP FHFVFFLASLYVMVTLTTWFR* DPCVSGMALNCSFLKIASSSGE YLRPTPSYLNQVVRVTMT |
| 15388 | 45756 | A | 15478 | 1 | 896 | CLPFGGPKPNPWDKDGCGQGR PQPRHLPGPGTAAQRRQQCPS KSL/CRWPSLTASTCSRLFYIL LHVGAS/CNLLPPAVKDSSGKG VGQDTQVLSGSGAVYRVCAGT ATFHLLQAVLLVHLHSPTSPRA QLHNSFWLLKLLFLLGLCAIAF CIPDEHLFPAWHYIGICGGFAFI LLQLVLITAFASWKNKNCNEAS YLAEVFGPLWIVKVYSYEFQKP SLCFCCPETVEADKGQRGGAA RPADQETPPAPPVQVQHLFLQL FCLPLRLLPWLTLCHGYPYQLV QASAGCGCKPFAPYSL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15378 | 45746 | A | 15468 | 528 | 1413 | QTERNSTSTSKTPSEGHQHQRPKVDKSTKMGRNQCKKA*NSK SQNACCPPKDHSSLPAREQTMENEFDELTEVGFRRWVITNSS KLKEHVL TQCKEAKNLEKRLE ELLTRITNLEKNINDLMELKNT ARELREAYTSINSRIDQAKERM SEIVDQLNERNDRENGTKLENT LQDITQDNFPYLARQVNIQIET QRMPQRYYSRRVTPRHIIVRFA KVEMKEKMLRAAREKDTSVK QKVNKDIQELNSALHQVDLIAI YRTLHPKSTEYTFFSAPHHTYS KTDHIVHSILCDSG |
| 15379 | 45747 | A | 15469 | 368 | 679 | SSQLNKAPSLFNPVSEEFCLWL LLLQKELLTRITSLEKNTNDLV DLKNTA*ELHEAHTSINS*IDQV EERISECEDHLTEIRHSEKMKTA LLK*DMQTRREKKK |
| 15380 | 45748 | A | 15470 | 865 | 2055 | QTERNSININKKDNIAKTPSKG HQQQRPKVDKSTKMRKNQHK KA*KFPKPGMPSSPPK\DHNCSP ARE\QNW MENEFNEFDEL TGA GFRRWVITNSSSELKEHVVTQCK EAKNLEKRL\QELLTRITSLEKN INDL MELKQDITQENFMKHTQ VSIAQADQGRKERVSEIEDPTL MDIKCEDKIREKK/IKKRNEQSL QEIWGYVKRPNLRLISVPESDG ENGK*ENILQDIIQENF/PFPNL TRQANIQIETQRTLQRYPLRR ATPRHIIIRFTKVEMKEKMLRA AREKGRVTHKGKPIRLTENLSA ETL*ARRE**PILNILKERNFQPR ISYRAKLSFISK/GKREIKSFIDK QTLRDFVTTRPALQELLKEAVN MERKNQYQPLQKHTKLKRPLT |
| 15381 | 45749 | A | 15471 | 1 | 315 | |
| 15382 | 45750 | A | 15472 | 1 | 2775 | |
| 15383 | 45751 | A | 15473 | 1 | 1017 | |
| 15384 | 45752 | B | 15474 | 1 | 3105 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15369 | 45737 | A | 15459 | 1 | 744 | |
| 15370 | 45738 | B | 15460 | 337 | 1515 | |
| 15371 | 45739 | A | 15461 | 1 | 1197 | |
| 15372 | 45740 | A | 15462 | 1 | 714 | |
| 15373 | 45741 | A | 15463 | 142 | 601 | HQRTKVYKFTKMRKNQPKKPE NSK/TQNPSSPSKDHNSLPAREE NWMENEFDKLTEVGFRRWVIT NSSELKEHVLTQCKEAKNPKD RLEKLLTRIISLEKNINDLVELK NTA*ELLEAYTNINSQIDQVEEK I/S/SIEDQLNEIKLEDEIREK KKK |
| 15374 | 45742 | A | 15464 | 153 | 474 | QTKSNNVNIKKQDVHTKTPSEG HQHQRPK\DHNSLPAREQNWIE NEFDELTEVGFRRWVITNSSEL KEHVLTQCKEAKNLEKRLQEL LTRITSLEKNINDLMELKNTA |
| 15375 | 45743 | A | 15465 | 1 | 2172 | |
| 15376 | 45744 | A | 15466 | 1 | 1640 | MKLMETLNQCINAGHEMTKAI AIAQFNDDSPARKITRRWRIG EAADLVGVSSQAIRDAEKAGR LPHPDMEIRGRVEQRVGYTIEQI NHMRDVFGRRLRAEDVFPPVI GVA AHKGGVYKTSVSVHLAQ DLALKGLRVLLVEGNPDQGT SMYHGWV PDLHIHAEDTLLPF YLGEKDDVTYAIKPTCWPGLDI IPSCALHRIETELMGKFDEGKL PTDPHMLRLAIETVAHDYDVI VIDSAPNLGIGTINVCAADVLI VPTPAELFDYTSALQFFDMLRD LLKNVDLKGFE PDHLTPAGNC YVVRNEDCIGFFSGFY NVISL GVYLVEQQKGWEDTHSKTPSK GHQHQRSKVDKSTKMRKNWS KNAENSKNQNALSPNDRNSSP ARAQNW MENKFDKLTEVGFR RQVITNTSELKEHILTQSKEAKN LDKRLQELLTRITSLEKNINDL MELKNTARELREAF TSFCVNCE AVSLITSLREDSHWLEDSKGHR M/RRHQE*KCEYFHPPHPGLQF YQLPESDSHSDPLWPHGGSFLS |
| 15377 | 45745 | B | 15467 | 50 | 1603 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15357 | 45725 | B | 15447 | 707 | 1826 | |
| 15358 | 45726 | A | 15448 | 108 | 397 | |
| 15359 | 45727 | A | 15449 | 1726 | 2464 | SKAVQLEAGGLLQLFCCCKMAP DPNITDVFGRTALHYAVYNEDT SMIEKLLSYGANIEECSEDEYPP LFLAVSQRKVKMVEFLLKKKA NINAVDYLGRSALIHAVTLGEK DIVILLLQHNIDVFSRDVYGKL AEDYASEAKNRVIFELIYER KKHEELSINSNPVSSQKQPALK ATSGKEDSISNIATEIKDGQKSG TVSSQKQPALKDTSKNDKNDVSN TATEIKDEQKSGTVSSQKQPAL KDTSDKNDVSNNTATEIKDEQK SGTSVFSETTGLEGYK |
| 15360 | 45728 | A | 15450 | 2 | 675 | |
| 15361 | 45729 | A | 15451 | 1 | 467 | DHSSSPAREQNWMEFEDEL EVGFRRWVITNSSELKKHVL TQCKEAKNLEKRLGELLTRIT SLEKNINDLMELKNTARELHEA YTSINSWINQAEERLSEIEDQL NEIKREDKITEKMKNSTTVRVA ASMQSKLLQGVAEEGPLRLTR SASF |
| 15362 | 45730 | A | 15452 | 2 | 632 | |
| 15363 | 45731 | B | 15453 | 355 | 894 | |
| 15364 | 45732 | B | 15454 | 99 | 716 | |
| 15365 | 45733 | A | 15455 | 1 | 1140 | |
| 15366 | 45734 | A | 15456 | 1 | 1476 | MEVNREKQLNELEVIGSEEQNL EEGLMIGGVAVRLVPDDIVIP GGVNATNGTEARDALRVKVA MSVTLLSGIIQYLLSALGWSY YTVDGVSQKNPRALGVTA DQLHAIFTTMSDEQASFRFG FVAIYLTEPLVRGFTTAAAVH VFTSMKLYLFGVKTKRYS GIFSVVYSTVAVLQNVK NLNVCSLGVGLMVFG LLGGKEFNERFKEKLPA PIPLEFFADHNSSPAREQK WMENEFDWTEVSFRRWVIT NSSELKEHILTQCKEAKNLE KRLEELLTRITSLEKNINDL MELKNTAQEFHEAYTSINS /RNQTEERVSEIEDQLN EI*CKDKIRIEKKRMKRNE QSLQEIWDCVKRPNLRLT GVPESDGENGTKLENTLQD IIQENFHNLARQANSQIQEI QRTQRYSSRRATPRHIIIR FTKVEMKEKMLRAARE KGRVTHKGNPIRLIADLS ADTLQARRQWEPFIFNILK ENFQTRISH |
| 15367 | 45735 | A | 15457 | 1 | 1185 | |
| 15368 | 45736 | A | 15458 | 1 | 2367 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15347 | 45715 | A | 15437 | 2 | 881 | HARCTGIAARAGLLDPRHTGEA LAARSRIDLARRPHWPRGCGTG GGGGGCAGLGGAWLGRNDVA VPARALVTAAPASSSMSPPIPA AARPVSSSPAASPSRCGLRAG PAELRCPRRLRQARAEPPRAG PAPGRRRPTPGICAPLSPRLRA GGTAPSLPGVTRGSRVGRRLRP SLGGAGCRVVKRPPRLPPGRR CSTGLPPPAGTGAPAGVCWED GDPGHELAALLRLGGQIRAL AGHRTAGWAQHGLSPREAVRP APAARGTLLRRSNSRRHLQNP ANFGGTLAT |
| 15348 | 45716 | A | 15438 | 3 | 502 | GRRDSCLPGVVAPRACLHPRG QVPRLGSGKMATPGMSWQQ HYYGGSAAKFAPSPATAQLAG HSMDYSQEMHLKMSKKIAQLT KVIYALNTKNDEHESAIQALKD AHEEEIQHILAETREKILQYKS KVTEELDLRRKIQVLESSLEDHI KMKQQALTEFEAYKHR |
| 15349 | 45717 | A | 15439 | 29 | 230 | LQIDCKNKPAILRGPTDPLKEA DCYCRTWERPQILLPKWEGTR KPILVI*QNKAHQHAPQITLLHQ |
| 15350 | 45718 | A | 15440 | 73 | 335 | FFWGGIEEPCFVILSGSVFWFL IWVGASASPVVGDVFGRGGSPP PTSTVGFTVLWGVSWVLKRV CGSSWDC*FVLAINLELKFTM |
| 15351 | 45719 | A | 15441 | 373 | 513 | |
| 15352 | 45720 | A | 15442 | 1585 | 1649 | KNSNIQHSPKITLVHQWQWFQTK KKFLIYLKKNSGGLVDP*MVHT TRLCADNPQYQPRARKSHS*VK GESTTLREHPMGQKNLNNSLQP |
| 15353 | 45721 | B | 15443 | 1 | 696 | |
| 15354 | 45722 | B | 15444 | 49 | 525 | |
| 15355 | 45723 | A | 15445 | 113 | 474 | SIPYKNKEEEEGKGGEYYIKGT CHGTKGSEQQPSALDLPDRAY PNEKEPEN*LI*QNKAL*HS PKNHTSSP/RNGSKPRKSLNL KKNSGG*LLS*LGRHQRKVKN ARKSKNQYKK |
| 15356 | 45724 | A | 15446 | 47 | 614 | TGCPRCQNSTCIAAVKMEGPL SVFGDRSTGETIRSQNDVTITN DGATILKLLVEVHPAAKVLCEL ADLQDKEVGDTTSVVIIAEL LKNADELVKQKIHPTSVISGYR LACKEAVFYLTENLIVNTDELG RDCLINAAKTSMSDDIINGDF FAN/MVVDVLAIHARHRGQ/P RYPVTLLY*SHGES |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15343 | 45711 | A | 15433 | 26 | 963 | FMIWAGQNRKVQDFVIQLRML TPVVPPPQAAPNAQQPRAAASA PQTRVRAPRWPLGNVVVLGTE DAAGPSRPASEPPASPALPGPAL ELGLPNHPKQT/HRPRLAPRRSH PKDSCTIFKLNSFLKNIKFNNSV GDQVNLDYKLISGTEYDILNFW NFRILAKTGCSKDGHNRNPRSRP TQEEGSGKPKKSLVKERSGAQE DLPVPPEEKLELSGTSMPCCFS KTSYGIPHIYILSYKGTATAG HRWPAAYPAPLNCSPPPETTM PVSDLGSPHWAASRIATPPSMW LCCLLAAALRVLAVSNSAEVY SQS |
| 15344 | 45712 | A | 15434 | 803 | 1305 | RSKPCRSSHNVFSWWAHSRPC CPWSGYSSRLCCLSCCITLGPY QLKNRQQRNGSYKSGNYLCV GNRLLFWVWIIFQGGKGRS/WLP RSDWVTSYKVMVSNDSHTWV TVKNGSGDMIFEGNSEKEIPVL NELPVPVMVARYIRINPQSWFDN GSICMRMEILGCPLPGWEH |
| 15345 | 45713 | A | 15435 | 2 | 377 | ARELLKAVWRPHKVA VMHCR GHQRASTLVGLGNSRADSEAR KAPSAPFRASVTAPLLPQAPDL VPTYSKEENDFLQAKGGQVME EG*IRLPDGRVA AVVLAVHETT HRGQELLEKLLGWYFYISH |
| 15346 | 45714 | A | 15436 | 77 | 679 | KMKTNQMGLKSKVVEMNATIS EIRLNINRKDVEYQQEILQLEAV WKLHKVAVMHCKGHQRASTL VGLGNSRTDSESPKAASAPLRA SVTAPLLPQAPDLVPTYSKEEK DFLQVEGGQVMEEGCIRLLDG RVAVPQLLGAAIVLAVHETTHL RS/ESSLGKLLGQLFSTISHFVSL CQNLTRQCVTCRQHNARQGPA VPPGMQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15341 | 45709 | A | 15431 | 129 | 444 | WGGPGRQPDGGRVPGRCGPRR PATWESPAACRPRPQSRHHSFE *GGSRS GSSSHKRPCPSSPAVLRA RDQVVLHTSFEATEGDSSHEDR STPLARRCLCSHRSGEA |
| 15342 | 45710 | A | 15432 | 1 | 2446 | METSLMVQVCGRDCNALLPG NLCSQPTQVLPLEVDGDDGPG GLPLNAAPPSSVPPVPPSEALPP PACPSAPAPWRSIISRLFGTSPA AEA AHPPP GGALDFGALRTSSC LSQSHGHIPGGPGLGLGAVRVP VPSEEDPASLFTEPVPAEAPAT VQSVEDFVANDRLDRSFLEDM TPARDEKKVGAKAAQQDSDTG RASRAPEQQIPHGGHWRGHSRS YERFRPPDMVSAGPGPSDGEAL GGNPIVAGFQDDVDLEDQPRGS PPPPAGPVPSQDITLSSEEEAEV ADPPKGPAPAPQCSEPETKWS SIPASKPQRGTAPMTAAASPWP GGASVHTGLEKCSSTRPPAEIEP GKGEQASSSESDPEGPIAAQML SFVMDDPDFESEASDTQCRAVR RVLPAQRAENAYGSFAFQPGAL KPECRPTLKGGPGVPVSKAGKK TEATSPRPTGGASPLAHGATVG AAWGLGMASWPIGSSLAPTRA RTREPLQRRVGSELPGDPCSG SGASCRQVCARGRATSVRLPAL ESLWPLSSDGSAAREGLEGPR LRQAAAPGGPGPPLPPLSRPPSP ARRMRGGA AVAGRGAAAPLE GRVRLGVGFLAETAVRAGAGA LAAADAPPGSRTPRARPLVAAG SGAAGGRCPVPSRRQREAPSPL GGAGVDLQLECLTSEKAGVGA ATGGVLEALARAIQKKEIEEIQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15337 | 45705 | A | 15427 | 1 | 2658 | MIINTIITTTTTITITIIITIMSSSPIT ITNIITIIQHSHHHNDQRPSLGK CRGLYIRVRKVPGERATANSRC PINAQGIESCWNGVMALWLGP NSTCSRLPELTDSEDCQPADSP GDEDPKPWWDPPEAPLTGYF HPYGAAFPVRHAGNFKDRREV PHQDTSFCSAGQFWILPSACKT GRVALTLTLIGAYQTLTEADV KGLTAARAASPGAKWRTQFPC PAGTCSSQAGNGQLEDCLPYPP GPSAPVGSLSRSSANGEFIIGRVI KAMNNSWHPECFRCDLCQEV ADIGFVKNAAGRHLCPCHNRE KARGLGKYICQKCHAIIDEQPLI FKNDPYHPDHFNCANGIKLG VFLTDRKDLTADAQELKGELY CLPCHDKMGVPICGACRRPIEG RVVNAMGKQWHVEHFVCAKC EKPFLGHRHYERKGLAYCETH YNQLFGDVCFHNRVIEGDDE GDGFAHRYSPYDSCEVDQSPL GQQLKSIRKGPLAQSQPLTPV MLHPGCKTQIREAPGSAALSV RRRPRGLVPEESESAAVEAV RHIHLQNFSSRLLETNGQKLG GHFCDVTVCIEASLRAHRCGL AIGSPSFQDKLLGPSEIRVPSV VPVQTVRQLVELLYSGSLVVA QSEAPQVLMAASVLRIDSYRR MHADYRTRSSAPASTSAPALP TPVPPPLAPEQLRHRLRHLLAA |
| 15338 | 45706 | A | 15428 | 708 | 892 | |
| 15339 | 45707 | A | 15429 | 2 | 713 | |
| 15340 | 45708 | A | 15430 | 212 | 1246 | DLPLAVHGVQSDSGAQAVASR SGDESSIVCLKEESTVNMTFRCS LPLAVISVVSFTAKCQVKSEFII GRVIKAMNNSWHPECSAVTSA RKFWQILHLSRMLVDRKDLTA DAQELKGELYCLPCHDKMGVP ICGACRRPIEGRVVNAMGKQW HVEREQYMDPGILSALIDPKYL LILSHRGLHMKSMKGFYFAKL YYEAKYDLAKKYICTYINVQE RDPKAHRFLGLLYELEENTKA VECYRRSVELNPTQKDLVLKIA ELLCKNDVTDGRAKYWVERA AKLFPGPSAIYKLKN/DGWVRG QMVPKPDDEGVQVRGRSGRPD AGWRLNRRSSVGGSAWRLRPQ |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15330 | 45698 | A | 15420 | 1 | 530 | SRTTPGKAPKETWGQDAGSGK GGQGPTRKPPRRTSSHLPSSPA AGDCPILATPESPPLAPETPDE AASVAADSDVQVP\GPAASPKP LGRLRPPRESKVTRRLPG\ARPD AGDGDHLSAVAERP\K\SLHFD TETDGYFSDGEMSDSDVEAED GGVQRGPREAGAKE\VVVRMGV LAS |
| 15331 | 45699 | A | 15421 | 1 | 2989 | MLLVMYWAPPPPVHMSQFLT TGPKCLESLDHGRDSQEITAS GLLWLQHAACGLAQWNQKPH PPFLTLLQAEPPFERARSCDIYIR IKMLQTAQQHQVGLAPTERKE ALRGSQSPQKSASGQRPGLDR ELLMLIKISKCLRVPSGPSSVLG TESTGPVPGELVLCQQDAGATQ EGVCYGRELMICRCDSPRLME PWGVKGTPEVFRDITAMKIP DSYQLSPDDYYILADPWRQEW EKGVPAGAEAIPE |
| 15332 | 45700 | A | 15422 | 218 | 404 | |
| 15333 | 45701 | A | 15423 | 1 | 422 | |
| 15334 | 45702 | A | 15424 | 160 | 470 | LTMLFAACVFSGDEIMASEERQ PMEEEWSRSSTISGEDGERWTP DTAGKAAQGIAGDVVWVSPLP PSKVSAASKPPKS\HHPFFKWH NFSNLMKMFYKMYFSKN |
| 15335 | 45703 | A | 15425 | 21 | 375 | TFENTRFWDVQIPVPTGERRNE WALPPPGAGSV\PAAGWSRPLTP GRCD\SGRGRSRRRAAPLSRPL PPLRRSPTLPGEPPAHRPLRVH PRHGPRPSHL\ACLNSQAPDASR LRASANQ |
| 15336 | 45704 | A | 15426 | 155 | 340 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15325 | 45693 | A | 15415 | 1 | 1272 | MWSGAGPGLAVWPQLVTVLSL SLSRLNCKWGLSFLACLLLG MADAAMQHYGVNGYSLHAM NSLSAMYNLHQQAQAQAHA PDYRPSVHALTLAERLADIILEA RYGSQHRKQRRSRFTAFTAQQL EAEKTFQKTHYPDVVMRERL AMCTNLPEARVQVWFKNRRA KFRKKQRSLOKEQLQKQKEAE GSHGEGKAEAPTPDTQLDTEQP PRLPGSDPPAELHLSLSEQSASE SAPEDQPDREEDPRAGAEDPKA EKSPGADSKGLGCKRGSPKADS PGSLTITPVAPGGGLGPSHSYS SSPL/SPLPSAGAIPPAHGGHQ PGALLVLRSRGSGPCCCSGGCC CALPGRQHGPAGLTA/SASPTTS PCQQPLP/SQGVWGSPLLAPP AGLAPASATLNSKTTSIENLRLR AKQHAASLGLDTLPN |
| 15326 | 45694 | A | 15416 | 1 | 1152 | |
| 15327 | 45695 | A | 15417 | 8 | 82 | |
| 15328 | 45696 | A | 15418 | 1 | 1350 | MGSEKDSSEPRSTSLHAAAPDP KCRSGGRRRLTLHSVFSASAR GRRARAKPQAEPPPPAAQPPPA PAPAAAQGPPEALPAEPAAEA EAEAAAAAEPGFDEEAAEG GGPGAEEVECPLCLVRLPPER PRLSCPHRSCRDCLRHYLRLEI SESRVPISCPECSERLNPHDIRLL LADPPLMHKYEEMLRRLAS DPDCRWCPAPDCGYAVIAYGC ASCPKLTCEREGCQTEFCYHCK QIWHPNQTCDMARQQAQTLR VRTKHTSGLSYGQESGPADDIK PCPRCSAYIIKMNDGSCNHMTC AVCGCEFCWLCMKEISDLHYL SPSGCTFWGKKPWSRKKKILW QLGTLIGAPVGISLIAGIAIPAM VIGIPVYVGRNIHSRYDGKENS KHKRNLAITGGVTLSVIASPVIA AVSVGIGVPIMLAYVYGVVPI SLCRGGGCGS |
| 15329 | 45697 | A | 15419 | 2 | 540 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15321 | 45689 | A | 15411 | 399 | 1089 | LLTPRTDLQEMPLDNAEIEWYT DGSYLRGEVFQWYDHLALIFVP QTGIEDVIWHIEALPNYIQKVCE RRNPYNQILSLQCAQHEIFLVS WKL VCKQLEGDDDM LVGTTA SNLLESEQSTS NLNEKINHLEY EDQYKDNNFGEGNDGGILEDK LISN/NMGGPDSPDSVNPVE/P/M PTMTDQTTLVPNEEEAFAL EPI DITVKETNAKRKRKLIVDSVKN LDSKTIRAQLNDY |
| 15322 | 45690 | A | 15412 | 3 | 809 | FKDDDM LVSTT SNLLESEQS TSNLNEKINHLEYEDQYKVDNF GEGNDGGILDDKLISNDGGIF DDPPALSEAGVMLPEQPAHDD MDEDDNVSMGGPDSPDSVDPV EPMPTMTDQTTLVPNEEEAFAL EPIDITVKETKAKRKRKLIVDSV KELDSKTIRAHLSDYSDIGTTLD LAPPTKKLMMWKETGGVQKLF SLPAQPLWNNRLLKLFT RCLTP LVPQDLIKRRKGGEADNLDEFL KEFEHPEVPREDQQQ*HQQRD VIDEPII |
| 15323 | 45691 | A | 15413 | 1 | 595 | MVNRSHFRGVGEPCHQQNSHG HLNSITETSN SPTLRAAPLQPTR DPSDMAVFEIDELPEGAVKPPA NKYPIFFFGTHETAFLGPKDLFP YKEYKDKFGK\SNKRKGFNEGL WEIENNPGVKFTGYQAIQQQS SSETEGEGGNTADASSEEEDR VEEDGKGKRKNEKAGSKRKS YTSKVTKLLIVINVICISIKHF |
| 15324 | 45692 | A | 15414 | 41 | 785 | GKGWAGGASGPANHGPAAGG RSPGMLRGDQGLPGRGAAGM ARPRSRE\YKAGDLVFAKMKG YPHWPARIDELPEASVKPPTNK\ YPIFFFWHPMKPAFLGPQDLFP Y*EYRGKFGK\SNNRKGFNEGL WEIENNPGS/IRFTGYQAIQQQ SSFRTEGEGGNTADASSEEEDR RVERDGGKGKRKNEKAGSKRK KSYTSKKSSKQ\RKSPGDED\D KDCKEEENKSSSEGGDAG\NDT RNTTSDLQKTSEGT |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15311 | 45679 | A | 15401 | 1 | 406 | MEEGWIRLPDGRVAAPQLLGA AVVLAVQETTHRGQESLEKLL GRYFYISPLSALAKTVRQRDFA DFGTTIKQDFRLLGQTSVDRLL QLSQGQAVKGNQLLPVSLTSQ CQVYKCVWNWWVLGLTDFKN EATDPPGVKLQTFVSVTTHKG SVDPNSEKQQDLLQRAKEQSFH SVEGDPSRDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSR*RAI SCCPSH*LPSAKCISVSGIGGFL VSLTSRMKPRTLLE |
| 15312 | 45680 | B | 15402 | 1 | 930 | |
| 15313 | 45681 | A | 15403 | 391 | 617 | LQLQPTG/CNFLYFYVGYMKIL GFCFHHIVEERGGCLWYPCFYC NLSLLGG*RSCSHTRIVPSLLMP KLGP GGQVC |
| 15314 | 45682 | A | 15404 | 1 | 1860 | |
| 15315 | 45683 | A | 15405 | 1 | 531 | |
| 15316 | 45684 | A | 15406 | 2302 | 2691 | |
| 15317 | 45685 | A | 15407 | 520 | 2883 | |
| 15318 | 45686 | A | 15408 | 3690 | 4727 | ENCHWGCHEPCDIGSSIIISPLA YWEQYHRVTYISRDEGSIIVFP ALVTMLRNLFILAGSSDPHFHT PMYFFLSNLSWADIGFTSATVP KMIVDMQSHSRVISYAGCLTQ MSFFVLFIACIEDMLLTLMAYDR FVAICRPLHYPVIVNPHLCVFFV LVSFFLSLLDSQLHSWIVLQFTF FKNVEISNFVCDPSQLNLACS DSVINSIFIYLDSIMFGFLPISGIL LSYANNVPSILRISSDRKSKAF STCGSHLAVVCLFYGTGIGVYL TSAIVSPPPRNGVMASVMYAV VTPMLNLFYISLRNRDIQSALRR LLSRTVESHDLLSQDLLHPFSC VGEKGQPH |
| 15319 | 45687 | B | 15409 | 1 | 3195 | |
| 15320 | 45688 | B | 15410 | 1 | 1819 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15304 | 45672 | A | 15394 | 1 | 1515 | MGQVFRVVTGVGEQPGHPDQF PYIDSWLSIIQNHPKWLQACFET YCKTLMAQIKPGTIERDCKASV KEKDSQEKQKKPVLQAPPEELE SPALYAPIYPSLARLRQEAAPA APRGSDSEESTPQATPCREEPEP LPEKETSSSYRSNAVHFLIHNPT WADCKQLLQSLFNTEEHHRVI QAAFQWLENNAPAGTGYIRQY AQQALPIEADTGWDPNQAQGL QSLQWYREALNGIKAGGKKA TNIGKVSEVCQKPDESPSEFYER LCEAYQLYTPFDPEAAGNQCM VNVAFVSQAQGDIKRKLQKLE AKAVLRGKFIALNTYIKKAERA QTDILRSHLKKELKKQEQTSKA SRRKDVTKIRAELEIETTTTKI QKINETKSWFEKINTINRPLAR LTKKSREKLQITSLRKEMGDTT TDTEIQKIIQGYEHLIAHKLE NLEEMNKFLEKYNAPSLNQEEL HTLNRPIRNSEIEVVIKKLPTKK/ SPGQDGFRASQYIFKEALV |
| 15305 | 45673 | B | 15395 | 1 | 1077 | |
| 15306 | 45674 | A | 15396 | 69 | 290 | YYFDSPIHPLHLSGTLRPGGSRQ FPCDPQFLCRLHHTLASL*SLPG DLLRGLLHKLVCRRVERLDLASL YAVGR |
| 15307 | 45675 | A | 15397 | 62 | 201 | |
| 15308 | 45676 | A | 15398 | 3 | 429 | LPSSVPRQPKMQARCLSRISRA VEIYESDLEEGQGLHEFSQFVL DRPPPTQSRYAQELVHTCYLHT LASL*SLPGDLQRGLLHKLVCRR AERLDLASHHAAVGRSEFFW TPYTHSPPGAGVGHPFPWHTRL PWGVPAEGHQ |
| 15309 | 45677 | A | 15399 | 303 | 612 | PSSSIPVYHCSLRGICIPVLGLKR AANVGVSLEASPLLSTPGGLGI CLSCGGTRTVGSRVGSIFPW*G EGTTGITGSISCKGSSDVGSNRT SGVDFPRRVE |
| 15310 | 45678 | A | 15400 | 1 | 273 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15297 | 45665 | A | 15387 | 207 | 605 | FQASAERFGTEDD/GSLRTRPPV MQSHQWPWRRPRPLVSRGRPQ TTPERHDSGGSLPLTPRMESH EDEDLA/EGCRWP/EAGTVGVP GPRAQGAAQR/QAVLARKKHR RRPSKRKRHWRYLELSWAEEK QQRDERQS |
| 15298 | 45666 | A | 15388 | 193 | 407 | ACPKTSKNLRQRLWNLAKHE F/SVDMTCGGCAEAVSRVLISLE VRVKYDIDLPNK/KVCIESEHS MDTLLATL |
| 15299 | 45667 | B | 15389 | 321 | 625 | |
| 15300 | 45668 | A | 15390 | 275 | 690 | SLWPPVIRG/SPKGNRPAILTYH DVGLNMANKKSGDHPEREGTP RSFREVVSAFGPGSSKLQIPKGS APRCGVPGRGARRELQSFRAGP RTQGSPVGPRCQSRRLRSAQEE SAKARHGGLRAHRSFSWDIRM SSKERKFS |
| 15301 | 45669 | A | 15391 | 2 | 137 | PGRYRPN*LLLSASPAGNEF QSTFLTPTILPSLRFPVLYTPNS |
| 15302 | 45670 | A | 15392 | 1 | 648 | MSLRKLTIMVEGKGGPNIPHAC GCRQRSSIKVSLPAVTSKSESP KEPEQLRKLFIGGLSFETTDESL RSHFEQRRTLTDCAVMRDPNT KCSKGFGFVTYATMEEKYHTV NGHSCEARKALSKQEVASASS QR/GRSGSGNFGGGHGGGFGG NDNFGHGENFRGHSSFGGSHG GSGYGGSGDDYSGFGNDGSNF GGGGSYNDFGNYSNQSSNFGP |
| 15303 | 45671 | A | 15393 | 1 | 3629 | MTGICYTEDERSYKKNAPTA ASKKQKETQKFCLRVDGQQKV KLSVLQEKSAQLTVQLKSQKFL GHPTAGRGRSELCLDLPDPED PVALETRSVGTWVRERDLGMP DGEAALAAKVAVLETQLKKAL QELQAAQARQADPQPQAWPPP DSPVRVDTVVRVVEGPREEVV ASTAAGAPAQRAQSLEPYGTG LRALAMPGRPESPPVFRSQEVV ETMCPVPAAATSNVHMKKISI TERSCDGAEMKWEDQNIGD |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15291 | 45659 | A | 15381 | 352 | 822 | DPRRVQAFPAKMKFNPFVTSR SKNRKRHFNAP\SHIRRKIMSSP LSKELRQKYNVRSMPIRKDDEV QVVRGHHYKGGQIGKVVQVYR KKYVIYIERVQREKANGTTVHV G\IHPSRVVITRLKLDK\DRKRIS DRKAKSRQVGKEKGKYKEETI EKMQE |
| 15292 | 45660 | B | 15382 | 80 | 432 | |
| 15293 | 45661 | A | 15383 | 11 | 888 | VKCRKAEGRRRESRLQTFEESQA VEAAMANVPWAEVCEKFQAA LALSRLVELHKNPEKEPYKSKYS ARANMEEVKALLGPAPEDED ERPEAEDGPGAG\DHALLPAE VVEPEGPVAQANRLRLA\NMF HLGVNHIDTEELSAGEEHLVKC LRLRLRYRLSHDCISLCIAQT WRCIGVRDPPTSSCAFLSTSPTP VHSVKKIQTPGRLRPSNSTLVD DMESSFQTCFASPLSQDYVNGS NQEEIGTGVDRCIHKFLDIARQ NISFLQKRLQLSVQKPEQVINED VDVSELRNE |
| 15294 | 45662 | A | 15384 | 1864 | 2705 | WPGKVLAHRLHPWHRDPHGS GGGAGQELRRQGGCLEQLLYD AAHAQRLPPLDSVLPRAALPQD CQRASACEGDPTLLRPSHSPGH PRGAEER/VPSTACLQRSWEGR/ WNRALQQVGGGLKSPWRGEYK EPRHPPPNQANYHQTL/ACPAE R/CFRQGPQGPQQLRRQQAEP SSSLLSHQSPQSQTSLLP*L*AR RSLGCGNPYLCPPWSQPLPETP AHQSGKQPSRSRNCSSWK*NYS STACPSHFLWRSRKFSTRASAST ASPCRMTVRRTHQRPLKARGTP |
| 15295 | 45663 | A | 15385 | 1113 | 1378 | RPHAESFVSGGIPDPGPGPGST GPGPL/ERQPCSLTSWPREPSSS SMKMLTQGPSLTAPYKGTILGE VNPAHAISSARNTSSRTSV |
| 15296 | 45664 | A | 15386 | 285 | 722 | TPAHPGVPPGQSGRHRHW/QSA ARSQLQPSAW*PKTGSFATTW RCQTRASTCSAHWPLMAASPG AGGSSMASWR/DRP*PCPPPPAP HLPEAAFLLR/CHDACP*NTGSA VPRGSCQPPAQWQDQGLAATR WGQAERLPRIYNWALAPP |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|--|
| 15279 | 45647 | A | 15369 | 2 | 621 | RFIKMLSRHHQHVVHVLPLLRA PLPVAMEEEIPALFIDNGSGM/C KSSFA/GDNALRAIFPSIIGHPRH QGVMVGMGQKDSYVGDQAQS KCGILTLKYPIKHGIVTNWDDM EKIWHHVIFYNELCVALEEQVV LLTEAPLNPRANREKMTQIMFK TFNTQAMYVAIQAVLTLHSSGC TTGIVMDSGDGVTHTVPIYERH TLPHTILHLDL |
| 15280 | 45648 | B | 15370 | 1 | 966 | |
| 15281 | 45649 | A | 15371 | 2 | 228 | |
| 15282 | 45650 | B | 15372 | 1 | 816 | |
| 15283 | 45651 | A | 15373 | 256 | 384 | RKLLNEAPC*PMR*HSLLNRLA TSCNSWTVPVVPKFSKLRRGL |
| 15284 | 45652 | A | 15374 | 145 | 375 | KIAGKNRLNRNQCKERKVQVL WISEKKKQREAVEDSPSLDCCH KFPPGS*ERLHG*KRGQWF*PP HTVEKQMRSCLL |
| 15285 | 45653 | A | 15375 | 319 | 482 | |
| 15286 | 45654 | A | 15376 | 4776 | 5910 | VCSTAGDVNGVCLLYDLLHIA VASGSAKGEFFARKPLLAEGV IYDCLQEFKEKKLVPAATPHAQV LSYEALLSAHDTIAQKDFEPLLP PLPDNIPESSEAMRIVCLVKNQ QPLGATIKRHEMTGDILVARIH GGLAERSGLLYAGDKLVEVNG VSVEGLDPEQVIHILAPRPCLS MSLADLPPLPREVLVLAKLPV PSSSFLLQPREDCQGPQPSLIT WFAPLETEPGVDRAMSRGTIMF KVVPVSDPPVNSQMVYVRA MTEYWPQEDPDIPCMDAGLPF QKGDILQIVDQNDALWWQARK ISDPATCAGLVPSNHLLK/RIWT EPGICIFTKRLRCSGKQREFWW SQPYQPHTCLKSTLCEYCNCPT |
| 15287 | 45655 | A | 15377 | 2 | 405 | WSLVTRRALARVGLPG/SPPRL LLLPLLLGWGLRVAAAASASS GAAEDSSAMEELATEKEAEES HRQDSVSLTLFILLTLTILTIWL FKHRRVRFLHETGLAMIYGLEK ITIGVLDITGWPYCTIQPYNGFL |
| 15288 | 45656 | A | 15378 | 1 | 3804 | |
| 15289 | 45657 | A | 15379 | 349 | 622 | RPDVANLAFLARKEGTRKGFSL KKTAEASRWHEKWFALYQNV LFYFEGEQSCRPGMYLLEGCSS GGTSPRSFRSSSRDSPISIPLHPT AK |
| 15290 | 45658 | A | 15380 | 314 | 483 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15276 | 45644 | A | 15366 | 3 | 841 | STPKMPKGKKAKGKKVAPAPA VVKKQEAKKVVNPLFEKRPKN FGIGQDIQPKRDLTRFVKWPRY IRLQRQRAILYKRLKVPPAINQF TQAL\DRQTATQLLKLAKHYRP ETKQEKQRL\LARA\KKA PKGTFTKRPVLRAGVNTVTT LVENKKAQLVVIADVDPIELV VFLPAL\CRKMGVPYCIK GKAS LGRIVHRKTCTTVAFTQVNSD KG\ALAK\LVEAIRTNYNDRYD EIRRHWWGGNVLG\PKSV\ARIAK LEK\AKAKELATKLGLNVHC |
| 15277 | 45645 | A | 15367 | 2 | 1006 | WINLKGNLLRKRLTSNFWPCK LRSRKRHTTRNLRLMNLWLSSH PPQQSNTKPWCCQLSCSTSLT LLGTSLPLLSYLIHLIPPGRQYP VIHRTSTLLLQHISVGKEKFHKS QHWGFCNNVMMMLQLQLSPLK GLSLVDKVNRPALSGTRVLAS KTAWRIFQEP/SEPKTAAAPG VEDEPLLRGNPCRFVIFPIEYHD IWQMYEKAEASFWTTEEVDLS KDIRHWESLKPEERYFISHVLVF FAASDGIINENLVERFSQIVQITE ARCFYGFQIAMENIHSEMYSLLI DTYIKDPKEREFLFNAI/ETMPC VKKKADWALRWIGDKEATYG |
| 15278 | 45646 | A | 15368 | 3 | 1368 | QAQPMGRVGGMAQPMGRAGA PKPMGRAGSARRGRFKGCWSE GSPVHPVPAVLSWLLALLRCAS TMLSLRVPLAPITDPQQLQLSPL KGLSLVDKENTPPALSGT\RVL ASKTARRIFQEPTPEPKTKAAAP GVEDEPLLRENPRRFVIFPIEYH DIWQMYKKAASFWTAEVVD LSKDIQHWESLKPEERYFISHVL AFFAASDGIINENLVERFSQEV QITEARCFYGFQIAMENIHSEM YSLIDTYIKDPKEREFLFNAI/E TMPCVKKKADWALRWIGDKE ATYGERVVAFAAVEGIFSGSF ASIFWLKKRGLMPGLTFSNELIS RDEGLHCDFACLMFKHLVHKP SEERVREIINAVRIEQEFLTEAL PVKLIGMNCTLMKQYIEFVADR LMLELGFSKVFRVENPFDPMEN ISLEGKTNFFEKRVGEYQRMGV MSSPTENSFTLDADF |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15270 | 45638 | A | 15360 | 40 | 1030 | RGDPRVRRRTQSLSPVLSLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL VESKIREHLEKKGPQVRDWSHY FKIIEDLRAQIFANTVDNARIVL QIDNARLAADDFRVKYETELA MRQS\VEN\DIHGLRNVIDDTN YHTDLQLETEIEALKEELLFMK KNHEEEVKGLQAQIASS\GLTV E\ADAPKISQDLAKIMA\DIRAQ Y\DELAR\KNREE\LDKYWSQOI EESTTVVTTQSAEVGAAETTLT |
| 15271 | 45639 | A | 15361 | 1 | 438 | LHSDDSLQMLRCSPVATAASY TSGPGAPISSSSFVRVGSSSFQGG LGGGFGGASGIGGITAVMVNQS LLRPLNLEVDPNIQARF/VHTQE KEQIKTF/NNKFASFIDKVRFL EQNRMLEAKWSLLQQQKMAQ SNMDNMFQSYINNL |
| 15272 | 45640 | A | 15362 | 176 | 1455 | EIFPLVIQKSYKVSTSGPRAFSS R\SYTSGPGAPISSSSFVRVGSS FQGGGLGGGFGGASGIGGITAVM /VQVLHTQEKEQIKTF/NNKFAS FIDKVRFLQQRNMLEAKWSL LQQQKMAQSNMDNMFQSYIN NLRWQLETLGQEKLEAELG NMQELVEDFKKKYHDEINKHT EMENEFVLEIKDVDEAYKNKV ELESLEGLTDEINFLRQLHEEE IWELQSLISDTSVVLSDSSHSLD MDNIITEVKAQYKEIANCSWAK ADSMYQIKYEDLQMLARKHGD NLRCTKTDISEMNQNVSWLQA EIKGLKGQRASLEATITDAEKR RELAIKDANTKLELEAALQW AKQDMAQQLRVYQELMNVKL ALDIKTATYKKLLEGEESWQES RMQNMSIYSKTTSGYAGGLSS AYGGLTSPPLSYGLSS |
| 15273 | 45641 | B | 15363 | 70 | 915 | |
| 15274 | 45642 | C | 15364 | 62 | 217 | |
| 15275 | 45643 | B | 15365 | 1 | 612 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15259 | 45627 | A | 15349 | 3 | 354 | EAFGGERVSSTMSGLSGPPARR GPFPLALLLLFLLGPRLVLAISF HLPINSRKCLREEIQGPASDW RVRDLRPVWGRWRPAQ/RTSRS QILLAIFSTPKRMQPRGNLPLTT EDYDMF |
| 15260 | 45628 | A | 15350 | 283 | 393 | YVYRRYGRFE*NDPSSALMST* GKRCQDCLDQRENKK |
| 15261 | 45629 | A | 15351 | 1 | 351 | |
| 15262 | 45630 | A | 15352 | 1 | 867 | |
| 15263 | 45631 | B | 15353 | 1 | 1323 | |
| 15264 | 45632 | A | 15354 | 1 | 3669 | |
| 15265 | 45633 | A | 15355 | 362 | 1039 | LESYLQLPSAEGKTVSVFGETC ATPVGP/AAGPHTQ/LAQNIVTS WLTGGRFIELKTVQILDRLELE KPCIDAEDECFTNEWSTFTLL KAWDEYLKAWFALHLEAMF QPSDSGKSFIFNMSVGYNLEGQ PLNPKNYP SQGVPRVLKSHRQD YLVGNKLSWADIHLVELFYYV EELDSSLISSFLLKPHTHVDNT KKGSHPHMCA YTDYVNNPND RMPQREITFVS |
| 15266 | 45634 | A | 15356 | 74 | 208 | QRLTKLRETSRRLLSWQRSPSS TSMHGAEWSPPRWLLAAAGV EFEEKFIKSAEDLDKVRNDGYL MFQQVPRLRLMG*SWSRV |
| 15267 | 45635 | A | 15357 | 308 | 735 | NQRCTWAYSMTMEIFLISCVKT LSVRYAVQQLKTGVFCSLETQP SKMAPAKKGSKKKKGHS/AIIE VVTQENTINI QKHIHEVGFKKC APRALKEIQKFAMKEMGTPVV LIDTRLNKAVWAKRIRNVTNRI HLCLSRKCNEDE |
| 15268 | 45636 | A | 15358 | 3 | 323 | LSSLASMSFTTCSAFTNYWSPG SVQVPSYGTQPVSHAASVYAG LGGSGSRISVSHSPMAGGLAG MGGIQNEKETMQSLRDLASY LDRVRGLETENWKLESKIQEH |
| 15269 | 45637 | B | 15359 | 1 | 991 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15254 | 45622 | A | 15344 | 1 | 4320 | |
| 15255 | 45623 | A | 15345 | 1 | 966 | MNVNLA EESK GKETV GDEIKG GGIQMV MLASQ PLTSYCAARFI TGHGQK LKSELK KTLQVIMLNI QKVRIP TRDGYNEKDILSTGKN VEKLELS NIAGYPSNIEKKEYQE QSVLSCC SERKDANPKSVVCSF FMQEQT KGEKRFLIPGTLSD RHLRYFG ILPTVSNA AVVKEVP TVSNA AVVTEAPTGSNA AVVT EAPTGSNA ARVMEVPTGSNA VVTEVPTGSNA AVVTEAPTGSN AAVVKEAPTGSNA ARVMEVPT GSNA AVVKEAPTGSNA ARVME VPTGSNA AVVKEVPTGSNA AV VKEVPT/GSNA AVVKEAPTGSN AARVMEVPTGSNA AVVKEAPT GSNA ARVMEVPTGSNA AVVKE VPTGSNA AVVKEVPTGVTLRW SRKRPRE |
| 15256 | 45624 | A | 15346 | 1 | 702 | |
| 15257 | 45625 | B | 15347 | 238 | 546 | |
| 15258 | 45626 | A | 15348 | 632 | 2361 | FQSR TFLKNW NPGEQS QKII/CF QLGERAY QTDVL VKVPRQSSV FSENQRM NNPWFESTGCGK TYNQNR AFNQHQRFHSGEKTY EHNECGK AFSWPSILSKHQRIH TGKKLYT CEDCGKSFSVHSYFI QHCKIHTREKPYECIKCGKAFS THSSYVQHLKIHTGEKHHECNQ CGKAFSHSSNLIHHQRIHSGEKP YKCKEKGKAFNRQSNLIHQHRI HSGEKP YDCKEKGKAFSTQLFL IQHQRIHTGEKPYECNECAKSFS LNRTLTVHQRIHTGEKPYRCNE CGKSFSQCSQVIQHKRIHTGEK PYICNECGKSFGARLSLIHQHRI HTGEKPYGCREKPYECSECGK AFSQSFNLIHHQRTHNGEKSYE CNECDKAFSLSSLVQHQRIHN GDKPYECHKCGKAFSQGSHLIQ HQRSHIGEKPYECNECGKTFGQ ISTLIKHERTHNGEKPYECSDCG KAFSQSAHLIHHQRIHTGENPY ECSECGKAFNVCSSLIQHHRHT GEKPYECSDCGKAFSQHSQFIQ HQRIHTGEKPYMCNECEKSFSA CLSLIQHKRIHTGEKPYVCAKC |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15248 | 45616 | A | 15338 | 1 | 2800 | SISGPGQEA VPLRPKAEPPEGSG MVWDRQTKMEYEWKPDEQGL QQILQLLKESQSPDTTIQRTVQQ KLEQLNQYPDFNNYLIFVLTKL KSEDEPTRSLSGLILKNNVKAH FQNFPGVTD FIKSECLNNIGDS SPLIRATVGILITTIASKGELQN WPDLLPKLCSLLDSEDYNTCEG AFGALQKICEDSAEILSDSDVLD RPLNIMIPKFLQFFKHSSPKIRSH AVACVNQFIISRTQALMLHIDSF TENLFALA |
| 15249 | 45617 | A | 15339 | 8 | 450 | TWSWSPQAPSWARPSSQARAV SLLVARGQLCQGSRRRSGVGSR VDAGAARTALRTLGT RPRLRRP CGLGSHEKAAASGQDQGRGS RGRGSLGGRELGANEPYQ/WR AHTLTVLFILTCTLG YVTLL EET PQDTAYNTKSEIAVVHLS |
| 15250 | 45618 | A | 15340 | 246 | 559 | MPVAVMAES/AFSFKLLDQCE NQELEAPGGIATPPVYGQLLAL YLLHN/GQRIWQRDFPGIYTTIN AHQWSETVQPI MEALRDATRR RAFALVSQAYTSIIADDF A |
| 15251 | 45619 | A | 15341 | 129 | 915 | RSGTQGRSAATAALNVIAGATP EGQSWGLAVRTVQRRGRPAK MPVAVMAESAV\SFKLLDQC ENQELEAPGGIATPKVYGQLL ALYLFHNDMNNARYL*KRIPPA IKSANSELGGIWSVGQRIWQR DFPWG/IYTTINGHQWSETVQP IMEALRDATRETAPLPWVSQA YTS\IAR*FCQPLLGLP\EEAV KGILAEQGWQA\DSTTRNGSCP GKPVCRGPWDVFPFNKFISLYS EPAPV\PIPI NEQQLARLTDYV AFL EN |
| 15252 | 45620 | A | 15342 | 1 | 529 | MATLTISRAQTEDEADYYCHRI KLVKEGLDERTHKAYLSSSGK GCEFHMVKPGSPLGPDILGSWA QSALIQPPSVSGSPGQSVTISCT GTSSDVGSYDYVSWYQQHPGT VPKPMIYNVNTQPSRVPDRFSG SKSG\NTASMTISGLQAEDEAD YYCCSYAGSYPPVFGGGTKLT |
| 15253 | 45621 | A | 15343 | 399 | 737 | WISGGNSCATT/LSDAGLSTTSN SIGSATGARQAESASSQSGGGA LGRHCGASGKCAESLRREP VGS ATNQWAPGWVVG RPASDSSHV VIGLGRSAWSPA EVTPSLIPGRG RTK |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15244 | 45612 | A | 15334 | 1 | 1754 | MRNEISDLTEELHQKEITIAVT KKAALLEKQLKMELEIKEKML AKQKPWACLVNAMPAIQVVFN LGRFRKCQDPHKAQEWVYPGY SGSDCEVFPEIMTSKNREEAMP EWKLWKKVVLSGATDAPSWD GPTFTDLNVFAGNMGLSDCTL LGKIWKIPGHFLHTSGPVSFHT KGLLNTPTKERWVGFGSEGR GVPEPGGCFGVLA VPRRTPPSA AAMTGGERLGRA WAGDRAAA SRSAPVPGTFGMMGWRPVAFG KNAKAYRGFGGIVTSLTPSCDK VTLLFVRILPGSGQSRDQSSPEK LTDTKSTSNKAYGFPECLRRPE STHIFYDHLGSEQPRGTKGT PLKWVSQKTLERETRQCQALVI WTD CDREGENIGFEIHHVCKAV KPNLQVLRARFSEITPHAVRTA CENLTEPDQRVSDA VDVVRQEL DLRIGAAFTRFQTLRLQRIFPEV LAEQLISYGSCQFPTLGFVVERF KAIQAFVPEIFHRIKVTHDHKD GIVEFNWKR/LSTL*PHGLPSSL SVVCGVRSLSRCSVGF CWRSTP DPVCLCITSGGCRTASIAEQQKL LPDPSYRSFIPEGQPPI |
| 15245 | 45613 | A | 15335 | 3 | 125 | |
| 15246 | 45614 | A | 15336 | 764 | 1005 | |
| 15247 | 45615 | A | 15337 | 1 | 3533 | MELVNCVLMSTLGNTCCPMAI AMFRSSSSLPRPGHSLTGSPLRV NLIHIKFPLNDFHQNVVKIKNK DPPLGAAIGKESCPIADNELHSL ERRPLSPKL VQALGVAGLSRPG PPHTGCAIWLLITDHKLLSEIL YDLLHQGLDILADPPDEGGIPR GKNLVELLQLPGLEEDKAFQKE IGLKILVFKAYSTLSSDGPP LFS ALRSLQGVQSSKVGESREEKSQ TEEDPGNPWVPQSLGASVSSS GKWGCLRTKP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15235 | 45603 | A | 15325 | 3 | 343 | |
| 15236 | 45604 | A | 15326 | 1164 | 1648 | PLMTSAPWPSCCCWRSLSGRP AGRQRQLPTSITTANQPAPSR KKSTSRKKQRNLPAVSPAMVAI VRRSCDLYRWSVLHYASQERR VRDAAKPESD\RKRTTTKTRR/H WRYIKELESRQPGVADMRQQP TQLVEVPWNEQTPEQRQQTLQ RQHGRETRCSV |
| 15237 | 45605 | A | 15327 | 28 | 417 | |
| 15238 | 45606 | A | 15328 | 2 | 440 | |
| 15239 | 45607 | B | 15329 | 1 | 441 | |
| 15240 | 45608 | A | 15330 | 22 | 584 | IRGRVDPPSAVEPPPKMQIFVKT LTG\KTITLEVEPLGYG*KNVK AQASRDK\EG\PPDQQRL\IFAG KQ\LEDGRTLSD\YNIQK\ESTL/ HIFVLRRLRGGAKKRKKKSYTT PKK\IKHKRKKKG*SLAVLKYYK \VDE\NGKIS\RLRRECPS\DECGC WGVYGGVTFDRHYCG\KCCLT LLFQQTRMTSNCMS |
| 15241 | 45609 | A | 15331 | 3 | 954 | LDARRHWEGTPGFTHTSPDAW ADAWGKMAGEKVEKPDTK KPEAKK\VDAGGKVKKGNLKA KKPKKGKPHCSRNPVLLRGIG RYSRSAMYSRKAMYK\RKYSA AKSKVEKKKKEKVLATVTKPV GGDKNGGTRVVKLKMPRY PTEDVPRKLLSHGKK\PFSQHV RKLRSITPGTILITGRHRGKR VVFLKQLASGLLVTGPLVLNR \VPLRRTHQKFVIATFTKIDISN VKIPKHLTDAYFKKKLRKPRH QEGEIFDTEKEKYEITEQRKIDQ KAVDSQILPKIKAIPQLQGNLRS VFALTNGIYPHQLVF |
| 15242 | 45610 | A | 15332 | 670 | 1008 | WCILGVTPSLMSRTALFLSRHT FFA/RSHAASKL/EKKKKEKVL ATVTKPVGGDKNGGTRVVKL KMPRYPTEDVPRKLLSHGKK PFSQHVRLRPSITPGTILITG RHRG |
| 15243 | 45611 | A | 15333 | 1 | 708 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15230 | 45598 | A | 15320 | 240 | 924 | NGEQKCILCHIVYSSKRRH\SHE CRRCGPTEVLSAYAKHISGQL HKDNVDAQEREDDGKGEEEE DYFDKELIQLIKQRKEQSRQEPS SSSQEVNSDDSSSATFSVSFVYV WLKTILLTWPKEVKRLDTPGL ELWLVPNMAELSEPEGPVDWK ERCVALESQLMKFRVQASKIRE LLAEKLHHNERLEYRDQRKDS ASFQRKKQFTYKASGIEMASDL SKAPLEIRG |
| 15231 | 45599 | A | 15321 | 3 | 755 | LRLPRRSTRTRRGIWVRTGAAM GKVNVAKLRYMSRDDFRVLTA VEMGMKNHEIVPGSLIASIASL KHGGCNKVLRELVKHKLIawe RTKTVQGYRLTNAGYDYLALK TLSSRQVVECvGvNQMGVGKIE SYIYIVANEegQQFALKLHRLR RTSFRNLKNKRDYHIHRHNVS WLYLSRLSGMKFCYMKQFCD EQGSQRLRIHMMGGQMWAVPIC QPRDLFVWFVLRAEACAGCGA TSQQRGALGVTSTCYRD |
| 15232 | 45600 | A | 15322 | 1 | 1028 | MNKTITTQEEVLPQADVQRE EELNSLKQKLAAALLAEQEPQP ERLVSELQL\PRKAAVFQDEILR SSRQLVLPGLGVHRHVLVCC GGLRCPLAGGLAAASVGRGLGL VDCDVVEMSNLAYQVLHGEAL AAQAKAASAAASLRGLNLAPP PAETVTNCADGGMLRVLTGVL GCLQPLKVLKIAASLGPSSGS LLFDALRGHFCCIRLRSCRLDC AACGKWPTVTHLLDYEAFCGS SATDKCRSLQLLGPEDRVSVTD YKRLLDGAPHLLLDIRPKMEL PRKAAVFHDEILRSSRQLVLPGL GVLRHLLVVGCGGLRCPLAQY LAAAIvGRGLVAYDVV |
| 15233 | 45601 | A | 15323 | 92 | 778 | QGTRRWSLGTCSLMTRTQFEV CTKVVCVQESLQRPGEELKTRCP SVGAGYVNYGTPAHERI/GAAV KTGREADKPEVTKQTQFSTRK DE/TSLFGVPLQ*LLARHRAPP* RRT/RRLLEVARTPMLPAQASR SELAARQDSAWASPAAPASPN/ RSVLRCLLSARPPLCGPL/LRV LPSWRRQQIRENSAED*LHSEY RANRIRRRRGHPEN/WTKS*LE NPENLTRRSSAPAPC |
| 15234 | 45602 | A | 15324 | 142 | 500 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15225 | 45593 | A | 15315 | 3 | 3027 | AMEQAGTRPAATEHPRLRRPM PWLLLLPLLLLLLLLLPGPAASQ LRYSVPEEQAPGALVGNVARA LGLELRRLLPGCLRLNHLGAPSP RYLELDLTSGALFVNERIDREA LCEQRPRCLLSLEVLAHNPVAV SAVEVEILDINDNSPRFRPNYQ LQVSESVA PGARFHIESAQDPD VGANSVQTYELSPSEHFELDLK PLQENSKVLELVLRKGLDREQA ALHHLVLTAVDGGIPARSGTAQ ISVRVLDTNDNS |
| 15226 | 45594 | A | 15316 | 1 | 775 | MPCVNGKYNSTIQAGLQMAQI LQDEGPYEVGIDEETGSQKGDG IIRSSRKL LFTMALFLETNLLKD PLSRERRWRLDELDSGGREKG VAVFLRSAGIRQVQVAMEQAG TRP/AATEHPRLRRPMPWLLL/L PLLLLLLLLLPGPAA/SQ LRYSV PEEQAPGAL/VGNVARALGLEL RRLGPG/CLRLNHLGAPSPRYLE/ LDLTSGALFVNERIDREACLGS AGANPVAVSAVEVEILDIN/DNS PRFRPNYQLQVTARCWWTSW |
| 15227 | 45595 | A | 15317 | 2 | 165 | |
| 15228 | 45596 | A | 15318 | 1239 | 2251 | TCSSRARRPRRGRTVSQVRGPA PWAPRRARLQQRGSLRGAARS PASPTSA/PSYSRASASAGPAAL QPQGAVTPGPSANLAAPGGTL VPAEGPRMPPVTAQSASSHPAP SASQPSSPAAASRGSLSVPEVT ATLLASASSPTLDATRDAPATP RIAAPPGSATSSRGLGSQAQGSS LGTKESISDSFGLGSPAVTQRTT APPDSAALSQDTRPEAAGSWPG PQTGACSVGSGTDRRD TAAAT EAQHLSSSESKEKTS AQKSGNCF GILKADFTISTLMDPEEMKDQF LRQVRLPSTDALKKQSI SNYRP PGKGKPQQYLGDSAWN MVSA GTIEGFYKE |
| 15229 | 45597 | A | 15319 | 46 | 2859 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15217 | 45585 | A | 15307 | 1 | 785 | MWDVQGQDSSLLRGAGGPGQLQ WFGRLQLHLGGLREHRDAWV HSRGLGSCSGMQGAATPTQNG RGSCSPAPASSMEHAAPAVPP CCSWCDSSSRSRWPATATTETG PRTVPSAQESAVGLLTASLLKG DSGSTGFCPLLSLAAPGTQQC SLGFCCTFERKRSSVSPAAPGTA APELAAAALMLMPRKNQIAVYE LLFKQGVMMVAKEGVHLPRHPE LADKNVPLNLHIMKAMQ\SLKSQ GHREEQFAWRHFYWHLTREGI QSIQ |
| 15218 | 45586 | A | 15308 | 1 | 392 | |
| 15219 | 45587 | A | 15309 | 1 | 716 | |
| 15220 | 45588 | A | 15310 | 150 | 372 | RRSNEWGVVPVVPARTGGG/HG QKTPPSPLPPSSPPSPSPPPPPA \APAKIPPLPLPPLPPREAPPAP GPALP |
| 15221 | 45589 | A | 15311 | 218 | 740 | KSCPETVSRKRVGSIKKHQGD KFNPVCLKMTTKTEFVLCGWV PCRCL/REGEEETVTTLDYSHCS VLEQVP\KEIFTFEKTEELYLDA NQIEELPKQLFNCQSLHKLSPD NDLTTLPASIANLINLRELDVSK NGIQEFPENIKNCKVL TIVEASV NPISKLPDGFSQLNLNTQ |
| 15222 | 45590 | A | 15312 | 96 | 297 | |
| 15223 | 45591 | A | 15313 | 469 | 5174 | KMTSLAQQQLQRLALPQSDASLL SRDEVASLLFDPKEAATIDRDT AFAIGCTGLEELLGIDPSFEQFE APLFSQLAKTLERSVQTKAVNK QLDENISLFLIHLSPYFLLKPAQ KCLEWLIHRFHIHLYNQDSLIA CVLPYHETRIFVRVIQLLKINNS KHRWFLLPVKQSGVPLAKGT LITHCYKDLGFMDFICSLVTKS VKVFAEYPGSSAQLRVLLAFYA STIVSALVAAEDVSDNIIAKLFP YIQKGLKSSL |
| 15224 | 45592 | A | 15314 | 267 | 495 | GCLL**CLCIRL/SKNRAERALR PYSDVEALRLSSDFPFRQRPKG GSGWSLLSVEINQYYGPRVMIG RSNSEVVLVL |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15214 | 45582 | A | 15304 | 184 | 370 | |
| 15215 | 45583 | A | 15305 | 40 | 1411 | RGDPRVRRRTQSLSPVLSLSPDS MSFTTRSTFSTNYRTLGSVQAP SYGARPVSSAASVYAGAGGSG SRISVSRSTSFRGGMGSGGLAT GIAGGLAGMGGIQNEKETMQS LNDRLASYLDRVRSLETENRRL ESKNPEHLEKKGQVRDWSHY FKIIEDLRAQIFANTVEQCPTTV L/LRIDSARLA\ADDFRVKYE\T EAGPCAQSVENNIHGLCKVIDD TNVTRLQLETEIEALKEELLFM KKNHEEEVKGL*AQIASSELT EVDAPKSQDLAEIMADIRAQYD ELARKNREELDKYWSQQIEEST TVVTTQSAEVGAAETTLTELRR TVQSLEIDLDSMRNLKASLENS LREVEARYALQMEQLNGILLHL ESELAQTRAEGQRQAQYEAL LNIKVKLEAEIATYRRLLEDGE DFNLGDALDSSNSMQTIQKTTT RRIVDGKVVSETNDTKVLRH |
| 15216 | 45584 | A | 15306 | 392 | 1449 | GPWEMLMTIKSHPDARQPQR VKKLTQVFWSSASLRER/GKTY LFWPKLKAAEIPAAAYREALDE ALGISGGGRDVGERVYKGPSM MANPQKPVLEALSSNKYLHILC AKHCDRHEGYKDEIKVKEASS RVNGCVEAMLSAPLPLDRRNE HVESKGKPFMGLSPRVLSASR RDGLRERKGSFFRTTVVLHDTKT DSNSDTETNSSTPPRTLLEMQIL SPTWTYEISSRTLGCGPSVFQQ RASYSPPSVSGPRLGCPLMDGGR MRCPPGNPESCVSEANLIPISVP VAPHAHQHLVLSVFWKITIVIG GKTCVAQNHSNEAKMKQRPEI NHASPPGAFAWSQSGEPIASAM TVPA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15210 | 45578 | A | 15300 | 710 | 1831 | IRMKSKEIIARCIKPYHSMARTQ PGTRNKENGPGAPTALDNVASS DDTGRHRPQTTQLAPGFAHPLQ LASFRRMVLFSLSGEGRSRGGPE LQFPASCRREGSGSPGVRESGSG GIAATSTPNYPNPQDSKEHDIR GAEHQKQEQPAKPPHTARSAY PPQKSSYPANAKATRHSPETAA AKEARAPAAAQQRHQPNPSP APHTRPATAATRQPERRVPSPT HRHPAATRLSPRRQSPSPRPHH DRRGFPRLAETLQHPCMPLPLV ASAGHHRHRLLLLLAPQAPER EASDEIVFSGRSRSGCPTFEQE SAMCFPNPGLPDSCGESQAVTI LILRKFKQVIWVIEVPLDYKKG SWEYFSRMETIIMPFEINIQSE |
| 15211 | 45579 | A | 15301 | 77 | 1041 | IPSCVVSGIAAAF/HPGLASDAP ARASSWWTHVEMGPPDPILGV TEGFKRDTNSKKMNLGV SAYR DHNGKPYSIHKAEAQIAAKNLD EDYLSIGRLAEFCKASAEVALG ENSEVSKSGRFVTVTISGTSAL RIRASFLQRFLKFSQDVFLPKPT WGSRTPIFRDTGMQLQGYRY DRKTCGFDFTDVEDISKTP EQ SLLLLHACSHNPTGVDPGPKQQ KEIATVVKKT/RNFLALFDMAY QGFASGNGNKDAWAVRHSAN IRHCRCQSYTKNMVLHSEGVA GFTMVCKDADEAKRVESHLKI LMCPMYSNPPLNGTRLLLLPF |
| 15212 | 45580 | A | 15302 | 1 | 1263 | |
| 15213 | 45581 | A | 15303 | 1 | 1146 | MTGRQSLSPVLSLSSLDMSFT TRSIFSTNYLFLGSVQVSNYGA RPASCMA SVYAGAGGSGSRISV SRSTSFRGGMGSGDLAAGMAG GLAGMGGIQNKKETMQSLNDR LASYLDRVRSLETKNRKLESKI REHLEKKGLQVRDWSHYLKT EDLRVQIFANTVDNAGIVLQID NACLAADDFRVKSLMTNVTWL PLETEMEALKEELFMKKNHEE EVKGLQAQIASSELTVEIEKSTT VVTQTSTKVGD AEMTLTELRR TVQSLKMDLDSMRNLKASLEN SLREVEARYTLQMEQLNRILLH LESEMAQSRAEGQHIGEYEAL LNIKVKLEAESATYHRLDDDD FNLGDALDNSNSMQTI/QKTTT RRKVVSETNDTKVL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15208 | 45576 | A | 15298 | 1 | 2104 | MKHLKRWSAGGGLLHLTLL LSLAGLRVDLDLYLLLPPPTLL QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLLREVRALGVFPVPTSV DAWL VHSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGG\CASEE NGVLREKHEA\VDHSSQHEENE ERVSAQKENS LQQNDDDENKI AEKPDWEAEKTTESGNE\RHL\ NGTDTSFSL\EDLFQLLSSQP\EN SL\EGISI\WGDIP\G\SISDGHEF FKHIYHVNFQPR\IS\QD\VNLH EAILLCPNNTFRRDPTARTSQSQ EPFLQLNSHTTNPEQTLPGTNLT GFLSPVDNHMRNLTSQDLLYD LDINIFDEINLMSLATEDNFDPI DVSQLFDEPDSDSLSDSSH NTSVIKSNSSHSVCDEGAIGYCT DHESSSHDLEGA VGGYYPEPS KLCHLDQSDSDFHGD LTFQHVF HNHTYHLQPTAPESTSEFPWP GKSQKIRSRYLEDTDRNLSRDE QRAKALHIPFSVDEIVGMPVDS FNSMLSRYLTDLQVSLIRDIRR RGKNKVAAQNCRKRLDIILNL EDDVCNLQAKKETL KREQAQC NKAINIMKQKLHDLYHDIFSRL RDDQGRPVNPNHYALQCTHDG SILIVPKELVASGHKKETQKGK |
| 15209 | 45577 | A | 15299 | 2 | 342 | RRRFRVAAA AVGTA*AVVLSA RPSETWETRGRR*RICPSSWP* GI*VNNG*K*RRHSVCQCSLWF PARCIKPYHSMARTQPGTRNKE NGPAGPTALDNVASSDDTGRH RPQT |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15205 | 45573 | A | 15295 | 3 | 1024 | CGGIHSLVLRGCSLEPAFFYLRSA FSPTISACRHPMEDSMDMDMSP LRPQNYLFGCELKADKDYHFK VDNDENEHQLSLRTVSLGAGA KDELHIVEAEAMNYEGSPIKVT LAATLKMS\VQPTVFPWGAFEIT PTQWSLRLKCG\SGPVH\SGQH FSKLLEEDAE\SEDEEE\EDVKL\ LSISGK\RSAP\GGGSKVPQKKS KTL LLMKDDDDDDDEED\DDDED DG*WMDFGWMEEAEEKAPSE RNPIRDTPAKNAQKSNQNGKD SKPSSTPR\SKGQESFKKQEKTP KTPKGPSSVEDIKAKMQASIEK GGSLPKVEAKFINVVKNCFRMT DQEA IQDLWQWRKSL |
| 15206 | 45574 | B | 15296 | 1 | 1107 | |
| 15207 | 45575 | A | 15297 | 1 | 1968 | MLASMGVVAKEMKYLSSPYQP HAFHTRIKSLMTVNFQAQLWL PNEAGPTGDGDWGGDTHGCPS FSPHLPRFIQKQPWGTGRLLQ EHFCKSLVPVIPS RDIEAFHLH ADLILNTLPSLVIIHQIESHSEEL RARVSTYESGEDTIQCITVTWK PKYGATR WKDPGSPDGPLEER RLEDLSTRNNSIRLFRGCGYRV KQNSSQRPNKVCGLPDTGVLL QTKCGLVRNSQRSAQTNTKQH EELFSTAGIPENLSRRQEVLP GH GFTGWVGWTVKLTSGEGVTF HHL SATHKL SHASCRQGNFKP KGAMSVTRSTVHPHLAFLSAEI NGKCGRPCVFLGIWAINCGMAI LYERLSALVCVSVSERHLDYT MRFLFDIPPSTLEARIGSPLWAL SLHPLRSSTVTSSVELILPECTV AVLEIQYVFLGDTILFTTVGKA RSGTRDRDGGRAQIMQVLQ GK GRELDAAAQPEGQLLREVRVL GV PFIPRARVDAWL VHTVAVG SADEAHGLLGAAAASSTGGAG ASVDGGSQAVQGGGGDPRAAR SGPLDAGEEEKAPAEPTAQVAD AGGCASEENEVLREKHEAVDH SSQREENEERVSALKENSLQQN NDDENKIAEKPDWEAEKTSER NERHLNGADTSFF\SLDLFQLL |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15198 | 45566 | A | 15288 | 1 | 278 | MKFHDRGQMOPKPSPAEAVNS APQREPEGSILRAADPLVWAAK AMSASR/RGS/CGGSSADPRHTE RTPTEPDADTRFQPAETLAGPK TRAAGAG |
| 15199 | 45567 | A | 15289 | 5 | 545 | SFMTEAKSSPNPAQQLSTQRP SESARKVPSELQTLSCGLQRPCL HPGRPGDPYYASASTRTRSPS ARHAVWGRRGCYPEA/AVRAR EGPHPTLAPASTYGLASPPRAD SAHRPRHRSLTRLLPNRKLGG SADPRHTEPTPEDADTRFQP AETLAGPKTRAAGAGGQPWDS ANASPP |
| 15200 | 45568 | B | 15290 | 121 | 822 | |
| 15201 | 45569 | A | 15291 | 1 | 1308 | MLRMVGIEISNGQWSTPPCQVL HLEGNDIYNPKEQGLGNTCRW GWMAAGTRRNLCWAPFPFLNP VASLVLHSTIQIALQESKDRVL GTLINSPLVTSTDKANWSLRLA LEVGDGGGLVGLSPQPVGSGA MSRCPNCTRKLIGSGISPTSSTL AEEQGSVVKTHSHQGGARCSK EKGWQILLILVAGLCQLVVVV QNVGVRKIPRKYLAALRVAIGH ALAIERRRIRVDVADQAQDTDR DDRSFGRDRNRDSDKTDTDWR ARSATDSFDDYPPRRGDDRFGD KYRDRYDSDQYGRGYWYEYR DGPCRDMDRYGVGSGRRAFG SGY/RRDNDYRGGRDRYEDRY NRWDDGSCSSRDDFSRDDCRY NDRRPPQRPKLNKPHNTPKGD DSSASTSQSSRASVFVGGAKPV DRAARETKVEEWLQKEQDKLQ HQLDEAKLE |
| 15202 | 45570 | A | 15292 | 2 | 293 | |
| 15203 | 45571 | C | 15293 | 56 | 298 | |
| 15204 | 45572 | A | 15294 | 1 | 273 | TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFGSLGAGAKDE LHIVEAEAMNYEGSPIKVTLAT LKMS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15192 | 45560 | A | 15282 | 362 | 1323 | HQLGRSALLDTRTVSMQKAKN GDAVTEPQVA/ENEANGKDTA EVDLLTKELEDFEMKKATARA VTGILASHPCSTDVHIINLSLTF HGQELPSDTKLELNSVRHYGLI GLNGTENSMLLSAVGKHGVPIPI EHIDIYHLTREMPSPDKTPLHSL VTVSSPRQRDDMSDGHLCSTAR RHTDIRDDRSPDAPDTARSLAR STITTRJFALATPSRTLQQVCS ALAYTSHPAARTQPLASTALTR RYMLPSPQLPSLRDHRRTNPLH SAVATIPHTTTGEADVSLLCIGL STLHYALVYHVSVLTAQSAQS MSATDASIIFFEPKR |
| 15193 | 45561 | A | 15283 | 3 | 537 | |
| 15194 | 45562 | A | 15284 | 1 | 455 | MPRPEKLGKTQVPPLAECLTKD SFLGQKQASLGPLTFRDVTIEFS LEEWQCLDTVQQNLYRDVMLE NYRNLVFLVISS/HFTQDFWPD QSIKDSF/QRIILRTYARCGHKN LRLEKIVKVSMRKHQIIHTGKK PYKCEECAKLLASQPLENMR |
| 15195 | 45563 | A | 15285 | 1 | 397 | FAVLMAHYDVQEEDPVLTVIT YMGLSVSLCLL\LAALTFLLC KAIQNTSTSLHLQLSLCLFLAHL LFLVAIDQTGHKVLCSIIAGTLH YLYLATLTWMLLEALYFLTA RNLTVVNYSSINRFMKKLMFPV |
| 15196 | 45564 | A | 15286 | 191 | 1332 | AIETQAITDNCSEERKTFNLNV QMNSMDIRCSIIQGDQTGPSVI AFISYSSLGNIINATFFEEMDKK DQVYLNSQVVSAAIGPKRNVSL SKSVTLTFQHVKMTPSTKKVFC VYWKSTGAG/CSQWSRDGCFLI HVNKSHTMCNCSHLSSFAVLM ALTSQEEDPVLTVITYVGLSVSL LCLLLAALTFLLCFAIRNTSTSL HLQLSLCLFLAHLFLVGIDRTE PKVLCIIAGALHYLYLAFTW MLEGVHLFLTARNLTVVNYS SINRLMKWIMFPVGYGVPVAVT VAISAASWPHLYGTADRMLAF KATAQLFILGCTWCLGLLQVGP AAQVMA YLFTIINSLQGFFIFLV YCLLSQQAHHKFTPMEVPRQN HRCLQQN |
| 15197 | 45565 | A | 15287 | 263 | 397 | GRPPAPAAARVSGPASVSAG*KR VSASGSVGVRSMRRGSALLPPN F |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15182 | 45550 | A | 15272 | 94 | 4505 | YLDMMSFVQKGSWLLLALLHP TIILAQQEAVEGGCSHLGQSYA DRDVWKPEPCQICVCDSGSVLC DDIICDDQELDCPNPEIPFGECC AVCPQPPTAPTRPPNGQGPQGP KGDPPGPGIPGRNGDPGIPGQP GSPGSPGPPGICESCPTGPQNY PQYDSYDVKSGVAVGGLAGYP GPAGPPGPPGPGTSGHPGSPGS PGYQGPPEGPGQAGPSGPPGPP GAIGPSGPAGKDGESGRPRPG ERGLPGPPGIKG |
| 15183 | 45551 | A | 15273 | 1628 | 1832 | RRRRKARERRRLAAEQGRRMK EQCKDGFSE/QASGALKLMGSN EGEFKAEGNSKFTYTVLEDGCT KHTG |
| 15184 | 45552 | A | 15274 | 1 | 362 | |
| 15185 | 45553 | A | 15275 | 1076 | 1240 | LRQLL*LCPSWRLCLLGWQL HLFF*RHFFVHLVSQRCSAMS PSPRRCFSLHL |
| 15186 | 45554 | B | 15276 | 480 | 1167 | |
| 15187 | 45555 | A | 15277 | 3 | 379 | |
| 15188 | 45556 | B | 15278 | 13 | 369 | |
| 15189 | 45557 | A | 15279 | 112 | 1112 | WPPASPSASVIRTVKEFALTNP KSSTKETERKETKAEELDAEV LEVFPHTHEWQALQPGQACPC RNPTYGLNLQTGEREAKLQYE DKFRNNLKGKRLDINTNTYTSQ DLKSALAKFKEGAEMESSKED KARQAEVKRLFRPIEELKKDFD ELNVVIETDMQIMVRLINKFNS SSSSLEEKIAALFDLEYVHQM DNAQDLLSFGGLQVVINGLNST EPLVKEYAAFVLGAAFSSNPKV Q/EWEAIEGGALQKLLVILATE QPLTAKKKVLFALCSLLRHFPY AQRQFLKLGGLQVRLTLGAGE GHGGARRARGHTALRPCHREK CSPRRRLS |
| 15190 | 45558 | B | 15280 | 54 | 385 | |
| 15191 | 45559 | B | 15281 | 274 | 776 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15176 | 45544 | A | 15266 | 1 | 743 | PPLLIFRQTGSGVDLQQTPTNLQ LRVLTVRRKTDKRGHPHQKPI CSSPSSKTKEGFRRSNYSKLKEE VQTHGKEVKNLKLDKWLTR ITNAEKSLKDLMEKTKARELC DECASLTSQFDQLDKRVSVME DQMNMKQEEKFREKRIKRNE QSLQEIWDYVKRPNLCLIGAPE SDGENGTKLENTLQDIIQENFPN ITRQANIQEIQRTPQRYSSRR ATPRHIIVRFTKVEMKEKMLR AAREK |
| 15177 | 45545 | A | 15267 | 1 | 618 | |
| 15178 | 45546 | A | 15268 | 200 | 618 | EVSRRNTRTKTSYKQDMNTSK GF*KDTST*PVT/KERSSSPATEQ CWTENDFDELREEGFRRSNYSE LKEEVRTNGKEVKNLKLDK WLTRITNAEKSLKDLMEKTM ARELCDERTSLSSRCDQLEERV SVMEDEMNM |
| 15179 | 45547 | A | 15269 | 158 | 594 | SGSSICCSPISTVLQPPLLTPRQT GSGATSSK/SPTDLQRECSSSP AKEQSWMENDFDELREGFRRS NYSELKEEVQTHGKEVENLEK KIDEWLTRITNAEKSLKDLMEK KTMAREQCDECTSLSSRRDQLE ERVSVIEDQINEMK |
| 15180 | 45548 | A | 15270 | 3 | 1453 | LSDLELAAQSIIFAGYETTSSV LSFTLYELATHPDVQKQLQKEI DAVLPNKERSSSPATEQSWTEN DFDELREEGFRRSNYPKKEEV RTHGKEVRNLEKKIRQM\VTRII NAEKSLKDLMEKTMARELRD ECTSLSSQFNQLEERVSVMEDQ MNEMKKEEFRRKRIKRKEQS LQEIWDYVKRPNLRLIGVPESD GENRTKLENTLQDIIQENFPNLA RQANIQEIQRTPQRYSSRRAT PRHIIVRFTKVEMKEKMLRAAR EKEIQTIREYYKHLANKLEN LEEMDKFLDTYTLPRLNQEEVE TLNRPITGSEIEAINSPTKKSP GPDGFTAIFYQRYKEDLVPFFL KLFQSIEKEGILPNSFYEASIIIP KPGRDTTKKENFRPISLMNSDT KILNKILANRIQQHIKKLIHHDQ VGFIPGMQGWFNIRKSINIIQHI NRTNDKTHMIISIDAEKAFNKIQ QPFMLKTLNKL |
| 15181 | 45549 | C | 15271 | 111 | 269 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15173 | 45541 | A | 15263 | 3 | 845 | PPKMPKGKKAKGKKVAPAPAV VKKQEAKKVVNPLFEKRPKNF GIGQDIQPKRDLTRFVK\WPRYI RLQR\QRAILYKRLKVPPAINQF TQALDRQTATQLLK/LVAHKYR P\ETKQEKKQRL\LARA\EKKAA WQKGTSP\TKRPP\VL\R\AGS*HP VTTLVEINKKASAGWWIAHRR GFPSSLVVFLP\ALCREKWGSPY \CIHKGKARLG\RLVTRKTCTTV AFTQVNLGRQRALLKLVEAI RTNYNDRYDEIRRHWG\NVLG PKSVARIAKLEKAKAKIELATK |
| 15174 | 45542 | A | 15264 | 1 | 5796 | |
| 15175 | 45543 | A | 15265 | 1 | 2212 | MPRVEKNIPGRRNSKGFEDPLE VTQDVTREWAKKVVKREKA SKINGAYFCEGRVRGEAIRRT MKMRQQATLTMTVDKGDNVN ISFKKVLIKEEDAVIYKNGSFIH SVPRHEVPDILEVHLPHAQPD AGVYSARYIGGNLFTSAFTRLI VRILPPQPENIKISNITHSSAVIS WTILDGYSISSITIRYKVQKNE DQHVDVKIKNATITQYQLKGLE PETAYQVDIFAENNIGSSNPFS HELVLPESQAPADLGGGKML LIAILGSAGMTCLTVLLAFLIILQ LKRVANVQRRMAQAFQNVREEP AVQFNSGTLALNRKVKNPDP TIYPVLDWNDIKFQDVIGGNF GQVLKARIKKDGLRMDAAIKR MKEYASKDDHRDFAGELEVLC KLGHHPNIINLLGACEHREGRD RRHLENQVPTLILRFSNTLSKR HTRRLYPEPGSEGPTPEPRSL AQQSEIKLHGGSEPPLIFRQTG SGVDLQQTPTNLQLRVLTVRR KTDKRKGHPHQKPICSSPSSKT KEGFRRSNYSKLKEEVQTHGK EVKNLEKKLDKWLTRITNAEK SLKDLMEKTKARELCDECASL TSQFDQLDKRVSVMEDQMNE MKQEEKFREKRIKRNEQSLQEI WDYVKRPNLCLIGAPESDGEN GTKLENTLQDIIQENFPNITRQA NIQIQEIQRTPQRYSSRRATPRHI |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15167 | 45535 | A | 15257 | 1 | 890 | MSKSESPKEPEQLRKLFIGGLSF ETTDESLRSHFEQWGTLTDCVV MRDPNTKRSRGFGFVTYATVE EVDAAMNARPHKVDGRVVEP KRAVSREDSQRPDYFEQYGKIE VIEIMTDRGSGKKRGFAFVTFD DHDSVDKTVIQKYHTVNGHNC EVRKALSKQEMASASSSQRGRS GSGNFGGGRGGGFGGNDNFGR GGNFSGRGGFGGSHGGGGYGG SGDGYNGFGNDGSNFGGGGSY NDFGNYNQSSNFGPMKGGNF GGRSSGPYGGGGQYFAKPRNQ/ GGYGGSSSSSYGSGRRF |
| 15168 | 45536 | A | 15258 | 1 | 286 | |
| 15169 | 45537 | A | 15259 | 1 | 1674 | |
| 15170 | 45538 | A | 15260 | 235 | 1370 | KREGEGRLADTFVSLLLSARGR RRRSIVKVS LHPAVMSKSESPK EP\EQRLRKLFIGGLSFETTDESLR SHFEQWGTLTDCVVMRDPNT KRSRG\FGFVTYATVEEVDAAM NARPHKVD\GRVV\EPKRAVSR EDSQRPGAHLTVKK\IFVGWH* RKTTFWGGKKKRAKKHHLRD YFEQYGK\EVIEIH*LDR\GQWP RKRGF\AFVTF\DDP\DSVDKIVI QKYHTVNGHNCEV\RKALSKQ E\MASASSS\QRG\RS GSGNFGG GRGGG\FGGN\DNFG\RGGNFS\ G\RGGFGGT\RGGGGYGG/SVG DGYNGFGNDGSNFGGGG\SYN DFGNYNQ\SSNFGPMKG\GNF G\GRSSGPY\GGGGQYFAKPR\N QGGYGGSSSSSYGSGRRF |
| 15171 | 45539 | B | 15261 | 1 | 660 | |
| 15172 | 45540 | A | 15262 | 2 | 486 | KMRQRERAQGKK/VAPAPAVV K/KQEAKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVKWPRYIR LQRQRAILYKRLKVPPAINQFT QALDRQTATQLLKLAKHYRP/G DKGALAKLVEAIRTNYNDRYD EIRRHWWGGNVLGPKSVARIAKL EKAKAKELATKLG |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15164 | 45532 | A | 15254 | 1 | 2423 | MNGKNKTNIYQEPTVCQALHW TLARIGKEEPRRGQRGEGLLCS RERQPRGLSSPGTAAPAAPAAP TPPALPGHRTSGSPEGPEPILR RGGSADAPGRVKTWVNRPAAF VGKCLGDGSADTACDQAMKG QRGSNRKRKTSLSLTFTSSDM HAGGLSAAHPCAHSRAPPPASP SPYKGS LGTRTDGLTDSRADSA ASGARALGVDGQPQSPRRRAP PRPVGADGSSRGPPGRRRVER RGPATQPGDSRALPEPRGVPAV HPAGSGSEWERPPPAAPSPEHR DKMLPGLRRLQLASARRPQFPF EAARWVWSPCFSSGTLCPSFQS ERPLL PFQGFPGTTLHQRLCP VAALHGS GKGQKWQQSHCYA AAVMEEPPAPGRSSES LQGPLS WAGGAPASACLLLMLLALPLA APSCPMLCTCYSSPPTVSCQAN NFSSVPLSLPPSTQRLFLQNNLI RTL GARHL WVQPAHPVALLQQ PLHHLPGHFPPL\QALEELDLGD NRHLRSLEPDTFQGLERLQSLH LYRCQLSSSLPGNIFRGLVSLQYL YLQENSLHLQDDLFADLANLE PTSFLHGNRLRLLTEHVFRGLG SLDRLLLHGNRLQGVHRAAFR GLSRLTILYLFNNSLASLPGEAL ADLPSLEFLRLNANPWACDCR ARPLWAWFQARARVSSSDVTCA TPPERQGRDLRALREADFQACP |
| 15165 | 45533 | B | 15255 | 47 | 482 | |
| 15166 | 45534 | A | 15256 | 1 | 636 | MRDPNTKRSRGFGFVTCATVE EVDAAMNARPCKVVGR TVEPK RAVSREDSQRPEDTEELHLRDY FEQYGKIEVIEIMTDQGS GKKR GFAFVTFDNHDSMDKT VIKY HTVNGHNCEARKALSKQEMAR ASSSQRGRSGGNFGGGRGGGF GGNDNFGRGGNFSGHGGFGGS HGGGGYGG/SGDGYNGFGNDG GGGSYNDFVNNYNNQSSHFGPM |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15159 | 45527 | A | 15249 | 378 | 1744 | QTERNSININKKDIHTKTPSVRH HHQRPKLHKTTKMGKKHSRKA ENSKNQSGSLPPKECSSPAVE QSWTENEFDEFTEEGFRVIESQ MNEIKGEEKFREKRVKRNEQSL QEIWDYVKRPDLRLIGVPDS DG ENGTRLENTLQDIIRENFPNLAR QASIQIEIQRTQPQRYSSRRATP RHIIVRFTKVEMKEKMLRAARE KELKIKKLTQNCLTTWKLNNLL LNDYWVHNEMKGEIKMFFETN ENIDTTYQNLWHTFKA VCRGK FIALNAHKRKQERSKIDTLASQ LKEIEKQEQTHSKASRRQEITKI RVELKEIETQKSLQKINESRSWF FEKINKIDRPLPRLIKKKREKNQ IDTIKNDKGDITTNPTIEQTISRE YYKHLYANKLENLEEMDKFLD TYTSLGLNKEEVESLNTSITGSE VEAIINSIPTKKKSRTRWIHSRIL PEVQGGAA |
| 15160 | 45528 | A | 15250 | 935 | 1269 | LIEGKLTERNSININKKDIHTKT PSVG/PPSSKTKDRSSLPAIEQS WMENDFDELTEVGFRRSVITNL SKLKEDVRIPHKEATNLEKRLD EWLTRINSIEKTLDDLMEKTM |
| 15161 | 45529 | A | 15251 | 401 | 497 | KTFSPFYFS*RRRTVRDINGFTE Y*EPEKLLG |
| 15162 | 45530 | B | 15252 | 220 | 940 | |
| 15163 | 45531 | A | 15253 | 1 | 1476 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15157 | 45525 | A | 15247 | I | 1808 | MAEETQHNLAAAKKKSATGF HREGPTSSATLKDLESPCQERA VVL DSTSVKISRLKNTIKSLKQQ KKQVEHQLEEV TAPDNLVPWV GLSWGIGGILGACLLLCHLCLP LEKKANNERQKAERELEVQIQT LIIQKEELNTDLYHMERSLRYFE EESKDLAVRLQHS LQCKGELES ALSAVIATEKKKANQLSSRSKA RTEWKLEQSMREEALLKVQLT QLKESFQQVQLERDEYSEHLKG ERARWQQRMKMSQEICTLKK EKQQDMRRVEELERSLSKLKN QMAEPLPPEPPA VPSEVELQHL RKELERVAGELQSQVKNNQHIS LLNRRQEERIREQEERLRKQEE RLQE QHEKLRQLAKPHCAFSRS *TMRTRAHLQLEQQVKELQE/Q ALARVFLQVELKSQEAQSLQQ QPDHYLGHPAAEHLEAASQQN QQLTAQLSLMALPGEHGGEH LDSEGEEAPRPMPSVPEDLESR EAMVAFFKSAGASAEKQAQL QEQVKEQRVCCQRLAHPVASA QKEPEAARGPGAPGPGGESSF MDHLKEKADLSE/PGEKRTLLH P/PTG/GDRRHQKTHHLLSEPGG CAK/DAALGPGHHQAGAQQGD |
| 15158 | 45526 | A | 15248 | 2085 | 2700 | YPGKRGLEWT*ANSNRPA AEG PDE\SSSLPATEQSWMENDFDE LRKEGFRRSVITNFSKLKEDVQ THRKEAKNLEKGLDEWLTRINS IEKTLNDL MEMKTMA*ELHDT CTSFSSRVDQVEERLSVI*DQM NEMK*EEKFREKRVKRNEQSL QEIWNYVKRPNLHLIGVSEIDR ENGTKLENTLQDIFQENFTYLA RQANIQIEI |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15149 | 45517 | A | 15239 | 1374 | 2220 | QAENSHININKKDVHSETPSEG HQRKRPKDHSSSPAREQNWME NEFDELTEVGFRRWVITNSSEL KKHVL TQCKEAKNLEKRLGEL LTRITSLEKNINDLMELKNTAR ELHEAYTSINSWINQAEERLSEI EDQLNEIKREDKITEKMKNSTT VLVSTWGSQLEQNNLPHIISPLF HSTHDLNISFYGGCLLQACSSK LLQGLAEGGPLRLTRSASFFAA KLCLTKHFLPTMILIKSRKTP DTQPRRLYLLQGVVDQTSRKG PTALNIRQKTFAAAPPHR |
| 15150 | 45518 | B | 15240 | 1 | 1311 | |
| 15151 | 45519 | B | 15241 | 46 | 212 | |
| 15152 | 45520 | A | 15242 | 3 | 371 | EPLPPEPPAVPSEVELQHLRKEL ERVAGELQSQVKNNQHISLLNR RQEERIREQEERLRKQEERLQE QHEKLRQLAKPQSVELK\SQEV QSLQQQPDHFLGHL\QQYVAT LSAARWAAYQQLD |
| 15153 | 45521 | A | 15243 | 392 | 558 | |
| 15154 | 45522 | B | 15244 | 52 | 689 | |
| 15155 | 45523 | B | 15245 | 400 | 603 | |
| 15156 | 45524 | A | 15246 | 5 | 1158 | RKFWRWMVVMQAQHSQAAQ GQRR**VSKGP**PGPMGGPVL GHWVHSGGISLAVPSLPPPGKS SVFLFLFSASFSDMKLNPGTVSP RLIFGSYDDGFLVETVVKFDFQ LWQKTPLHRAAGERRRAEQRG KLSFVMP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15130 | 45498 | A | 15217 | 1 | 964 | MNVKGGDTQGNTRVRVDNIGG VGAQTVNGIELIEVGGNSAGNF ALTTGTVEAGAYVYTAKGKG NDEKNSPSVYRP/EAGSYISNIA AANSLFSHRLHDRHSLQPLKI LVTGGAGFIGSAVVRHIINNTQ DSVVNVDKLTAGNRESLADV SDSERYVFEHADICDAPAMARI FAQHQPDAVMHLAAESHVDRS ITGPAAFIETNIVGTYVLLEAAR NYWSALDSDKNSFRFHHISTD EVYGDLPHPDEVNNTTEELPLFT ETTAYAPSSPYSASKASSDHLV RAWKRTYGLPTIVTNCSSNYG PYHFPEKLIPLVILNALE |
| 15131 | 45499 | B | 15218 | 44 | 405 | |
| 15132 | 45500 | A | 15222 | 1 | 498 | MTRSLLSVFEEDAGTLTDYTNQ LLQAMQRVYGAQLNLLHTELA KQL\ETQWFYLSYNSEKRISQTL SAMWRGRAAQA/TQGHVWVG MVEAVCSKVSTLKDLFGLASN EHDLSMAKYSRLPKKKENEKL AAFGQPTWCDPAERVGFLEPV GPDGPAKSAPSPRDRASTL |
| 15133 | 45501 | A | 15223 | 1 | 1224 | |
| 15134 | 45502 | A | 15224 | 1 | 1353 | |
| 15135 | 45503 | A | 15225 | 1 | 2580 | |
| 15136 | 45504 | A | 15226 | 1 | 3117 | |
| 15137 | 45505 | A | 15227 | 1 | 1260 | |
| 15138 | 45506 | A | 15228 | 1 | 2142 | |
| 15139 | 45507 | A | 15229 | 1 | 1413 | |
| 15140 | 45508 | A | 15230 | 1 | 4049 | |
| 15141 | 45509 | A | 15231 | 1 | 381 | MLMLNIGFKNFQFEHLKCSHGS YSEDIGFPNAGALSGAMFLLEE KHLLFGLKEEERLRASIRRESQ QRRMREKQHQGRGLSASY\WNLI DTMRRRKARSP/YSLAAIKNRY KGGIRDQKPSYDSLNLCT |
| 15142 | 45510 | A | 15232 | 1 | 467 | DHSSSPAREQNWME\EFDELT EVGFRRWVITNSSELKKHVLTO CKEAKNLEKRLGELLTRITSLE KNINDLMELKNTARELHEAYTS INSWINQAEERLSEIEDQLNEIK REDKITEKMKNSTTVRVAASM QSKLLQGVAAEEGPLRLTRSASF |
| 15143 | 45511 | A | 15233 | 1 | 1140 | |
| 15144 | 45512 | A | 15234 | 1 | 2640 | |
| 15145 | 45513 | A | 15235 | 1 | 714 | |
| 15146 | 45514 | B | 15236 | 1 | 546 | |
| 15147 | 45515 | B | 15237 | 1 | 735 | |
| 15148 | 45516 | B | 15238 | 50 | 1603 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15126 | 45494 | A | 15213 | 3 | 471 | GRPSSPGVHGSSTQTPAHVGSF PGCGPIPPD/ACRRSKIRGPGGW GGVGG/CRDGRNSR/DLRNLPC PFLFLPGP*AAAPSPWPAAAGA APCGQCLDGWPHSYSHGHSSA AGRGGICRSPLLAGELRPPGIQ YNGRTEVRGILSGSPCPPFSGAG |
| 15127 | 45495 | A | 15214 | 3 | 449 | PHQDLEEAMVLL*PPSP/PAWPT MRTRKRPSSKVSSTSRPLRKSIM TTYAVPSRAPTPA*PSASKPTNA FS/HMVGSEPRSHAHL DGRHRD SR*RKPRPLSGPRTLGGKSLRGS AGAGRGGVPRPRPLPENLDAPL WNSPGNSAGAAVQLA |
| 15128 | 45496 | A | 15215 | 26 | 1126 | EGPSSEAAHPGGTPREQDGAM DPARKAGAQAMIWTAGWLLL LLLRGGAQALECYSCVQKADD GCSPNKMKTVCAPGVDVCT\ EAVVAVETIHGQFSLAVR\GCG SGLPGKNDRGLDLHGLLAFIQL QCAQDRCNAKLNLT SRALDP AGNESAYPPNGVECYSCVGLSR EACQGTSPPVVSCYNASDHVY KGCDFGNVTLTAANVTVSLPV RGCVQDEFCTRDGVTGPGFTLS GSCCQGSRCNSDLRNKTYFSPR IPPLVRLPPPEPTTVASTTSVTTS TSAPVRPTSTTKPMPAPTSQTTPR QGVEHEASRDEEPRLTGGAAG HQDRSNSGQYPAKGGPQQPHN KGCVAPTAGLAALLLAVAAGV |
| 15129 | 45497 | A | 15216 | 1401 | 1983 | AQRAQALECYSCVQKAD/DGC SPNKMKTVCAPG/VDVCTEA VGAVE/SHPFWIWPRPFNAAPP LSAWPGPYDTALQARPLY*QL QARGAES*ELVH/GQFSLAVRG CGSGLPGK/NDRGLDLHGLLAF IQLQ/QCAQDRCNAKLNLT SRG LDPAGTSPPVVSCYNASDHVY/ KGCDFGNVTLTAEPPTVASTTS VTSTSPQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15123 | 45491 | A | 15210 | 1 | 1297 | MGKIMSSYQHVDLIVDCDFEA YHRQPSSGTSVVTGPSAQALI TEKIVTYHWDQHVGDVVLVNI YCVINVLDHTVKAVIDDRFMG GITTINLQLMAHIVRYFFASGSA YIVAMLVPVFAMLANVSGAPLM LTALALLFSNSYGGMVTHYGG AAGPVIFGVGYNDIKSLCFDER TRIDVADTYASNWRSRCNQITF NGECPNTRQHIAAVRRGIDTLL MNDYLRKQIIDISTRIAGTANN GDFTGQWITAANTVNFQIVAGT HNCHQYFIALRLIFGILKYIQDR AREGLKQRDLAEALSTSPQTVN NWIKRDALSREAAQQISEKFGY SLDWLLNGEGSPKKDLESNIPP ESEWGTVDADWKNTPLPDDEV EVPFLKDIEFACGDGRVHDEDH NGFKLRFSKV\VQPRVGC*QG* G*LLYLDV**GDPLEST |
| 15124 | 45492 | A | 15211 | 62 | 301 | SWMSSPRAFSSSTCLETAAPTR MATALTSAACRLPPAAGSGSP WAPAPYRWRARRRTGPMSDR Q*RTSQPCPEPAAASR |
| 15125 | 45493 | A | 15212 | 1 | 1665 | MQDSAHLRRLPPAASRRVWLA LGSCPLPLESSPAHRAYERPSVA HQPAVPGARRSLEVPSEVPLTV PALTPPRIPAMLTAVCGSLGSQ HTEAPHASPPRLDLQPLQTYQG HTSPEAGDYPSPLQPGELQSLPL GPEVDFSQGYELPGASSRVTC DLESDSLAPGPFKLLQPDMS HHYESWFRPTHGAEDGSWWD LHPGTSWMDLPHTQGALTSPG HPGALQAGLGGYVGDLQLCAP PPHPAHHLLPAAGGQHLLGPP DGAKALEVAAPESQGLDSSLD GAARPKGSRRSVPRSSGQTVCR CPNCLEAERLGAPCGPDGGKK KHLHNCHIPGCGKAYAKTSHL KAHLRWHSGDRPFVCNWLFCG KRFRTRDELQRHLQTHGTGKKF PCAVCSRVMRSDHLAKHMKT HEGAKEEAAGAASGEGKAGGA VEPPGGKKGKREAEGSMASSSPD SPCSCDCFVSVPASAIPAVIFA HELGPTPGRGAGGGVCPRRHS HSWEPAPGL*AVGGGGGASGQ AGDRGCHA*EAGRS/SCSRRGS GL*RAGTS*ISASS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15119 | 45487 | A | 15206 | 31 | 1981 | RWLMRGMGIALPAAMASTVSP STIAETPEPPPLSDW/LRASG/DV WVHLLGLDPHLLSSLLLSICLF SLIWIF*LQP*SV/ALAFQMGAS LFASNIGVIEGEGPQAKPL*CLT VSYFEMLNLLNAQGPQKGLSP CQCLSLQVMTMPEYLKKRWTL GQRSQWPQMHSVFS*LFPP*A DIFAGAIFIKQPSGEGKYMRT G*NALVLFFLSLGGLEVVIINIG CLRQ*DISFYSDAFLAFNEVGG YESFTEKYVNATPSVVEGDNLT ISASCYTPRADSFHIFRDAVTGK GR*LPLKSSPGLFHECVTFSRQV IVQRCLICGKDMSHVKAACIMF LFV*WLLVLPWASLDSLLNSSP DMVACVVPSECVISTLSGLARQ CPATNQCLYPFPAPGLRGLMLS VMLASLMSSLTSIFNSASTRTK AQWK*L*CFCLMFKLCCFLLR FVLLLTVVSVWVPLVQVSQNG QLIHYTEI***LT*ISFSYFLNLI FFLLLLQGAFWGLMVGLAMGL IRMITEFAYGTGSCCLAPSNCPII CGVHYLYFSIKVPFYTYIANICL LLMHFCMVVPVQLYRLCWVLR NTTLTRISSSFVI*IFCNHLLIFVP DYPEKSRGCLKKAYDLFCGLQ KGPKLTKEEEEALSKKLTDTSE |
| 15120 | 45488 | B | 15207 | 1 | 1392 | |
| 15121 | 45489 | A | 15208 | 57 | 1523 | |
| 15122 | 45490 | A | 15209 | 473 | 589 | LPRQLALSCVVHCQTLVPAIRCI DWGWLF*W*SVTPVM |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15117 | 45485 | A | 15204 | 1474 | 1511 | HS*VPANLYMELKACFTGA/NE KGELVVLGHNLA VSYFIALAAS LRADCCEIWTDVDGVYTC DPR QVPDARLLKSMSYQEAMELSY FGAKVLHPRITITPIAQFQIPCLIK NTGNPQAPGTLIGASRDEDELP VKGISNLNNMAMFSVSGPGMK GMVGMAARVFAAMSRARISV GLITQSSSEYSISFCVPQSDCVR AERAMQEEFYLAELKEGLLEPL AVTERLAIISVVGDMRTLRGIS AKFFAALARANINIVAIAQGSSE RSISVVVNND DATTGVRVTHQ MLFNTDQVIEVFVIGVGGVGG ALLEQLKRQQSWLKNKHIDLR VCGVANSKALLTNVHGLNLEN WQEELAQAKEPFLGRLIRLVK EYHLLNPVIVDCTSSQAVADQY ADFLREGFHV VTPNKKANTSS MDYYHQLRYAAEKSRRKFLYE HNTFVSPHIRPLIERRGRSSTRD KWCARPSTERQQDNSAARILSC QQGNTSFEHTSSIRVGT TNSLN |
| 15118 | 45486 | A | 15205 | 198 | 462 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15112 | 45480 | A | 15199 | 283 | 796 | FVG VKSAGNRLKTIDELANESR SSVGLTQAALKTLESSGAIRIER RGRNGSYLVEMDNKALLTHVD INNVCAMPLPYTRYEGLASG LKAQFDGIPFYAHMRGADIRV ECLLNGVYDMAVVSRLAAESY LPQKGLCLAL*LGPPPYVGE\YQ L*QVKAKSEYVKRVGHV |
| 15113 | 45481 | A | 15200 | 48 | 3376 | |
| 15114 | 45482 | A | 15201 | 49 | 681 | DPGADRRGSVWGLSDLRNTYN ALYLTHSGRLSECTPANEEKE PTNHNRTLNTQTQKEKKKTRT KDCTTRNKKNSTRPGSGIAGPSY YTVAGPPSAIDPRWLRPTPAL DPQ*MPHTSKRGKRADQSQPN ANKPNTEREKKDKNEGLHHKE QEQ\QRP GSGIAGPSYYTVAGP PSAIDPRWLRPTPALDPQTEPL IFQQLEIDHYVAGLTHEVMSLS HLTLVMRWGSVSAHLAHWA RCRWISTELTPNSITSTSSPLKD CSSSPAMEQSWLENDFDELTED KKTCLCDH |
| 15115 | 45483 | A | 15202 | 3 | 587 | |
| 15116 | 45484 | A | 15203 | 3 | 774 | MVLMAGFTAGNEKGELVVLG RNGSDYSAAVLAACLRADCCEI WTDVDGVYTC DPRQVPDARLL KSMSYQEAMELSYFGAKVLHP RTITPIAQFQIPCLIKNTGNPQAP GTLIGASRDEDELPVKGISNLN NMAMFSVSGPGMKGMVGMA ARVFAAMSRARISVVLITQSSSE YSISFCVPQSDCVRAERAMREE FYLELEESLLEPLAVTERLPIIS VGSDGNPPPCGGISPFFAALA PRPISKFVALCSGIPF |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15107 | 45475 | A | 15194 | 1 | 1388 | MIEHPRRRDNYRQSGPPVADKP TTKGEPLISDIVSDAQQANLLIP VDETPPVINDEQSTSTPLTTAQT MALAAVADKNTTKDEKADDL NEDVTASLSALFAMPLPGFDNTP KVTDAPSTVLPTEKPTLFTKLTS EQLTTAQPDDAPGTPAQPLTPL VAEAQSKAEVISTPSPPSISGVT RSKMRQREWLVLPEDSLVIRR SNKTSQLPAFNVPLSAKAAAS KPWRASNTACRNSRPSKVCSAE GEQWFSASGRGEIHSQSPARDM AQMCKLAAEGHFAEARVINQR LMPLHNKLFVEPNPIPVKWACK ELGLVATDTLRLPMTPTIDSGR ETVSGDETYLEAAPLAELHAPA GMILPVTSGDYAIPVTNGSGAV GSYSAITEPGAGSDVGS�KTTY TRRNGKIYLNGS/NVFYYQQL HPVHRGDGARRGFSQTCLHR MVC*YEQTGHQSDQT*KARSA YG |
| 15108 | 45476 | C | 15195 | 1 | 1905 | |
| 15109 | 45477 | A | 15196 | 285 | 1706 | YARVHSGRSSIRRSIPVSICIRSSI RGCVPVHHCIRSSIRRSIPVDHL YQIIHTKKHTRCPFVSDHPYEE APDYSASLLPDWLPVPSSKVVI TYPGFTSICGYTTSSKACFSVF AWCFVTSDVPGRFSDDEDDSE MWSLTALMGVMGGWKSARS EVSILCSTSSKVIHSSYPYADRA FQVWSLDARFAHINKPFGVDRF SGEAPSRATTMYGVKVLNRPA TGTAHRLVPPDVPVPHGGESN KPRVQTTVSSGISRLSIPISASAL QNVDPKTHDISNITDTVYHCPL SQSSRWYWRFPVRSPPLSNGQ TAVRPGGSRAGAAGGPLSEYS GSGFGVMKWTKDQLTVTVKV HHLPEVVEFLYKQGGWLSVL FGNDERKLNGHYAVYYVLSRE KGTKCW/ TDSMDYRQR/PAPT NDAETYEFINELGARKTTVPPI GPLHVTS/DEPGHLRLFVDGENI IEANNE*IHRTQC |
| 15110 | 45478 | A | 15197 | 3 | 1396 | |
| 15111 | 45479 | B | 15198 | 1 | 1399 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15101 | 45469 | A | 15188 | 1 | 1446 | MWRETKRYAAVLLLTPHYSAS LLPDW/PNLYLHQSGHHVPGVY LKFGISSNPIYPCVDSAKTVFPN APLHDRVQSVRRMGPFKGVFR KVFSNLGFEYSLSTWATMGSPG SLGVSPFGKTLFVESASGSLDA LWPTVEKEISSHKNYQKHSEKQ IYDVRIELTGLNALPNISLNFYK NSVSKLLNRKKGLIHLQPFILR LCVSLHKNREENLGITIQDVAM RLSALPNIVCRLYKKTASEVLK EWSTRWDEYTHHKEVSQKALP TLSVKIYKKNICQLLNQNNGNPN SEMNALITKKS VKSASGYLESI AALVEKEISSYKNYTEAFYNLL CDVYSHVTEMKLSSIEQIGNTL FVESASGVWRALRPRGKEVNDI FIDQIANSVLVDSSKDICKRFEA CGAMVKKENLHIKTRQKISEKL HWPFGAPRLTSLTGPEKTGKGE HPGAKARGELSGAPPLIHRKL SLMSNVETLLLEKLQGYTGAH |
| 15102 | 45470 | A | 15189 | 1 | 966 | |
| 15103 | 45471 | A | 15190 | 157 | 531 | GDHTTFLCLLMVNAEFKYNFK TIIS*DLLKKDSGQYGHFTIFFRS MSIGCFSIYLCIFNFFHQCFVVF LVEIFTFLVKCIPQVDSIEDTTFG HPEEATPHPFSSFMRLQFSHIF SSWPVSFTAH |
| 15104 | 45472 | A | 15191 | 9 | 494 | PTDRPRPRALAGARGPPGRAPR VPPAGGPRPSQYGHGGRPNPR HGWHDAFCPNNTPYRERPLDS RYLTPGPLDMRGDSGFRTGRGS DVGSLKPTDTRRNGKIYLNGS/ NVFYYQQLHPVHRGDGARRG FSGRTCLHRMVC*YEQTGHQS DQT*KARSAYG |
| 15105 | 45473 | A | 15192 | 1361 | 2038 | |
| 15106 | 45474 | A | 15193 | 1376 | 1906 | LAFPDGMASLIMMSLPAMRTL AWAMAVSGNCIPEGQFSALSC ADFGISPKLIL*SSSAPMYLAMG ISCPRADDLPEAGTAETDRACR SIPQYGTDLGWYPATAAGPQSE SVQGAV*PHRYEAG*ST/VWKP LKKK*KPLPRR*LARWQMIRFR KPSPLTTSKLTCARFLDFRW LE |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15095 | 45463 | A | 15182 | 881 | 2040 | MKAGWRQTQHLHDAGQLLHLI LPGEQGVARVQLRRDAAQAPH VNGHVVGVAQDHFWSVEPA LDVRVYCGGKTGGKQRRERREG RCGVEILMVGERKMENKEDT SKESEYKDESEKDLEGLTNEN EKSDASIIEMACEKEENINQDLK ENETVIEHSKQLSDPKSLQDE VSPRRNDFISVPSIQPLDPISDS SENSFQESKLESQKDLSEEEDEE VLPRSSNSCVSGIKKEDSAKID VVTHSSTGEPLAYI/ASTYKLAY IPPLNRKTCPSAAISDRSKNG KSN/HGQSAHISSVTSTYCLSP* QKEL/QKREQKREKLKREEEQQ KIEEEEKKRENGIVFKAWLQK KREQVLEMRRIRAKEIEDMNS RVSKTSLKNKFIQI |
| 15096 | 45464 | A | 15183 | 873 | 4292 | MVVSLGRVSSLSSESDPTGRVG R*VDCKVDRSIWAGVWISEDAP SEA*EIGGLGRK*MLSGGPQSPS KHVHIL*DQDSSSIPEPMGPCCP\ PHAPGKEPGTSCSIDTDGKLSG VSGDDS*T/GTDGGESEIILLPQ *QLPVTLPSPPLPG*VRYTSR SRSRSTRDPGRKSRPISGLRGLC GDGATS/PLTPRHAPARDVQ/PG VSMAFAGDR\GDGGRRGGASQ/ PAPPGPAVPRPCAQYSARAMPA SGRRES |
| 15097 | 45465 | B | 15184 | 1 | 2214 | |
| 15098 | 45466 | A | 15185 | 3 | 361 | |
| 15099 | 45467 | A | 15186 | 1 | 1035 | MKIHKSGGLKATPQLYASQFSG VAILATWGPHRPRNSSTSFSTQS KLRRPDESSVDFQKLMLCKEAT KKSKEKEPGMAFPQGHLIFSDV AIKFSVEEWKCLNPEQRALYRE MMLNRYRNLES/VG*LFKIHDG VLINRARQYRSVPHRDIGKT*FL LPRNQERYSGL*VSVARN*KK WP*STHDRNQVRN*VHTGEKP QKCNECGKTFQSQSYLQCHHR LHTGQKPYK*E*CDKVYSCRSQ LKTHRRITG\EKAYKCKVCEK AFWDNSCLSCQKRVHIGEPY ALVMHKAIHTGEKPYTCNECG KAFSRKANLALYHRLHTGEKP YKCEECDKVYSRRSHLERHK |
| 15100 | 45468 | B | 15187 | 1 | 1347 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15091 | 45459 | A | 15178 | 76 | 969 | KKSTALVIDNGSCMCKAGFAG DDAPQAMFPSTVGFPGHQGVM VDMGQKDSYVGNEAQSRSIL TLKYPIKHGIITNWDNMEKIWH HFYNELHGAPE*QPVLLEDPL NPKDNREKMTQIMFETFNTPA MYVAIRDVLSLYAFGRRTTGIVM DCGHRVTHTVPIYEGYSLPHAI LHLDLTGWDLTEYPCILLFSEK SYELPDGQVITIGNEWFWCPEV LFQPSFPCMESCRHQTTINSIKK CDVDIRKDNTVLSGGTTMYPG IADRMQKEITALAPSTMKIKIIA PPERKFSVWIGCS |
| 15092 | 45460 | A | 15179 | 1 | 451 | |
| 15093 | 45461 | A | 15180 | 130 | 227 | LMKMKKVM*RA*KEEERRTPP AEDDFEKDLEWLINENEKSDAS IIEVYIANSIHNNYITKCFAIL |
| 15094 | 45462 | A | 15181 | 104 | 1715 | KEEERRTPPAISVIPAAAFYTAY FLHKQKMENKDTDSKKSEY EDDFEKDLEWLINENEKSDASII EMACEKEENINQDLKENETVM EHTKRHSDPDKSLQDEVSPRRN DIISVPGIQPLDPISDSSENSFQ ESKLESQKDLEEEDEEVRRYI MEKIVQANKLLQNQEPVNDKR ERLLKFKDQLVDLEVPPLEDTT TSKNYFENERNMFGKLSQLCIS NDFGQEDVLLSLTNGSCEENKD RTILVERDGKFELNLQDIASQ GFLPPINANSTENDPQQLPRS SNSSVSGTKKEDSTAKIHAVTH SSTGEPLAYIAQPPLNRKTC PSS AVNSDRSKGNGKSNHRTQSAH ISPVTSTYCLSPRQKELQKQLEE KREKLKREEERRKIEEKEKKR ENDIVFKAWLQKKREQVLEMR RIQRAKEIEDMNSRENDRPQQA FRLWLKKKHVEEQMKERQTEEL RKQEECLFFLKGTTEGRERAFKQ WLRKRMEKMAEQQAVRERT RQLRLEAKRSKQLQHLYMSE AKPFRFTDHYN |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15088 | 45456 | A | 15175 | 777 | 1548 | SKIQRDSQAPLYSIEETQRANT HLVEGEPEAEIAFKTLKQALVQ APALSLPTGQNFFLYITERAGIA LGILTQTRETTPQPVAYLSKEV DVVAKVWLHCLRDGEPIKHDC QQIIVQIYAARDDLLEVPLANP DLNLYIDGSSFVENGIRRAGYAI VSDVTVLENSLAAVTLQNRQG LDLLTAEKGGCTFSGKECCFY TNQSGISSPLEDTTITAGPFLHPI QQEVARAIIGQFPTAFGVSCLE GRLRGEASWTSWVE |
| 15089 | 45457 | A | 15176 | 1 | 1359 | MGPEPKNTHPGSCTCPLACSSS HKGFECLAVEQGSYTPVASPIV GVKENQEILDLELKYNQTRSA VTRCVLGAASTARIKQAEEGGR SRLAESSGLRPFVLELPALAHQ TPSSSGFELDLHQRLATWSQA FNYRLKDTLLASLLLRFWDS WLPCCSVCSWPVGLHLVIIERN YSYQQGTETVSSWATGVSA ASVSATIPINRVQGHCGFLGKR CFYCCIGECNHS DHQPGTVAG SWARGVSATASQIQVDLGKFS DDPDYIDVLHLTWRDVMLLL DQTLAFNENNVAAAQEFGD TWYHRPVNDRMTAEQRDKFPT DIKTAAGIPWNHWLLLTMDPQ TQRDSQAPLYSI*ETQRANTYL VEWEPEAE/TSFKTLKQALVQA PALSILTGNFSLYVTERARLAL GVL TQTCGTTPLYQDEL RKKTL RHRDSESGFNQLEASAD |
| 15090 | 45458 | A | 15177 | 368 | 5192 | AAPAPQLGLGPCKLASHLLSQS HLSQSVRSEAEQKAGASPASSI QREPLFKDQLKAPLEQKRSL LTVPLLTFRQKCGPGSPLVAR GGATDSWLVSSEFRLSDSTAPP TELRGQEATGITKPPASLHPQPH AWDWARGRDRRHLLGTPELQ EHSEKTTTETLPADMGLRTW ERKEATAGQAAEGAAGGIHFE ATSLLRPSSYVPQTQGALSTTY KEAKMDRDLHLTPILAAQRAR GPRIHSFSPSEMIEPS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15083 | 45451 | A | 15170 | 1 | 1569 | MPIGKVG EYYIKGTLRATKESE QQSSALELSSDRVYLNEKEPGD QPWNAAFVFRGCGVALALRPP HLGWGEPRWAGFRGAFGFPFS TLNPSNWSLTLIIQGCKQEGFYS PSMRPRVVPKRGSAPKVRAEEN AALPSRCPPGPLPVAQPRGLLM GAHVSSAPAVGVGAASCHRLC PGFPDRPRPTLRSCIMNAVVG CDLRGQVYDPTGGWANEGTR DLSAVQGVNHPGGRPCPTPQS SRQLPVVSRRPVVRPGGEAPPP LDILPAALALHQSLTPQDPRE DRPSADLWAQDSWVGQPQEL PVGSRVRTGTETPDTHSGSVCTS RQKDGSGPLARESSVRVILQG PSSAWMMFPEYTPGPRARAGT AVVGAMARQTVNVCLTKVRL QHPEGIPGGGRGPLVPKPVCTC/ IVDVKGSRV\WHVHICMSMGC RNVCLCGRSVGSRMCTAGQT PKLARQASIELPSMAASSTKSW WETGEVQAQSAAKTPSCKDIV AGDMSKKSLWEQKGGSKTSST IKMDSVTT |
| 15084 | 45452 | A | 15171 | 328 | 641 | LLMRSWSLPSAPRGFSCSCLQP QYPCRTESWPQTEPVSPVSHR LLVLATAMLGSSME/RLAG*LG GPASGLDGLGVLFQPLINLGDG QVWLGLHTVTLLYGAV |
| 15085 | 45453 | B | 15172 | 120 | 1458 | |
| 15086 | 45454 | A | 15173 | 1 | 440 | IQQDSQAPLYSIKETQRANTYL VEWEPGAETAFKTLKQALVQA PALSLPTGQNFSLYITERAGIAF GVLTQTRGTTQPVVYLKDGE IEHDYQQIIAQTYATQDDLLEV PLANPDLNLYTDGSSFVVGIR RAGYAIVSNTVLE |
| 15087 | 45455 | A | 15174 | 288 | 376 | NHWLLLTMDPRIQQDSQAPLY SIKETQRA |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15074 | 45442 | A | 15161 | 666 | 1536 | FSSAGDTQANRVCSVPPTNHSR PAADRPVRRKVNKQKTATSTS TKRTSTQRPHPKVTNDHSSSPA REQNWMENEFDELTEVGFR WVITNSSELKKHVLQTCKEAK NLEKRVRVNCLTRIT*P*RRIT\ KTLMEKNTAREVLHEAYTSINS WINQAEERLSEIEDQLNEIKRED KITEKMKNSTTVRVAASMQSK LLQGVAAEGPLRLTRSASFSAEI SMCHQWLFSTFGNGKSRNRYH CEKAHIEGNQLVEETGRAFKSR HRYGTGPLHKFEIHEYTELHHV LMLQGKC |
| 15075 | 45443 | C | 15162 | 104 | 364 | |
| 15076 | 45444 | A | 15163 | 162 | 467 | |
| 15077 | 45445 | B | 15164 | 1 | 1122 | |
| 15078 | 45446 | A | 15165 | 188 | 456 | |
| 15079 | 45447 | A | 15166 | 485 | 1580 | GEGYKADLAAATVECPICQQQ RLTLSPQYSHIPQGDQPTTW*Q VDCIGPLLKGQRFVLTGIDTYS GYVFAYPVCNASAKTIISGLTE CLIHCHGIPHSIASDQGFHMA KEVWQWAHVHGIH*SYHVAD YPEAAGLIEGWNGLLKSQQLQC QLGDNTLQGWGKVLQKPMYA LNQHLYGTVSPATIHGSRNQD WNGSSLRGWTFILFTAPRREP GTYIASDQRTHFMAKEVWQW AHAHGIHWSYHVADYPEAAGL IEGWNGLLKSQQLQCQLGDNTL QGWGKVLQKPMYALNQHLY GTVSPATIHGSRNQGMEVEVA PLTITPGDPQAKFLLPVPMTLCS AGLEVLPPEGGLPPGHHTIPLN |
| 15080 | 45448 | B | 15167 | 10 | 2352 | |
| 15081 | 45449 | A | 15168 | 2 | 497 | WKPIAMRKSRRRQEKLLPVQK EGQPKEGEREEGGPVQAQKVP NRLHLHWTT/HLPSFFQLPLLD SLWRALKFVVLEAIVKMIRFNG VLGKCEAIRAQALHEGGPPLPL AVFHNRRLLQIVACSRISARLRGS PPPKSNNEQSSLSTDLRTDSQRL PPLSRNAQQKG |
| 15082 | 45450 | B | 15169 | 1 | 1911 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15070 | 45438 | A | 15157 | 1 | 1610 | MGLGKSLCILKDAVLALREIKG ISFYAPNTNRLWGYRQAKQT QHLSGISTLDCPQRYNGDDTGS VWALEPSCMLWACPLVFPSEIY YFISEDVWKHLDAQEKFAAVM GPSRRTSVRAVWKGNVGLEPP HRVPTGALPRVAVKRGPLSSRP QNGRSTYGLHCLKDPTPTQEDW LVSVLPEGSRVGVDP LIIPTALG HGRITFLKVLDFQGPAPCPAA MGVRLMAGPQCVCSSDYWKKM AKVLRSAHHILIPKENLVDKI WTD RPERPCKPLLTGLD YTG I SWKDKVADLRLKMAERNVM W F V \ V T A L D E I A W L F N \ L R G S D VEHNPVFFSYAIIRD*ETFMLFI DGD\RIDAPSVKEHLLLDLGLE AEYRIQVHPYKSILSELKALCA DLSPREKVWVSDKASYA/V*SE TIPKDHRCMPYTPICIAKA\VK NSAIESEGMRISDEKSAGNLTED PFYVIDRTLITTGVVCNSTEKSS LMSVASADTAENLWHLFFHILP SERALTRKLRVLKLGPNYSVQ NPTAQLHQQGPLGVA |
| 15071 | 45439 | A | 15158 | 1 | 756 | |
| 15072 | 45440 | A | 15159 | 1 | 1677 | |
| 15073 | 45441 | A | 15160 | 1220 | 2620 | GPTEPHTGELWLESGGCPSGTK LPEEGTGSNLCCSTASAGDTQA NRVCSGPPTNHSRPAADRPVRR KINKQKTATSTSTKRTSTQRPH PKVTNDHSSSPAREQNWME FDELTEVGFRRWVITNSSELKK HVL TQCKEAKNLEKRHSLGTK EPAALKGRTQYWQDSSPADLR PWL CATLLKQYKPTVFSHSTVA VHPRAGFLNLSTVDQHPVLDEP IAEAVCIIADTNKWSVQVATSQ RKVPHNLKLGQDVLVSSQVSSL LQSILQLYKLHLPADFGDILLD NNLKCVFQLGSILPVTFRSHDP YDGE GTDELRTAACSPDTEQLA RQSGTYPVSLGQATVLEDSKA ALPGLGPTLMAVTVVTEAAV DMVVGDRGEERGGLVAPGTR GLTEEIWFVPVSPSRWSSHPV VAFITLAKYGPTSSPPVFHHGPN IIRHGAQGAASAGDSGSSSRCD RLPCRQNA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15065 | 45433 | A | 15152 | 2095 | 2663 | LGLGDLPWEINPPSSCSLLREKD PPTTSGPQTYQPKKHLTNFKSA CFERIKACYHSPAKAWPFKAYK LSLQFPHTCLKTRHAI/PS*FSD LCLINQIVLPIHPMVNPYTLIC SIPPYTMHYSVLQLIRAFFTIPLH P*PSLY*VSLGLTLPIRLSKLP GLHCRKASQTTPTS VKPKFHP HLLPIST |
| 15066 | 45434 | A | 15153 | 678 | 1189 | LGSGDLPWEINPLSSCSLLCEKH PPTTSGPQTDQPKKHLTNFKSE TKETCFIHEPKTLAPVTD*GRQP SLGV*SLQGRPL*SFSHISRVS HAGMPALVLHP*RQVPLFWGR GKYPNPFSPCLLPLLCFSGDRG KYPNPFSPCLYSFSAFLGTGQVP QPLLSLSLPLLCF |
| 15067 | 45435 | A | 15154 | 649 | 1428 | QCISELQFLLASTVRQTPATSPA HKNFQTPELQRPQVPPEPPPTG ACYTCRKSGHWAKECPQPGIPP KA/HLTDSFPDLLSLAAIED*HC PIASEAPETITDAELPVTLTVEA HLHPGEINSHVAHTKPVWWSL HRDAHEIWCCSDRGTSLRRPI PCPPALCSVTKIHLRPQVLRPTS PRNISPISNPAAPHQAELGPNPS/ SSLCSSL*SFYHLPSSHLVWLT VSFRD |
| 15068 | 45436 | A | 15155 | 240 | 1208 | LRSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKHLTNFKSC KQ/DLFLSSPTSLTIPQLSPFN LGATLQSLPSLNFSHFVLVETK ETRFIRGPKTPAPVT/VLGRQPS LGV*SLQRCLSDYTPTFQGCQT TQGRLPWSFTLSGK/CPLFWGR GNTL*KD*SLLSLACYSMGLLN PINSFPSSHFTCPKTRQAVTS* VQDLRLINHIVLLPIHPGGAQPH TLFCPQYRPVVLPIILFVYVKHA FFTIPLQPLIPSLSLPSRLTLTPI RLNKLPGLCCKAFRDSPHYLN QAQISSSVTYLGIIKAHVLSL PIVSDW |
| 15069 | 45437 | A | 15156 | 1174 | 1623 | KFGLVQLTLGKPLPEPELWPK A/HLTDSFPDLLGLAAED*HCPI ASEAPYTITDAELRVTLTVEGK SVPFLINTEATHSTLPSFQGPLSL ASITVVGIDGQASKPLKTPQLW CQLRQYSFKHSFLVIPTCPVPLL G*DTLTKLSASLTIP |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15062 | 45430 | A | 15149 | 303 | 2028 | LGSGDLPWEINPLSSCSLLREKD PPTTSGPQTHQPKHELTNFKSD KGDMFYPTWQNYQCRSRTGK AAFPWCLITAGTPL*LYTHVSR VSDHAGMPALVLHP*RQVPLF WGRGKLLLARPS*VPILPQPLLL HPIIFLSPPLLTGPAYSFVL*LA LPHLPSNLLLKRWLEPKA*SSM/ TLKGLKPVITRLLQHGLLKPTN SPYNSPILPVLKPKPKYKLVQD LRLINQIVLPIHPVLGIIGLTSSV RRDAGQDLKRDRAEFLGDEV HHPHRRRIAIEARRLLLQGDFDP LHRLIGQVLELGEARYAPPVEQ HHRLAPARRTGQRLHPLEQFG QAGRAQRNRNLGIEHRDRLDRP DDGAGNALAGDGDFFRGCLFA GIGIRPRYCRYRQSQDDRRPSH AAPRPRALPIHRPATPIADV VMFSVAIMSQLRLVLRHIDGIS RWPPAVVFITDVKIWLVPSPDD CRIRSNDRDDMQGEAPAMSMN AAARVGDPIGHFSFSQGLFGEAL DGLFFARRSEVDMRAGNLGRLI ARGLSGGRWTPADGQTLGSR DVFINGPPATMTIRSTGQCRQH |
| 15063 | 45431 | A | 15150 | 653 | 1076 | RSKYPNLVSLCPSPLFPRPDLLS LWPNPLFLHPNLLYLCAPIPYFH APTSYLCTPTPYFHDPTPFPLFW KELATSARNLATRPRNACSPGF LLSCVPSVRDPTGNRTVQLTW QPLPELELWPKA/HLTDSFPDL LGLAAED*CCPIASESP*TSDILG RDTLLLALKVQTVVLQTACGE GHVAGNCGRPLETEGSLQLTAT KKLRDSVLQPKSPEFCQQFTRA WNRTQVPDETEAPAGTYAAQS GDLWEINPLSSCSLLHEKDPPT ASGPQTDQPKHELTNFKSGFRG VRPRRDACLGPSPLAASPAFLG KGQVPQPLLSVSLPLLRLSGGQ ETPNPFSFTLSGKSAFLEEQVPQ PRISVPQSLISTPRPLISVAQSLIS APQPLISLCPNPLFPCPDLLSLHP NPLFPRPNPFAFLEGACYKCQ KSGHQAKECLQGPICKLRPICA GPHWKSDCPHTLAATPRAPGT LAQGSLTDSFPDLLGLAAED |
| 15064 | 45432 | C | 15151 | 234 | 449 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15055 | 45423 | A | 15142 | 2 | 2107 | IDMIFTGPPSTPKHKKSQKGS AFTFPSQQSPRNEPYVARPSTSEI EDQSMGKFKVVERQVQDMG KKLDFLVDMMQHMERLQVQ VTEYYPTKGTSSPAEAEKKEDN RYSCLKTHICNYSETGPPEPPYSF HQVTIDKVSPYGFFAHDVNL RGGPSSGKVQATPPSSATTYVE RPTVLPILTLLDSRVSCHSQADL QGPYSDRISPRQRRSITRDS LTLMSVNHHEELERSPSGFSISQD RDDYVFGPNGGSSWMREKRYL AEGTDTDTDPFTPSGSMPLSST GDGSDSTVPLFLSSEILQKQVG QSITSMGLGFLSRGSPMKLCMGL ACVLSLWNTVSGIKGEAKKEK GMTFLPTTDSKKFFSLSVTSYS SFAFHKFSVAVYNISNLKTVD AKFPTRYCYCLNNRTNDLSDF ALLVDIIGNSTSYLTEIFKSTSIL SVNQSNESDCIFCVMTGKSGR NLSDFWEIEEKYPIINYTFTSGL SGVLALLLTQSLFGGLFTRTRM KFGAVTRIGGPPLGNQSPSSCSL LHEKDPPTSGPQTDQPKKHLT NFKSAARPTFLGQGQVPLNPFS FTLS/EQVLLS*AARTPQSLISTP QPLISVPQSLISVPQPLLYFSGG QEPPPPPLLCVSSLFSLASFTM GAFTHGTQTPSPTKATAPRYPQ TGDLSAEWPFTAGEEPVLVPRP |
| 15056 | 45424 | B | 15143 | 1 | 930 | |
| 15057 | 45425 | B | 15144 | 401 | 1093 | |
| 15058 | 45426 | C | 15145 | 1 | 843 | |
| 15059 | 45427 | A | 15146 | 1 | 498 | |
| 15060 | 45428 | A | 15147 | 112 | 669 | SLQGRSLDYTPTFQGCQTQGC LPWSFTLCSKSRFSGEGETRFKR IKACYHSPATAWPFKAYKLSLQ FPHFTCRKTRQALQVSSSAPY QPNCFAYPGRGAEPHSPILNTS LHNPLFCSGSQTCFLY/SFLCTL HPSLSSLGLTLTPIRLSKLPGL YCLKSSQTAPITSVKPKFLPHLL PISA |
| 15061 | 45429 | A | 15148 | 957 | 1100 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15054 | 45422 | A | 15141 | 1 | 1340 | CSEYEDSSPAPVPATDLSSTLSS SVPQPQDTGTSQQLHPLDPWHE LLRAQELQGATNHKGYSIAEH EHAGLG VQGGNGALAFSNSGH RHAVPTISSGTGRRRTPSSSAFG LLNLHQWFVSGFQAFSDRLKA ALSASLLLRFGSDWLPSSSAC KCLMLGLHFVIVGNICATLKEK YSSMLHLDVTMKNKEKRTRL QKRKKGMPPHPAYEDLNIAAIT LPANVVV LHQPSGFRTSGQLDPV WWSLDTDAHEIWCQDPGLGSG DFPWEITPLSSYSLLHEKDPPTT SGPQTDQPKKHLTNFKSKTKET GFIHGPKTPAPVTDWEGSLPLV FNHSGTPL*LFTHVSRVSDHAG MPALVLHP*RQVPLFWRRGKI* LTSPSRCTIIEKSCNSLPPL*DKP QPHLQHTRTSKCLNRSGQAF/L PEPPPTG/CLLHVPEIWPLGQGM PAARDSS |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15046 | 45414 | A | 15133 | 245 | 1033 | TALLLTQSLFGGLFTQTRMKFG AVTRIGGPPLGDQSPVLLFFVPR ERSTYDLGPQTDQPKKHLTNFK STSFVFSSCIPPP*PSSISLLPPW/T TDHAPLTISL/TT*SPLPCSMPI/ ASHSML*KD*SLLSLACYSMAF *SL*TLLTIPPFYLS*NQRRFTG* FRICALSTKLFCLSTPWCQTHIL SYPQYLPPQSIILFWISNVLSLLF LCTLHPSLSSLSLGLTLTPFRLS KLPGLYCRKASQTAPITSVKPK FLPYLLPISA |
| 15047 | 45415 | B | 15134 | 146 | 556 | |
| 15048 | 45416 | A | 15135 | 1 | 555 | LTSFLHCCLSHHYHGAQIHPRH FLHLICRCHCHQYCHHAYLDPC PQDSHHLHWCWQPLPELELRP KA/HLTDSFPDLLGLAAED*HCP IASEAALPPCFPRPDIMITSLQL QRRRQTALGVRYRNATYRTRT ASTNSLRPRGSPFPLALVTNDR QVRSQALWKRDRLLQLSPINR AIESSFT |
| 15049 | 45417 | B | 15136 | 1 | 555 | |
| 15050 | 45418 | B | 15137 | 499 | 769 | |
| 15051 | 45419 | A | 15138 | 752 | 1111 | MQPTIGNSQSVSRPTA*MPLAE SHPITQLVGTVTTPRVTPLSIRH PWRCRSANAGAMILTMKQLAI VMRVYQHQVRRSMRPGRNGA RSGMSAVGAYYSSCIRVMTAL QSCTGDDEAVLL |
| 15052 | 45420 | C | 15139 | 1 | 632 | |
| 15053 | 45421 | A | 15140 | 1 | 375 | PGVRGAQGGPSIPRQCEESAIGP KFAWISSFHWKQGMFNMEAP SSLFFVNMCAVKKQTTWGRPD RGIWQPLPELELWPKA/HLTD SFPDLLGLAAED*HCPIASEAPA LVYTAGLHCFKPSQ |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15032 | 45400 | A | 15119 | 144 | 298 | WQVPLFWQPFPEPELELWPKA/HLTDSFPDLLGLAAED*RCPIASEAPCTQVI |
| 15033 | 45401 | A | 15120 | 449 | 667 | |
| 15034 | 45402 | A | 15121 | 2 | 111 | |
| 15035 | 45403 | A | 15122 | 323 | 401 | LLLGLAAED*RCWIASEAL*TITDAK |
| 15036 | 45404 | A | 15123 | 2 | 593 | CTLPSH*NLITLTPLNANIPSHGML*KD*SLLSLACYSTAF*GL*TPLTIPPFYLFKNQTRLTG*FRICPLSTKLFCLSTPWCQTHILSYPPYLPPQPIFLFWISNMLSLLFLCTLYPSLSSLSLGLTLTPIRLSKLPGPYCRKPSQTAPTSNHPSSFSGSWYSVETSYPLSSSIFRKGRDTSWSLKDTPHQAQPPT |
| 15037 | 45405 | A | 15124 | 354 | 630 | |
| 15038 | 45406 | A | 15125 | 29 | 354 | RFLVSLMLPPAVVMLNHCYSLI FTNALVKRLFAWNMLSELATCAGNLATGPRNARSPGFLLSVPSVRDPTGNQTVQLTWQPLPELELWPKA/HLTDSFPDLLGLAAE |
| 15039 | 45407 | C | 15126 | 1 | 576 | |
| 15040 | 45408 | A | 15127 | 377 | 624 | RDQLQCLQLWDAGACYTCWK SATGPRNAHSTVFLLSHVPSVWDPTENRTVHLTWQPLPEPELELWPKA/HLTDSFPDLLGLAAED |
| 15041 | 45409 | C | 15128 | 1 | 462 | |
| 15042 | 45410 | A | 15129 | 44 | 340 | PCQTTQGRLLTAGTPL*SFTHVSRVSDHAGTPALVLHP*RQVPLFWGRGNHISGTQELPNT*TAV/VQAF/LPEPPPTG/CLLHVPEIWPLGQGMPAGQDSS |
| 15043 | 45411 | A | 15130 | 242 | 522 | RLVWPTATQRAWSQSEAAAAKTVDLALSARNSATGPRNACSPGFLLSCAPSVWDFTGNRTVQLTRQPLPEPELELWPKA/HLTDSFPDLLGLVTED |
| 15044 | 45412 | B | 15131 | 1 | 1080 | |
| 15045 | 45413 | A | 15132 | 1 | 642 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15023 | 45391 | A | 15110 | 1 | 1194 | MGFLHLGQAGLEFLTSGSSTDI SEDWEKDFDLDMTEEEVQMAL SKVDASGEPCFCWKGYPPGGEL ETLIRLLQKLFFLKTDPAFVLSP STLVKLHLWGNEGLQESLESLV LHDAALVILVPNLEKKGEISELL VGSPSIRALYTKMVPAAVSHSE FWHRYFYKVHGLEQEQARRVA RLKQRAEQSISEEPGWEEEEEE LMGISPISPKEAKVPVAKISTFPE GRTLAPQSPCEENLVTSVEPPA EVTPSESSESIPKSPLPTRALGTD |
| 15024 | 45392 | A | 15111 | 213 | 1031 | AGNKPDPWAGRNRATAVLPDVS VFHREDVGWWRSLQQSYQA VKEKSSEALEFMKRDLTFTQV VQHDTVCTIAATASVVKEKLA TEGSSGATEKMKKGLSDFLGI SDTFAPSPDKTI*RDVITLMGTP SGTAEPYDGTAKARLYSLQADP ATLLY*PDGPPELFDALWSQFC LEKKGEISELLVGSPSIRALYT KMVPAAVSHSEFWHRYFYKVH GLEQEQAPRDALKQRAEQSIFE EPGWEEEEEEELMGILPIFPKEAK FPLAKISYIP |
| 15025 | 45393 | C | 15112 | 414 | 557 | |
| 15026 | 45394 | A | 15113 | 98 | 467 | |
| 15027 | 45395 | A | 15114 | 1 | 155 | |
| 15028 | 45396 | A | 15115 | 16 | 94 | RCPIASEASWTITD*RCPIASEAS WTITDALGNSYSGGMAF |
| 15029 | 45397 | A | 15116 | 95 | 115 | IIRHLCND*TPREGCLPSP*PAW SDTFETWVNNQASLQ |
| 15030 | 45398 | A | 15117 | 3 | 282 | LKPVITCLLQLGLLKPINSPYNS PTLPVQKPDPRPYSKPNSLP*LNP SLLQRNYTSIFLLTLNMPISICT TMLLYGQKEISSLHKGPPLMP |
| 15031 | 45399 | A | 15118 | 548 | 1401 | SCTPCWHLTGRLWGITA VRQK RHVLSVDPKLRHQSRGKAAPF WCLIIAGTPL*LYTHVSRVSDH AGMPALVLHPLQQVPLFWGRG NTL*KD*SLLSLAC/VQHGLLK PINSPYNSPILPVVKPDKPYKL VQNLRLINQIVLPIHPVGEAPV PLETGGKSGKDCILWFECHLSHNTI EHQVSSSTFRIVVATGVLVSLH PQLYMAQNRERHAECLESGESK GREQESLSGNPENSRSFLLTSRRY LYKSTRITIVLLGLAGPLKQKKL RSQHPSLYKYLQSFNRNKDSYR |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15016 | 45384 | A | 15103 | 84 | 303 | EEQELPSLSVPSCLWGPCPRAG WLHSLHWPVSHSFSATSTFGM AIWT*SLASGIKPQSSSKVSSRIQ VPPTM |
| 15017 | 45385 | B | 15104 | 112 | 462 | |
| 15018 | 45386 | A | 15105 | 326 | 1323 | DRKAINLQVKLEGAVAL*KPG EAQLEFGKALGLFQ\STLGHHF VNNKEKILGDFQEATLQAATK LTRGRSLVMENMEQLLSMRME DQSQRNMPLSVVLIREKAHSPF ENRKQEQGEGASPENFRARIQG *FLAFKAAPPA*AASGPAAQER SVQEPSVNAPG*IPEGGLHTLA GVHHE*ALAWCSPLNKPRFLW KRLP/SRTFHFPEDESAPGSKP SGDLLTLLGGNAAGDFKLKVP CLVYPSENPCFLKGSFKPNLPL VWCSHKKA WVQPG*QSETPFQ KKKKKKKKKA WVTMSLFQEW LHFCSTVE/ARCTQYDLPYKGL PILDSTPGHPGC |
| 15019 | 45387 | A | 15106 | 3 | 375 | HASAHASGLQQSYQAVKEKSS EAEFMKRDLTEFTQVVQHDT ACTIAATASVVKEKLATEGSSG ATEKMKKGLSDFLGVISDTFAP SPDKTSTAMSSPYDGTKARLY SLQSDPATYCNEPDGPP |
| 15020 | 45388 | A | 15107 | 184 | 377 | YCTNNQKVN*TKEIITKRKTPSR QKKDSAFSPSHPLTEGLKWND LTLVSLTHDGFVWRRGKGV |
| 15021 | 45389 | A | 15108 | 3 | 816 | SWEDVGWWSWLQQSYQAVK EKSSEAEFMKRDLTEFTQVVQ HDTACTIAATASVVKEKLAIAA CSRGACFLCPFSIQTEGSSGATE KMKKGLSDFLGVISDTFAPSPD KTIDCDVITLMGTPSGPAEPYD GTKARLYSLQSDPATYCNEPDG PPELFDWLSQFCLEEKKGISE LLVGSPSIRALYTKMVPAAVSH SE/TFWHR/YFYKVHGLEQEQA RRDALKQRA/VSGDSCT*SGVL TNE*KGSWVRDTERVRSPLQT FSEGVGWREC |
| 15022 | 45390 | A | 15109 | 1 | 281 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 15008 | 45376 | A | 15095 | 16 | 545 | GLPWRQHVRVEECGRS/PLRPC SPGTPSPS*PLPAATRGPATCQS LSGLQPEKTT/SPS/CAAVAHER PPGPVPQCPAQGTGLIF*EGWT QPQQIRQGPHVAHE\CAHDLO QAAPGPGGAHQG/PSQPG*PDR QPDARA VVHPGAQ*DAEIQPG LPGEGGPLATRTERSPAQRPS QARG |
| 15009 | 45377 | A | 15096 | 320 | 1167 | MDLKTAVFNPARDGKLRLTLK *MASKSKEEVSSLISEKTNGAT PLLMAARYGHLDMEFLLEQC SASIEVGGSVNFGETIEGAPPL WAASAAGHLKVVSLLNHGAS VNNTTLTNSTPLRAACFDGHE IVKYLVEHKADLEVSNRHGHT CLMISCYKGHKEIAQYLLEKG ADVNRKSVKGNTALHDCAESG SLDIMKMLLMYCAKMEKDG GMTPLLSASVTGHTNIVDFLTH HAQTSKTERJNALELLGATLFT QKEISCDESGRTRDLSRRKPPH |
| 15010 | 45378 | A | 15097 | 187 | 623 | KLKTQKNNIGPQACNSQLASVS TRSPPTLSVPIIMTDDSQASQL LLAAVTIRKLWSRMAPMLALP TGQSGQTGAEGQGKEGERGQS PCWKPRLDPKLC/EPRQPAQLL* ADVCTGP/CGVRGCPADCRLPC LSPSSAQPKASRSA |
| 15011 | 45379 | A | 15098 | 789 | 1041 | |
| 15012 | 45380 | A | 15099 | 707 | 1373 | SAWPSCHCCHLDILSR/PGDDA CSVQILVPGLKGDAGEKGDKG APGRPGRVGPTGEKGEKGDG DIGPPGPNGEPGLPCECSQLRK AIGEMDNQVSQLTSELKFIKNA VAGVRETESKIYLLVKEEKPYA DPPLSWQGRGGLSMAQDEAV HGLKGAYLGQARLGRGFIGIHR PWKRRAPLLLF*TLSPLRSF*KG DGGGNTQKGSRRKRELQGIW GPCIRR |
| 15013 | 45381 | A | 15100 | 79 | 420 | WRRFLFLGLVFRGYLGCLRSRS VLGRLKVSDMRIFFFACGCGHL STLPSWPLRPSLWLRL*EEQELP SLSVSSGRSASRL*LGWRGF GPSPSPRLTVQFSGGRRRAQGPS |
| 15014 | 45382 | A | 15101 | 3 | 284 | |
| 15015 | 45383 | C | 15102 | 83 | 112 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 15001 | 45369 | A | 15088 | 216 | 1369 | EPVLRRRPRQPRAGAQGFPVFS PPGPPRKPPALSRVSRMFSVAH PAAKVPQPERLDLVYTALKRG L/QAYLEVHQEQ/DKLQGGQIR ESKRNSRLVMAGGVLWTVV*E RGAVTSLASAGVLLIPPKYLP LPTPAGLALYDLKQVKSIERFL/ RRLEFHASKVRVQHVCRWD\D ELYEAYCVQRRLRDGAYNMV RAYTTGSPGSRREARDSLAEATR GHREYTE/DEGWGPMRQRHRS MCLLES/ELEAQLGEFHLRMKG CAVDINDLGTIKLSLEVTGAAS SVNKASTVTKRSPPIARAHRT PHFGNSFLSTRKPNTYTANHRR RPIEQHPDMRTPPPPHRARTNT GRKDKVRAHEGEKATPTRTRG APHGKAQRLRPLYQYVTIATLS |
| 15002 | 45370 | A | 15089 | 1 | 940 | MSYNSKNYVETITTMNSVKFG ETTPRNRTHYLSTNEKKIFLSGV FSNAYPAGLSRGWDSPWGSTP WVRHFCYLSSTQLCDQNCILLS SLLPAGPSVCNRLLASAWQKSS SSASSEASETCQSVSECSSPTSD WSKVGSHEQPSGATLQRRKDR VE\PCETQSPGPASGGTLGPSGE EAPRPRMSPATIAAKHGEEVSP AASDLAMVLTRGMSL*HQKSS RDSLQYSSGYSTQTTTPSCSEDT IPSQGRPAGLGPTKPVSIESTYL QSPQRLKQEWATEGKIQLPPQ IQVVNFQVDSSPSLPLIMVPEH MHVS |
| 15003 | 45371 | B | 15090 | 1 | 777 | |
| 15004 | 45372 | A | 15091 | 26 | 336 | KISPMINVFCSESSPSGERRGA* TPPSPQSPPCGPKPSS\PPSCSPSR NYFLLFQGLCAEHPALAAPAAS VGTCPSPASGTHAAAPSGPWGR RCVHSGPGGRLW |
| 15005 | 45373 | C | 15092 | 46 | 423 | |
| 15006 | 45374 | A | 15093 | 1773 | 2219 | ELDYLCSNSSAQCPGALLPSL ALPGPAGSARQAGSPARRLCAP VQPSGRWPAPGGPGFPGSSCPA SPTRQ*LLTSGSGCPRPCHHPSG PPQ*QSTQAWDWVILGPGAHG PSGQRCERCLPSRSPGPQTHSG VGSEPRAVRGPVSVFV |
| 15007 | 45375 | B | 15094 | 1 | 7916 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14993 | 45361 | A | 15080 | 602 | 1257 | FGKRGRITLTCILAVGMLCCRK GHTKPRRRPGASPISTHLHSSPPI STHLHTSPPPHRREEARISGQ*R QSCGAAAAR*PWWWNC DGWG PKCQRFSKH*DIAQPDEVSWGQ *PWAVGALAGPHP\PQASEGPL GCTPASICGSTRKPSKPLSKKPP QAARTSSSRIVIFTPISTRPPTQG QPEKAKSATPTNDLEGPSAKVK FVNFLMDETFPEPSFFFI |
| 14994 | 45362 | C | 15081 | 140 | 175 | |
| 14995 | 45363 | A | 15082 | 2295 | 3089 | NLLGYQEINPPLQIFWDKLLAV SERDSSVKEESGDVESDDTML* MLPCP*ETTEFSS*PFRIS*LSS* STAQIPAETCFAGGWYSIFCPQ RIEQETMCLL*SWQSEVAVSCE SPWPTALHHSHPNRAPPICY/S KSTSSSLSSPLENSG*QNRPPSLL ITSVLPLRITCLP*VSFIPPIMQLG GSFLSNDRL*QSFILPKNVSLF VSFPLI*GAVSKPAISFNTSVSPL LVSDIFFALSLLP*GLGTWLIPSS SSLLLVRGF |
| 14996 | 45364 | B | 15083 | 143 | 1727 | |
| 14997 | 45365 | B | 15084 | 307 | 1017 | |
| 14998 | 45366 | A | 15085 | 1 | 959 | MSRMGLLGFGERKELPNHPAV SEWPLTLVTGCSSGTVAEGEGN LTTSGLFSIVPLHPDGVAAGQR HSSLPRWGSQAEALLTSQTVDG QAEMLLTPQTMGGQEEMLLTS QTTGEDFITRSTESGTHSKSHKG DEGEPRWMLGWMLWVCDIAE PLVKAKLLDCKHTCCSVCLQQ TRTSQKDVRCPWCSGVTKLPPD FSVSQQLDDPEVLAVITIPHASE HMPVFIRLPGSGCY\SCPCSPRS TRCCPEI*AATCCPGTGRSPSL\C DHPCWTAASARQSGPGGGGGG AGQAGHGEKLVHVEGVHCHL GGLRLGLPPQHRAP |
| 14999 | 45367 | B | 15086 | 112 | 672 | |
| 15000 | 45368 | A | 15087 | 2 | 530 | SGRSAALLSARVNRSQSFAGVL GSHERGPRSFVFPSPGPPRKPP ALSRVSRMFSVAHPAAKVPQPE RLDLVY TALKRGPDGLLGAVH QQEQEKLGQGIRESKRNS/RLG EWREGFLYDLKQVKSIERFLR RLEFHASKIDELYEAYCVQ\RR LR\DGALHMG\RAYTTGSPGSR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14982 | 45350 | A | 15069 | 383 | 756 | LNPSNKLALINPAASPIIKGVDL TANQI/PCIADIPLYDADVQQE* CFPATVEALGEQIRQADGVVIV TPEYNYSVPGGLKNAIYWLSRL RQILVFLDAMVMNKPEFMGGV IQNKVDPQTGKVIDH |
| 14983 | 45351 | A | 15070 | 343 | 924 | |
| 14984 | 45352 | A | 15071 | 223 | 308 | |
| 14985 | 45353 | A | 15072 | 57 | 5546 | NKMARKKFSGLEISLIVLFVIVT IIAIALIVVLATKTPAVDEISDST STPATTRVTTNPSDSGKCPNVL NDPVNVRINCIPEQFPTEGICAQ RGCCWRPWNDLIPWCFVVDN HGYNVQDMTTTSIGVEAKLNRI PSPTLFGNDINSVLFTTQNQTPN RFRFKITDPNNRRYEVPHQYVK EFTGPTVSDTLYDVKVAQNPFS IQVIRKSNGKTLFDTSIGPLVYS DQYLQISARLPDYIYGIGEQVH KRFRHDL |
| 14986 | 45354 | C | 15073 | 1 | 1818 | |
| 14987 | 45355 | A | 15074 | 493 | 576 | |
| 14988 | 45356 | A | 15075 | 381 | 498 | |
| 14989 | 45357 | A | 15076 | 48 | 514 | LLLFULLQSYDWSESGKRQSAL HGRQKGLPKSPTAARGGSDPW PSCRHP*GPNRKRKRS/R*PMET APRRPSVSPALTPARPPGLTATP RLHPRPP/RSPNPSANLLRRPTP DT*AHATFGPGRSRHHFPGQLS TE/RRRSAEGGRSRREASRRE GGE |
| 14990 | 45358 | B | 15077 | 1 | 1116 | |
| 14991 | 45359 | C | 15078 | 249 | 332 | |
| 14992 | 45360 | A | 15079 | 710 | 1326 | RAAGNCFPEPGFVKQLSAAAA VVAPAAAATEGSIPDTGKSPSSI SHWPNPQKNVICKRRGRVEQE QAWKGR*RVVFGL*KSMRCP VDLLPQSCLCQRFLHQ/GKWIL TKDYIIHSAKSGRWLDATTYE WGYKIEKDSRYSPQMMSAPKR WREELKRTGAPGAFHRWKVVL LVRTDKRSDSLIRFSDNFGDCDI RMEECTFRTLMS |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14977 | 45345 | A | 15064 | 1 | 1496 | SGGCAGLHGG LCSKEPFQASV QQGVAGHACAPAAALQVPVCGT LSDCGSRAASLCENPSFISLYGR LVATSLAKLPIPKLMRWGASD VHFVRPVHTVTLALGDKVIPAT ILGIQSDRVIRGHRFMGEPEFTI DNADQYPEILRERGRKVIADYEE RKAKIKADAEAAARKIGGNAD AKFEEKFLAVPAEALVYTMKG DQKYFPVYANDGKLLPNFIFVA NIESKDPQQI/DRIQALAGWIAE Q\IGADVNHATRAGLLSKCDLM TNMVFEFTDTQGVMMGMHYAR HDGEAEDVAVALNEQYQPRFA GDDLPSNPVACALAIADKMDT LAGIFGIGQHPKGDKDPFALRR AALGVLRIIVEKNLNLDLQTLT EEAVRLYGDKLTNANVDDVI DFMLGRFRAWYQDEGYTVDTI QAVLARRPTRPADFDDWHALG RAGTGDVVVGVRGR LAIVPLT DGLDEAGHSTGVLQGEVPQRL ERAATVPGVTLPQALQARGL |
| 14978 | 45346 | A | 15065 | 134 | 384 | VTPTGWRKRRIQWCS DAGCG VNALSGLRFSHSLALFSAAMFI LGVVSGITMSISP*ILSCVRSKNP LLVSGSGPLSCNSTIH |
| 14979 | 45347 | A | 15066 | 1 | 723 | TKSPKIARSRHIPLCHFIFERRPI MTNSNRIKLTWISFLSYALTGA LVIVPGMV MENIADYFNLPVSS MSNTFTFLNAGILISIFLNAWLM EIVPLKTQLRFGFLMVLPVAG LMFSHSLALFSAAMFILGVVSGI TMSIGTFLVTQMYEGRQRGYR LFLAASLF SMAGMIFPMIAAFL LAPSS*W*WVYACGLAYVTIF IMTFGCEFPALGKHAPKSYAPV EKVKWGILGGASSFRAV |
| 14980 | 45348 | A | 15067 | 422 | 1045 | LLEGKLTNRKQ*HQH*OKARPC KKPIQSAQN/WNREEYDELTEV GRRWVIITNSFELKEHVLTQWK EAKNLDKRLQEGLTRITSLEKKI NDLMVLKNTARELHEAYTSINS RIDQAEERISEIEDQLNEIKLED KIRGKRJK/RQTNKQSL*KMWD YVKRPNLRLIGVPESDEENVTE LENTLQDIIQENFPNARQANIQ IQEIQTLLR |
| 14981 | 45349 | A | 15068 | 1 | 1131 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14973 | 45341 | A | 15060 | 1 | 5621 | MSEKTFLVEIGTEELPPKALRSL AESFAANFTAELDNAGLAHGT VQWFAAPRRLALKVANLAEAQ PDREIEKRGPAIAQAFDAEGKPS KAAEGWARGCGITVDQAERLT TDKGEWLLYRAHVKGEGTEA LLPNMVASSVAKLPIPKLMRW GASDVHFVRPVHTVTLLLGDK VIPATILGIQSDRVIRGHRFMGE PEFTIDNADQYPEILRERGVIA DYEERKAKIKADAEEAARKIGA KAWGTNVEFHVQNQP |
| 14974 | 45342 | A | 15061 | 82 | 732 | |
| 14975 | 45343 | A | 15062 | 1 | 3849 | MDLGANGWQTFRYVVLNLS ALLAGGMLAFALSFDIIVTTFT AEQVDAAVRAADAFAEWGQ TTPKVRAECLLKLADVIEENGQ VFAELESSNNTAFARASSNGDL PTKADLQAQLDSL NKQKDL SA QDKLVQQDLTDTLATLDKIDRI KEETVQLRQKVAEAPKMRQA TAALTALSDVDNDEETR KILST LSLRQLETRVAQALDDLQNAQ NDLASYNSQLVSLQTQPERVQ NAMYNASQQLQQIRSRLDG |
| 14976 | 45344 | A | 15063 | 219 | 1186 | PPKLGRKRGIFLPSHSNPNTNRI CPNCCMNGVSTANTTSKSSLVI CAWTKHALLNAILQPEQLWKS GSRWRINLALPRGYRESLLQPW QAERLTDDKGEWLLY/RAHVK GESTEALLPNMV/ATSLAKLPI KLMRWG/ASDVHFVRPVHTVT LL/LGDKVIPATILGIQSDRVIAA TGKAKIKADAEEAAR/KIGGNA DLSESLLEEV/ASLVEWPVVLN AKFDEK/FLAVPAEALVYTMKG DQ/KYFPVYANDGK/LLPNFI/F/ VANIESKDP/Q/QIISGNEKSFVR LADAEFFF/NTT*KRLFLPHQKL PPSQILHQQTRNYASFCHRRD NWTSA |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14969 | 45337 | A | 15056 | 356 | 1205 | APASMTFEQFVREFA/VMVFTK RPAAMMIGIRADESYTVLSPSP V*INNVLPTITWTFPQTIYDFLW LIGEAIFF/YLPVGICWSAVKKM GGTRSLVSCL/AVTLVSPQL/MN AYLLGQQLPEVWDFG/VCSLIL/ AVFLAHALIGPFGRMI/GDGVA FAVRHLMTGSA/PIGAALFGFL YAPLVIT/GVHQTTLAIDLLMM QSMGGTPVWPLIALSNIAQGSA VIGIISSRKHNEREIPGEVFPRT GVGKGKSLG*PLH*LQPYRQHL GAGSYSQTLKKQIAESA VRLSIP |
| 14970 | 45338 | B | 15057 | 1 | 435 | |
| 14971 | 45339 | A | 15058 | 2 | 1785 | WLLYRAHVKG/STEALLPNM VATSLAKLPIPKLMRWGATYV HFVRPVHTVTLGLGDKVIPATIL GIQSDRVIRGHRFMGEPEFTIDN ADQYPEILRDSGKVIADYEERK AKIKADAEAAARKIGNADLSE TLLEEVASLVEWPVVL/TAKF/E EKF/LAISRTALVPYSADNMYQ LVNDVQSYQPFLPGCTGSRILES TPGQMTAAVDVSKAGISKTFTT RNQLTSNQSILMNLVDGPFKKL IGGWKFTPLSQEACRIEFHLD FTNKLIELAFGRVFKELAAANMV QAFTVRAKEVYSASMRYIYVIV YISYRPPNLLDSHIIGFSSITTHC AVTSHHYNSCDMTMTIHSYVT PYISVRVSLTQTYAPSPSRNLRI TDLTIYRAISSEKSIDDTRHIHTI ESRCRVCGAHDSDAERLDRF AQTADEIRJADRGFSSRPECIRS LAFGEADYIVRVHWRGLRWLT AEGMRFDMMGFLRGLDCALIS KTRLLSENRRKGRVVQAETLE AAGHVLLLTSLPEDEYSAEQVA DCYRLRWQIELAFKRLKSLHL DALRAKEPELAKVGIFANLLAA FLIDDIHQPSLDFPPRSAGSEKKN |
| 14972 | 45340 | A | 15059 | 1 | 993 | |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14964 | 45332 | A | 15051 | 361 | 837 | DGQQIALHRLALRELQQAVH AGLPQQAKILFDGGSEIGKIPSEI YFCQLVKLILCPVLFPCWRRVA ILWRRRDVLFSGSFSFSAVSPH LCG/SYLPFVFDVGDRL*LSVG WS\KEIWPC*KFGHLM SVLNT PMKSLVEGFKHFPLAGFGYEYL SFFCR |
| 14965 | 45333 | A | 15052 | 1563 | 1652 | |
| 14966 | 45334 | A | 15053 | 2756 | 2995 | AMRSAHRCTVFSALLNCWQITP HLTPSVMICGQLLTLVNRC*PSS TIFSIPLSKQVARMFRSAMSPL NRARCWKVPCN |
| 14967 | 45335 | A | 15054 | 762 | 2184 | WRAVPSEPISFILKADTEKYVY L*NSSSAQYSGSCTRAYYLDLTQ HPTPRLCLIFGGKDSGLMLHLT AELARQMGGKICVLFDWEAQ FSCTINYVQSLRELYTDVIEEFY WDALPLTTQNSLSQYQPEWQC WEPDVEWVRQPPQDAITDPDF CFYQPGMTFEQFVREFAEWFSQ KRPAAMMIGIRADESYNRFVAI ASLNKQRFADDKPWTTAAPGG HSWYIYPIYDWKVADIWTWYA NHQSLCNPLYNLMYQAGVPLR HMRICEPFGPEQRQGLWLYHVI EPDRWAAIGSPADREDAEEYL EAIMEARVTVAGMGLVMEVQ DYFDGEADRLAKAWLAEYTPQ IKSLKDERKEAYRQIVEMSTEP QDVDLVRPANKFEMTRVREGE KEADLPVWKHLLCDESGNYP ALLNHWETKVFEIETKREGFAF WYRNPQYTGQSSLGIAYVEAE QYKIVRPDLFFAEQDGKMVV |
| 14968 | 45336 | A | 15055 | 2069 | 2586 | PWLENLPVGICWSAVKKMGGT RSLVSCL/AVTLVSPQLMNAYL LGQQLPEVWDFGMFSIAKVG QAQVIPALYL VVPVCSLILAV FLAHALIGPFGRMIGDGVAF RHLMTGSFAPIGAALFGFLYAP LVITGVHQTTLAIDLQMIQSIGC TPVLPVNALSNI DLWHISILV |

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|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14953 | 45321 | B | 15040 | 1 | 4534 | |
| 14954 | 45322 | B | 15041 | 1 | 1826 | |
| 14955 | 45323 | B | 15042 | 1 | 1626 | |
| 14956 | 45324 | A | 15043 | 248 | 1212 | NSKHYSRGQKKKLPTLPRAAN SRWRSLKI/GFTVSFDETLKPFV RDVSGSRLKDLPKPNKSDDETR ANDAVNRYKLLKKDARTIAAQ QVARLESAMCLRRRWLENFQ LFLVEHPLVRHLTRRLIWGVYS AENQLLACFRVAEDNSSSTADD DLFTLPEGDISIGTPHVLEISPTD AAALLFADYELLPPFRQLDRNS YALTEAERNASELTRWAGRKC PSGRVMGLANKGWIKGEPQDG GWIGWMIKPLGRWSLIMEIDEG FAVGMSPAELSAEQLLSKLWL WEGKAERYGWGSNSTQEAQFS VIDAITASELINDIEALFE |
| 14957 | 45325 | A | 15044 | 1 | 1788 | |
| 14958 | 45326 | A | 15045 | 1 | 3048 | |
| 14959 | 45327 | A | 15046 | 1 | 3546 | |
| 14960 | 45328 | A | 15047 | 969 | 1205 | SPVRCCISAVHRTYHRRTSALL RLAELHRLLEKCASRQWMYEN I*SPFRQIA*CLPYSDHKNQRLH GLDSIFLARLLW |
| 14961 | 45329 | A | 15048 | 877 | 1248 | WPLTVPYCGVGYAS*A*VADN HRAVGYSRWAGRKCPSGRV MG/LANKGWIKGEPQDGGWI/G WMIKPLGRWSLIMEI/DEGFAV GMSPAELSAEQ/LLSKLWLWEG KAERYG/WGSNSTQEAQFSVID |
| 14962 | 45330 | A | 15049 | 854 | 1313 | DHGVASAATCVYTNEGHRQSY VRVCEYASRTRVSHHCSV*RVL RCEAIRIVSPDRSC*RDPEFSYL ALPENYNRLFLPNSTNQTNRI KTLNSIAIGKLLAAGGVYNGNI EGFRDTAEKLDGRTIDGYDQIL NEKTAVIAKATAISILLTKRS |
| 14963 | 45331 | A | 15050 | 1010 | 1396 | KPFGKLTYYKLFEGHAWLVKAE KVRVGYYRILGRLTYPFDIRFPAL PFGLVL*KGAHFTVPRIWAGHA C*LMPMALPMFRWKVTGLLFIP ICLVKPSFLTITIIAIRRISTSTN CRKTPKQPSRWCKPR |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in U/SSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|--------------------------------|---|---|---|
| 14946 | 45314 | A | 15033 | 965 | 5928 | TWKGTTSTSRCKIMPKYRSTRQ KVNKDTQELNSALHQADLIDIY RTLHTKSTEY/TFFSAPHHTYSK IDHIVGSKALLSKCKRTEIITNY LSDHSAIKLELRIKNLNQSRSTT WKLNNLLNDYWVHNEMKAE IKMFFETNENKDDTTYQNLWDA FKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKEKQEQTTHSKA SRRQEITKIRAELEKETQKTLQ KINESRSWFFERINKIDRPLARLI KKKREENQID |
| 14947 | 45315 | A | 15034 | 383 | 8708 | |
| 14948 | 45316 | A | 15035 | 2 | 3257 | WRKIYQANGKQKKAGVAILV/S DKTDFKPTKIKRDKEGHYIMVK GSIQQEELTILNIYAPNTGAPRFI KQVLSDLQRDLDSHTLIMGDFN TPLSTLDRLMRQKVNKDTQEL NSALHQVDLIDIYRTLHPKSTE YTFFSAPHHTYSKIDHILGSKAL LSKCKRTEIITNYLSDHSAIKLE LRJKNLTQSRSTTWKLNNLLN DYWVHNEMKAEIKMFFETNEN KDDTTYQNLWDAFKAVCRGKFI ALNAYKRKQERS |
| 14949 | 45317 | A | 15036 | 1 | 3508 | MELKTKARELREECRSLRSPCN QLEERVSAMEDEMNMKREG KFRDKRIKRNEQSLQEIWDFVK RPNLRLIGVPESDGENGTKLEN TLQDIIQENFPNLARQANIQIQEI QRTQPQRYSSRRATPRHIIVRFTK VEMKEKMLRAAREKAPHHTYS KIDHILGSKVLLSKCKRTEIITN YLSHSAIKLELRIKNLTQNHST TWKLNSLLNDYWVHNEMKA EIKMFFETNENKDDTTYQNLWD TFKAVCRGKFIALN |
| 14950 | 45318 | B | 15037 | 1 | 4760 | |
| 14951 | 45319 | A | 15038 | 1 | 3110 | |
| 14952 | 45320 | A | 15039 | 1 | 5546 | MELKTKARELREECRSLRSRRN QLEERVSAMEDEMNMKREG KFREKRIKRNEQSLQEIWDYVK RPNLRLIGVPESDAENGTKLEN TLQDIIQEDFPNLARQANVQIQE IQRTQPQRYSSRRATPRHIIVRFT KVEMKQKMLRAAREKDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSTLD RSTRQKVNKDTQELNSALHQA DLIDIYRTLHPKSTE |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14939 | 45307 | A | 15026 | 1 | 2053 | MKAEIKMFFETNKNKDDTTYQN LWDAFKAVCRGKFIALNAHKR KQERSKIDTLTSQLEKEKQEQ THSKASRRQEITKIRAELKEIET QKTLQKINESRSWFFERINKIDR PLARLLKKKREKNQIDAIAKNDK GDITTDPTIEIQTIREYYKHLA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPIGAEIVAIINSLP TKK\SPGPDGFTAELYQRYKEG AVLEVLARAIRQEKEIKGIQLG KEEVKLSLFAAGDMIVYLENPIV SAQNLLKLISNFSKVSGYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKN PCSWVGRINIVKMAILPKVIYGF NAPIKLPMTFFTELEK\TT*KFI WNQKRARIK*ILSQKNKAGGI TLPDFKLYYKATVTKTAWYW YQNRDIDQWSRTEPSEIMPHIY NYLIFDKPDKNKKWGKDSL KWCRENWLAICRKLKLDPFLTP YTKINSRWIKDLNVRPKTITTE EKLSENTIQDIGMGKDSMSKTPK AMATNVKIQKWDLIKLSFCT AKETTIRVNRQPTTWEKIFATY SSDKGLISRIYNELKQIYKKKT NPIKKWVKDMNRHFSKEDIYA AKKHMKKCSPSLAIREMQIKTT MRYHLTPVRMAIIKSGNNRC |
| 14940 | 45308 | A | 15027 | 3 | 3229 | |
| 14941 | 45309 | A | 15028 | 1 | 3907 | MGDFNTPLSTLDRAIRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFFSAPHHTYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNTQNRSTWKL LLNDYWVHNEMKADIKMFFE TNENKDDTTYQNLWDTFKAVCR GKFLALNAHKKKQERSKIDTLT SQLKELEKQEQTHSKASRRQE TKIGAELKEIETQKTLQKINESR SWFFERINKIDKPLARLIKRE KNQIDAIAKNDK |
| 14942 | 45310 | A | 15029 | 1 | 4005 | |
| 14943 | 45311 | A | 15030 | 287 | 2708 | |
| 14944 | 45312 | A | 15031 | 1 | 4602 | |
| 14945 | 45313 | A | 15032 | 1 | 4806 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 14933 | 45301 | A | 15020 | 1 | 2229 | MGKKQNRKTGNSKTQSASPPP KERSSSPA TEQSWMENDFDEL R EEGFRRSNYSELREDIQT KGKE VQNF EKNLEECITRITNTEKCLK ELMELKTKARELREECRSLRSR CDQLEERV SAMEDEMNEMKRE GKFREKRIKRNEQSLQEIW DYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHII VR FTK VEMKEKMLRAAREKEIQT TIREYYKHL YANKLENLEEMD TFLD TYTL PRLNQEEVESLNRPI TGSEIVAIINSLPTKKSPGPDGFT AEFYQRYKEELVPFL LKLFQSIE KEGILPNSFYEASII LIPKGRDT TKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFI PG MQGWFNIRKSINVIQHINRAKD KNHMIISIDA EKA FDKIQQPFML KTLNKL GIDGTYFKIIRAIYDKP TANIILNGQKLEAFPLKTGTRQ GCPLSPLLFNIVLEV LARAIRQE KEIKGIQLGKEEVKLSLFADDM IVYLENPIVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMGELPFTIASKRIKYLGIQ LIRDVKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKIGKTTLKF IWNKKSRIAK SILSQKN/KAGGITLLTQLYYKA TVTKTAWYWYQNRDIDQWNR |
| 14934 | 45302 | A | 15021 | 1 | 960 | |
| 14935 | 45303 | A | 15022 | 1 | 2928 | MEDEM NEMKQEEKFREKRIKR NEQTLQEIW DYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRY S SRRATPRHII VRFTK VEMKEKM LRAAREKDRSMRQKVNKDTQE LNSALHQADLIDIYRTLHPKSTE YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIITNYLS D HSAIKLE LRIKNLTQNRSTTWKLNNLLN DYWVHNKMKAEIKMFFETNEN KDTTYQNLWDAF |
| 14936 | 45304 | A | 15023 | 1 | 1782 | |
| 14937 | 45305 | A | 15024 | 1 | 4881 | |
| 14938 | 45306 | B | 15025 | 1 | 5962 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14928 | 45296 | A | 15015 | 1 | 1853 | MGRNQRSRKAENSKNQSASSPP KDCSSSPAMEQSWTENDFDELT EVGFRRSVITNFSELKEHVETNL KEAKHLEKRLDKWLTRIKSVE KILNDLMELKTMAQELHDTCR SFNSQFNQVEERSVIEDQINE MNIDGTYLKIIRAIYDKIPRNII LNQQKLEAFPLKTGTRQGCP PLLFNIVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLEN PIVSAQNLLKLISNFSKVSGYKI NVQKSQAFLYTNNRQTESQIMS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLKEIKEDTNKW KNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTL KFIWNQKRARIKSIQSQKNKS GGITLPDFKLYYKATVTKTA/W L/YHTPLSCLPP*WNRTEPSEIIP HIMAVAQIQVKKLLLLQGQHA SSRLQPTSSTKCGGWTASSASP RSMGLSSWKGNLASAIHYFPCK PLTLPSRISTSSSSWGCRQAHAV LEVLRWPPGLGWPGWHHLTLL HVPPVRITKSNGPRACTRASAS HARHHQYNQEPSLSPLHSPLPP PEQVLVSTAERTEDRSYHRTL RHSPYFKNEAADLRGEGYSS |
| 14929 | 45297 | B | 15016 | 1 | 3276 | |
| 14930 | 45298 | A | 15017 | 1 | 2274 | |
| 14931 | 45299 | B | 15018 | 440 | 3383 | |
| 14932 | 45300 | A | 15019 | 1 | 2646 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14922 | 45290 | A | 15009 | 1 | 3253 | MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQGDLIDIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKWKRTEITNYLSDH SAIKLELRIKNLTQSRSTTWKLN NLLLNDYWVHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFIALNAHKRKQERSKIDTL TSQLELEKQEQTTHSKASRRQE ITKIRAELEKETQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK |
| 14923 | 45291 | A | 15010 | 1 | 2816 | MEDEMNMKREGKFREKRIKR NEQSLQEIWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRY SRRATPRHIIVRFTKVEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFTTCICDDAEDLQSPSTA GPWFGVLYTKGGPYPQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPNQCH IGEVLLDGFTAIFYRRYKEELV PFLKLFQSIEKEG |
| 14924 | 45292 | A | 15011 | 1 | 3347 | MGDFNIPLSTLDRSTRQKVNDK TQELNSALHQADLIDSYRTLHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEITNYLSDHSA IKLELRIKNLTQNCSTTWKLNN LLLNDYWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQE TKIRAELEKETQKTLQKINESR SWVFERINKIDRPLARLTKKKS EKNQIDAIKNDK |
| 14925 | 45293 | A | 15012 | 1 | 3855 | MGKKQNRKTGNSKTQSASPPP KERSSSPATEQSWMENDFDEL EEGFRRSNYSELWEDIQTKGKE VENFEKNLEECITRITNTEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSAEMEDEMNMKRE GKFREKRIKRNEQSLQEIWDYV KRPNLRLIGVPESDVENGTKLE NTLQDIIQENFPNLARQANVQI QEIQRMPQRYSSRRATPRHIIVR FTKVEMKEKMLRAARQKAPH HTYSKIDHIVGSKAL |
| 14926 | 45294 | A | 15013 | 1 | 2559 | |
| 14927 | 45295 | A | 15014 | 1 | 2956 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14919 | 45287 | A | 15006 | 1 | 3891 | MKPEIKMFFETNENKDDTTYQNL WDTFKA VCRGKFIALNAHKRK QERSKINTLTSQFKELEKQEQT NSKASRRQEITKIRAELEKETQ KPLQKINESRSWFFKINKIDRP LARLIKKKREKNQIDAIAKNDKG DITTDPTIEIQTITIREYYKHLN KLENLEEMDKFLDMYTLPRLN QEEVESLNRPIGTSEIEAIIINSLP TKKSPGPDGFTAIFYQRYKEEL VSFLLKLFQSIKKEGILLNLFYE DSIILKPKGRDITTKENFRPISL MNIDAKILIKILANRIQQHIKKLI HHQVGFIPGMQGWFNIRKSIN VIQHINRTKDKNHMIIISDAEKA FDKIQQPFMLKTLNKLGIHGTY LKIIRAIYDKPTANIILNGQKLL AFPLKTGTROGCPLSPLVFNIIVL EVLAWAIRQEKEIKGIQLGKEE VKLSLFADDMTVYLENPIISAQ NLLKLISNFSKVSQYKINVQKS QAFLYTNNGQTESLIMSELPFTI ASKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKED\TNKWKNIPCS WVGRINIVKMAILPKVIYRFNAI PIKLPMFTFDLEKTTLNFIWNQ KRARITKSILSQKNKAGGITLPD FKLYYTATVTKTAWYQNS MVLVPKQRYRSMEQNRALRN NAACLQLSDL |
| 14920 | 45288 | A | 15007 | 1 | 4215 | MHSLCPDATGEGELYNSLGSLT WSFLSMIGVLLWVDFSGDSIDL CSPLWNRTNLEALQKKLEEL DEQQRKRLEAFLTQKQKVGEL KDDDFEKISELGAGNGGVVFK VSHKPSGLVMARKLIHLEIKPAI RNQIIRELQVLHECNOPYIVGFY GAFYSDGEISICMEHMLVLLQER PCPGFLWMENSDYGLLLPLDLL LCLSFSFSKVLSDLVSDILIHGM KARNRSIHGDVVVVELLPKNE WKGRTVALCENDC |
| 14921 | 45289 | A | 15008 | 1 | 2823 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14916 | 45284 | A | 15003 | 1 | 2375 | MSGFLISPKHKHGTNSGIVSWA DVQSQLRHIEAAFDQEAAAVL MARLGVFRAESEEGPDVLRWL DRQLIRLHSLTTLDIVPAGKGE VVKGPMSISQQAQKGCQKFGQY NKEDPTSFRLSDSFSLYPQFMF HLRRSPFLQVFNNSPDESSYYR HHFARQDLTQSLIMIPILYSYS FHGPPEPVLLDSSSILADRILLM DTFFQIVIYLGETIAQWRKAGY QDMPEYENFKHLLQAPLDDAQ EILQARFPMTRYINTEHGGSQK KREKNQIDAIKNDKGDITTEPTE IQTIREYYKHLKYANKLESLEE MNKFLDTYTLPRLNQEEVESLN RQITGSEIEAIINSLPTKKSPGPD RFTAKFYQRTNDQKHMIISIDA EKAFDKIQPFMLKTLNKLKID GTYFKIIRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPPLSLLF NIMLEVLARAIQEKEIKGIQFG KEEVKLSLFADDMIVYLENPIV LAQNLLKLISNFSKVSQYKINV QKSQAFLYTSNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYRF NAIPIKLSMTFFTELEKTTLEFI WNQKRARITKSILSQKNKAEGI TLPDFKLQYKATVTKTAWYSY QNRDIDQWNRTEPSEIVPCIYN YLIFDKPDKNKKWGKDSL FNK |
| 14917 | 45285 | A | 15004 | 1 | 1428 | |
| 14918 | 45286 | A | 15005 | 2 | 1975 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14906 | 45274 | A | 14993 | 687 | 2274 | LRDCKRINQHPVKTDQSAFCK M/API/MQDVVLEVLARAIQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLISNFSKV SGYKINAQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEITEDT NKWKNIPCSWVGRINIVKMAIL PKVIYRFNAIPIKLPMTFFTELE KTTLKFIWNQKRARMAKSILSQ KNKAGGITLPDFKLYYKATVT KTAWYWYQNRDQVQWNRTEP SEITPHIYNLIFDKPDKNKQW GKDSL FNK WG WENWLAICRKL KLDPFLTPYTRINSRWIKDLNV RPKTIKTLEENLDITIQDIGMGK DFMSKTPKAMATKAKIDKWDL IKLKSFCIAKETTIRVNRQPTKW EKIFATYSPDKGLISRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAAKHKMKRCSSSLAIRE IQIKTTMRYHLTPVRMAIHKKSG NN/R/CF*WQKPGPSG*ALRSWK EDIAGTSYVGMNQCMRKNTK TLI |
| 14907 | 45275 | A | 14994 | 1 | 3189 | |
| 14908 | 45276 | A | 14995 | 1 | 3351 | MGKKQNRKTGNSKMQSASPPP KERSSSPATDQSWMENDFDEL REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRITNTEKCL KELMELKTKARELREECRSLRS RCDQLEERSAMEDENEMK QEGKIKRDKEGHYIMVKGSIQQ EELTILNIYAPNTGAPRFIKQVL SDLQRDLDSHTLIMGDFNTSLL TLDRSMRQKVNDQTQELNSSL HQADLIDIYRTLHPKSIEYTFSS APHHTYSKIDHIVGS |
| 14909 | 45277 | A | 14996 | 1 | 3192 | |
| 14910 | 45278 | A | 14997 | 1 | 2742 | |
| 14911 | 45279 | B | 14998 | 1 | 2313 | |
| 14912 | 45280 | A | 14999 | 1 | 1542 | |
| 14913 | 45281 | A | 15000 | 1 | 3300 | |
| 14914 | 45282 | A | 15001 | 1 | 1824 | |
| 14915 | 45283 | A | 15002 | 1 | 2982 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14905 | 45273 | A | 14992 | 473 | 2385 | HSFLSFIVLMYLTMDLTRSQKH GWASSPSHGTSPWPVRLRTSLA KPCKWQVSLCWLSASPGSSF SLVRSSLLIIVPHAESVSRRPSLL SRVGLFPARY*HRVWQRSPSPQ TRDHLIKRNPSQDV*RRQQPRG TRVSNKCSLHTSALGIGRQPSC DATL*GQQGLP/VK*KRQQPAP/ MSQQQTGAALEVLARAIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPTVSAQNLLKLISNFSK VSGYKINVQKSQAFLYTNNRQ TESQIMSELPFTIASKRITYLGIQ LTRDAKDLFKENYKPLLKEIKE DTNKWKNIPCSWVGRINIVKM AILPKEPGWARSLVFGARGLQG QGRCGQSRGGGGSCLGGGGST ENWQHREPSARKTGSTENRRH REPAAPRTGSTENQHREPAAPR TGTENRHREPSARKTGSTENRR HREPAAPRTGSTENQHREPAAP RTGTENRHHQEPAPRTGGTENR QHREPAAPRTGTENRQHREPAP RTGSTENRQHREPAPRTGSTEN RQHRESAAPRTGSTENRHHQEP APRTGTENRHREPSAPRTVGTE NRRHREL VAPRTGGTENRPREP PAGTRPRHTPMRGGSEGALFH QRRFLEPTPDREQLEGIRYPPVA |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14903 | 45271 | A | 14990 | 1 | 1716 | MKA EIKMFFETNENKDTTYQN LWDTFKA VCRGKFIALNAHNR KQERSKIDLTLSQLKELEKQEQ TYSKASRRQEITKIRAELEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKRQKNQMDTIKND KGDITTDPTIEIQTTVREYYKHL YTNKLENLEEMDKFLDTYTLPR LNQEEVESLNRPIITGAEIVAIINS LPTKKSPGPDGFTAIFYQRYKE ELPGRDTTKEENFRPISLMNIDA KILNKILANQIQQHIKKIIHHDQ VGFIPGMQGWFNIRKSINVIQHI NRAKDKNHMIMSIDA EKA FDKI QQPFMLKTLNKL VLEVLARAIR REKEIKGIQLGKEEVKLSLFAD HMIVYLENPIVSAQNLLKLISNF SKVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFRENYKPLLKEIK EDTNKWKNIPCSWVGRINIVKV AILPKVIYSFNAIPIKIPMPFFTEL EKTTLKFIWNQKRARIAKSILSQ KNKAGAITLPDFKLYYKPTVTK TAWYSYQNRDIDQWNRTEPSE ITPHIYNLIF |
| 14904 | 45272 | A | 14991 | 1 | 702 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14898 | 45266 | A | 14985 | 1 | 2067 | MELKTKARELREECRSLRSRCD QLEERVSA MEDEM NEMKREG KFREKRIKRNEQSLQEIWDYVK RPNLHLIGVPETDGENGTKLEN TLQDIIQENFPNLARQANVQIQE IQRTQPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREKEIQTTIR EYYKHLHANKLENLEEMDKFL DTYTLPRLNQEKVESLNR PITG AEIVAIIN/SLPTKKSPGPDGFTA EFYQRGILPNSFYEASIIIPKLG RDTAKKENFRPISLMNIDAKILN KILAKRIQQHIKKLIHHDQVGFI PGMQGWFNIRKSINVIQHVNR TKDKNHMIISIDEEKA FDKIQQPF MLKTLNKL GIDGMYFIIIRAIYD KPTAHILNGKKLEAFPLKTGM RQGCPLSPLLFNIVFKVLARAIR QEKEIKGIQLGKEEFKLSLFADD MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQTFLYTNNR QTESQIMSELPFTIASRKIKYLG QLTRDVKDLFKENYKPLLKEIK EDTNKWKNIPCSWVGRINIVK MAILPKVIYRFNAIPIKVPMTFF TELEKTTLKFIWNQKRACIAKSI LSQKNKAGGITLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRT EPSEITPHIYNYLIFDKPEKNKQ WGKDSL FNKWCWENWLAICR KLKLDPFLTPYTKINSRWIKD |
| 14899 | 45267 | A | 14986 | 1 | 1293 | |
| 14900 | 45268 | A | 14987 | 1 | 3229 | |
| 14901 | 45269 | A | 14988 | 1 | 3352 | |
| 14902 | 45270 | A | 14989 | 1 | 1419 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|--|
| 14887 | 45255 | A | 14974 | 1 | 1240 | MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGWFNICKSI NVIQHINRAKDKNHMIIISDAEK AFDKIQQPFMLKTLNKLIGDGM YFKIIRAIYDKPTANIILNGQKLE AFPLKTGTRQGCPLSPLLFSIVL EVLARAIRQEKEIKGIQLGKKE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRLKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNIPCS WVGRJNIMKMAILPKVIYRFNA IPIKLPMPPFFTELEKTTLKFIWNE KRARIAKSIPSQKNKAGGITLPD FKLYYKATVTKTAWYWYQNR DIDQWNRTEPSEITPHIYNLIF DKPEKNKQIQKAFILHKEPWV MWNMGNTNR |
| 14888 | 45256 | A | 14975 | 1 | 2241 | |
| 14889 | 45257 | A | 14976 | 1 | 2802 | MYGTGYRDVAGKWAIDPDSK REFLDVTQEGIQGCDFSGTCRQ TLSILTQPLRQWGLEGIKKPNS WIIEESVSNGGPPLLIPQTAS GVDLQQTPDQLRLVLTVRRK TNKQKGIASSTKRTSTPKPHL YVTIHKDQSYIKPQRWGKNIAE KLKILKIRVALSLQRNAAPHQQ WNKAGRRMSLMSSQKKASEVI ESQMNEIKGEEKFREKRVKRNE QSLQEIWDYVKRPDLRLIGVPD SDGENGTRLENTLQDI |
| 14890 | 45258 | A | 14977 | 1 | 2739 | |
| 14891 | 45259 | A | 14978 | 1 | 2478 | |
| 14892 | 45260 | A | 14979 | 590 | 727 | |
| 14893 | 45261 | A | 14980 | 1 | 3255 | |
| 14894 | 45262 | A | 14981 | 1 | 3810 | |
| 14895 | 45263 | B | 14982 | 1 | 3127 | |
| 14896 | 45264 | A | 14983 | 1 | 3325 | |
| 14897 | 45265 | B | 14984 | 1 | 1734 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14877 | 45245 | A | 14964 | 1 | 832 | MPHVCAQRRLPVA AVLPPDGA QNCILLAGLSAGTFCHHGGVHI LLSNPVA T SLLVAIDRVGQIPPIPP PPPPALPYDCCCPPPSRHTEDRE HVPIPLHWKLMVNRWFLPVPT EWIATLSNSSRSSRTCSMQGLSF LDSQVHLKAMIEDLRGNVSKES SPCLADNADVGQFPMEGGQKD PKQRIIPFCQGVTNLSGPHGPGA VCGGSHYQKQESSEISLSVGQV WTSSRRMSQVGGSSHCRGARL GPCNVPRRPDGVQDEFSLQPEE DAG*QTSVDPMVLEQYVVVA/ NYQKQESSEISLSVGQ/VVDIIE KNESGWVFW/STAEQGWVPA TCLEGQMGC RMSFLCSLKKML DWIQR RVSL |
| 14878 | 45246 | A | 14965 | 1 | 346 | |
| 14879 | 45247 | A | 14966 | 157 | 413 | ALVCS/SSLAI REMQIKTTMRYH LTPVRMAIIKKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELEIPFDPAIPLL |
| 14880 | 45248 | A | 14967 | 1930 | 5781 | RAKSPANIIMTGSNSHITLTLN VNGLSNPIKRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLIMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSDHSAIKL ELRIKNLTQSR |
| 14881 | 45249 | A | 14968 | 1 | 2235 | |
| 14882 | 45250 | A | 14969 | 1 | 2148 | |
| 14883 | 45251 | A | 14970 | 1 | 1821 | |
| 14884 | 45252 | A | 14971 | 1 | 1248 | |
| 14885 | 45253 | B | 14972 | 4 | 2121 | |
| 14886 | 45254 | A | 14973 | 1 | 1137 | |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14870 | 45238 | A | 14957 | 434 | 1790 | GNFFRKTISACIISVLSYLVSCLR GASPTEASMDFCLKTSKREAAR ASRKICFVCKKKGAAINCQKDQ CLRNHFLPCGQERGLPFTIFWR VQIIL*QTSP/EHRTSNMGHVGE ESCILCCEDLSPTECLRTFQSPC CSQAIYHRKCIQ/TNMPHQSK HFFKCPQCNNRKEFPQEM/REN GNSYSRQRCCLGTRARGFLRLI SALSAL*CPHLVCMNKAETALR MKGGGASFCVLHADPTEPTGT APLLDLTVRNGSVRSVHL/PAA TDYIPENSGDIPCCSSTFHPEEHF CRDNTLEENPGLSWTDWPEPSL LEKPESRRGRS/VLLEVQGCQ NH*QLQKIQVTPSE*LLVPHNR V*TCAPPSGLGREHSGTVRQGS RASSETMS/LSKEKSQWSMRRE QSRCQQGNAFMATRVPLLSPL LPPRILPP*SCFHMPLLTSPMFV VMQIKVFSPKKKKK |
| 14871 | 45239 | A | 14958 | 146 | 484 | |
| 14872 | 45240 | A | 14959 | 228 | 353 | |
| 14873 | 45241 | A | 14960 | 214 | 722 | TARELPGRVLKEMYIQK*EGA ALGRPTRPGRQGQVRRAECR RLFRGVLRPCNRC |
| 14874 | 45242 | B | 14961 | 1 | 951 | |
| 14875 | 45243 | A | 14962 | 241 | 517 | QSCGQRLPTVLR/PLRTPWILPM YPQPLPAGGPTPCLRSRPYINITI LKGDKGDPGPMGLPGYMGRE GPQGEPPG*GSKGDKGEMGRP RRPVP |
| 14876 | 45244 | A | 14963 | 748 | 1055 | DRKQTS PGDAYHTIPGSLSSSSD HVLSEPD*GEGSHL**SVQHDD VPPTA**RLQY\RAVVLFPTATL PAILIM*GMRCPVPRNCSTW TAQIRAYIEVQQT |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Met hod | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|---------|-------------------------------|---|---|---|
| 14865 | 45233 | A | 14952 | 1 | 1513 | MIIALQKESLMSLQAQLDKALQ KEKHYLQTTITKEAYDALSRKS AACQDDLTALEKRTGRDWNP PPFRTQQRGSKSLTAIRPLCLFR KLNHVTSETKSLQQSLTQTQEK KAQLEEEIIAYEERMKKLNTL RKLRGFHQESELEVILYEEEMG NHNENTGEKLHLAQEQLALAG DKITSLERSLNLYRDKYQSSLS NIELLECQVKMLQGELGGIMG QLSKTSSDLSKM/RCY/TTW*M WTKLQFIHSILTSVIFHLLSFSSM GSI*KWIMALSGSSFLDDAHYIS QFGPRQLPSVCAEPEKEKATDG VVRNGKSTAGHQRYLCSHCRK TWQLQFTYTASQPAGQ*RHRL RG\MDEQWGYVGAKSRQRWLF YAYDSLRLKTVVAHHREQSGIK CKLEEDLQEATKLLDKREQLK KSKEHEKLMEGELEALRQEFK KKDKTLKENSRLKEENENLR AELQCCSTQLESSLNKYNTSQQ VIQDLNKSPMEIRFQLYIFTPDQ |
| 14866 | 45234 | A | 14953 | 125 | 363 | INVSVWSQPFPGG*QPEKGLKE HPADARPGSC\PPAGRVPQGRA EVASAAPPRGSSPAAAPGQSH PSCLRAPLYWSFSR |
| 14867 | 45235 | A | 14954 | 306 | 583 | TCSTRRRKNDLSVKYVSVWSQ PFPGG*QPEKGLKEHPADARPG SC\PPAGRVPQGRAEVASAAPP RGSSPAAAPGQSHPPSCLRAPL YWSFSS |
| 14868 | 45236 | A | 14955 | 225 | 407 | LRGMVTFSPFSSILNGQFEPNSG CPL/CPVCWVCLREPGDPEKLG EFLQKDNISVHYFCLVS |
| 14869 | 45237 | A | 14956 | 484 | 722 | NTCRCGHNRSPEVNSRRGGLRS IPRMPDAGSCS/PPAGRPSAGPG RRSPPLLPRGSSPAAAPGQSH PSSSQGAHVLEL |

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|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14857 | 45225 | A | 14944 | 1 | 333 | LNLVLFQQRAELMIS*PQ*FSRA LLVIFPLLQTELQQLFLLHVNP AAVEAPPSVPIGLYSENVNRNR LPETVIRVKQPALARFSPDIAPL FVHFRADDDVTARRVEKRCK |
| 14858 | 45226 | B | 14945 | 1 | 1794 | |
| 14859 | 45227 | A | 14946 | 1183 | 1899 | LNRRDSYVEYLADKVADREED AEEYLEAIMEARVTVAGMGLV MEVQDYFDGEADRLAKAWLA EYTPQIKSLKDERKEAYRQIVE MSTEPQDVDLVRPANKFEMTR VREGEKEADLPVWKHHL/SV*R KRELSGSVEPLGNQVFEIETKRE NS*EL**KSLKDERKEAYRQIVE MSTEPQDVDLVRPANKFEMTR VREGEKEADLPVWKHLLCDE SGNYPALLNHWETRFLRSKPN VKIHRSSDKSPTYFVFFISQYDL PAFYPINGHFLVERVVKVRIVFI EEFADHHHLAIFQFNNRLQRHA FVVTLANVTNQPFSSVVVVVNL |
| 14860 | 45228 | B | 14947 | 1 | 3099 | |
| 14861 | 45229 | A | 14948 | 1174 | 1545 | |
| 14862 | 45230 | A | 14949 | 1 | 945 | |
| 14863 | 45231 | A | 14950 | 62 | 576 | |
| 14864 | 45232 | A | 14951 | 1 | 1642 | MLANIGFYNSNVIHRSKGAIGE GPPDPRGIVEQNLGGDISIPCYN GPRPRRSAQKTTLGPLNQPRIPS AQCAGAFPRVAAAGAGGGGG GGSGGSGFCLGWRLRRRRQRR RRWRRGEGEGDGDAGHMRPR PAGRAEARRRRRLRGNPPPGAR LPNREGNGSGVSWAAEVSGDG RGARTEAARTRRRPGGADNYP GAVPPVQLLTGWCVTAKAPPDI SAISALTAVKHGNCSSLTPLLNP PGSDVIVCAEMDEQWGYVGAK SRQRWLFYAYDSLRTVVAHV FGERTMATLGRLMSLLSPFDVV IWMTDGWPLYESRLKGKLHVI SKRYTQRIERHNLNRQHLARL GRKSLSFSKSVELHDKEELAAL FSELKQEKKVDELIAKLVKNR TRIVNESDVFSWVIRREFQELR HPVDEEKARCLEGIGGHTRGLV ASLDMQLEQAQGTRELAQAE\ LCWNSSEMRTTMSSSGSSTPWP PVSRRRPWTERRLGSVRGDRLR ERSRPAVNRTPRMSRVPAGAPR GTPSRRWMMKCWDHQMGRG LVEEEVG |

| SEQ ID NO: | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/540,217 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion) |
|------------|--------------------------------|--------|-------------------------------|---|---|---|
| 14846 | 45214 | A | 14933 | 1 | 1429 | MVLAAGDPVEKGITWARENAG IYISCTMMKLSMIPGDQSYRNL IPLKFVACILIEGNAKCWPLPEF DPSQIRLIVYQDCERRGRNVLF DSSVKRRNEDISVSRIKYLGIQL TRDVKDLFKENYKPLLNEIKED TNKWKNIPCSWIERINIVKIAILP KKLGSDAQVKVFGKCCQLKPG GDSSSSLDSSVTSSSDIKDQCLK YQRTVDLSAQLSSSGKGQTTSS SGSLTPMTPHWEIPPSGGQQTSS HTGELRLASGRGSSGMKLPEEG TDRNLCCSAASSGDTQANRDW SGPPANTSRPAAEGPDCDRENG TKLENTLKDIHENFPNIARQAN IKIQEIQRTQQRYSRRATPRHII VRFTKVEMKEKMLRAAGEKH WVIHKGKSIRLTVDLAETLQA RREWG\PIFNVLKEKNFQLRISY PAKLSFISEGEMKSFPEKQMLR DFVTIRLALQELLKEALNMARE /NR*QPLQKHM |
| 14847 | 45215 | A | 14934 | 2320 | 2811 | ESKLTRGVKDLFRENYKPLLNE IKRGHKQMEEHSMLMGRKNQ YREKWPYLPKVN*IQCHPHQA TNDCFHRIGKLL*SSYGTKKE PALPSQS*DKRTKLEASHYLTSS NYTTRLQ*PKQHRYWYQNRDI DQWNRTEASEIMPHIYTILILWT NLRKTSMERHP |
| 14848 | 45216 | A | 14935 | 2 | 872 | |
| 14849 | 45217 | A | 14936 | 769 | 828 | |
| 14850 | 45218 | B | 14937 | 1 | 669 | |
| 14851 | 45219 | A | 14938 | 1 | 807 | |
| 14852 | 45220 | B | 14939 | 35 | 212 | |
| 14853 | 45221 | A | 14940 | 235 | 837 | QQAHKTPQRRHSAFTEYVRNN RLPETVIRVKQPALAIFSPDIAPL FVHFRADDDVTARVIHAIIMIF WCDRVEKRVSDAVACFTLESEI AEVGVLCRTHIRQ*RQVTPARM *ALSRILHACRSEDVRHNRPPYP VIRVKQPA\RRDLAPT*PHCSSIS AQTITSLPGCMREVT/ELRPEFF K*RKTVLRPTPIMRARAERRCK |
| 14854 | 45222 | C | 14941 | 1 | 1755 | |
| 14855 | 45223 | A | 14942 | 1 | 747 | |
| 14856 | 45224 | B | 14943 | 1 | 2466 | |